Run on:

```
April 18, 2003, 04:46:26; Search time 278.727 Seconds (without alignments) 2192.677 Million cell updates/sec
                                                                                                                                                                                                                                                                                         4109280
GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                                       2054640 segs, 14551402878 residues
                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                     OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                             1 gaaagtatcttcaaggacgcc 21
                                                                                                                                                                                                          IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    em_htgo_mus:*
em_htgo_other:*
                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                 US-09-270-437D-9
21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 em_htg_hum:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mue:
                                                                                                                                                                                                                                                                                                                                                                                                                                       9b htg: *
9b htg: *
9b om: *
9b om: *
9b pat: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
                                                                                                                                                                                                                                                                                                                                                                                                                        GenEmb1:*
                                                                                                                                                                 Perfect acore:
                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                       Searched:
```

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		•				
Result No.	Score	Query	Query Match Length	80	ID	escription
н	. 21		174	y	. 65	AX365954 Sequence
7	21	100.0	1743		AX366054	56054
η•	21	100.0	1743		AX366057	56057
<b>7</b> L	7 7	100.0	1764	φ (	AX366035	5603
n	7 7	100.0	4155		HSU76705	U76705 Human puta
0 1	7.5	0.00	4154		ARI71863	AR171863 Sequence
٠ ۵	7 .	90	41/1		AF11/108	
0 0	7 7	700	4181		AX333233	AX333233 Sequence
7	7 .	100.0	4181		AX365782	Seguenc
7 :	77	100.0	4181		HSU97188	
1 .	77	100.0	4602		AX397963	
	21	100.0	51119		AC090865	Homo
בו ט	21	100.0	54379		AC079780	_
	21	100.0			AC090245	Homo
	21	100.0	176547		AC092447	Ношо
c 16	21	100.0			AC087709	
	21	100.0	188389		AC024199	
18	8	87.6	1740		AB046173	) E
19	18.4	9	192406		AC115321	_
c 50	r	œ	96009		AC114540	AC114540 Mile mile
21		8	109198		AC078891	CO TEST OF COURT
22	r	0	129432		HS497,T21	ALOUSON OLYZO BOL
c 23	_	σ	104983		110101104 00101104	Action October
24	_	. 0	167274		AC112310	2 t
25		٥	20000		2000011	מבנ
26		٠.	143498		יסניסניטל	ACUSSII Kattus no
	17		159768		2010101	
	11		176348		AC1101.0	מננ יננ
	17		177435		ACTOR 30	ACIOSSO MUS MUSCU
0			104775		ACIOSES	ACIZB3ZI KATTUB NO
	11				AC102586	AC102586 Mus muscu
	٦,				AC12/286	AC127286 Mus muscu
י ני	ċ	90.0	2/59		TGSUCSANI	X96938 T.gesnerian
	ė,	80.0	7661		AF012923	AF012923 Mus muscu
# I	٠,	80.0	31170		CEF35E12	Z81527 Caenorhabdi
	٠,	80.0	35016		AL603838	æ
36	<u>.</u>	80.0	w		AC015133	2
	Ġ.	80.0	102477		AC110687	58
G 38	ú	0	~		AC103498	æ
39	'n	0	128750		AC007307	200
c 40	'n	0	2875		AC007307	307 Mus
41	٠,	0	3217		AC008370	370 Drogonhi
42	'n	0	3327		AC068586	THE CHOICE SEE
c 43		_	3327		PODERSE	
	16.8		140186		ACOSTRODA	0 0
	٠,,		775		200000	Social Homo Bap

DNA 1740 bp 1 Sequence 347 from Patent W00200174. AX365954 AX365954.1 GI:18697455

RESULT 1
AX365954
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCES
ORGANISM

ALIGNMENTS

PAT 16-FEB-2002

linear

Homo Bapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. human.

Wang,T., Wang,A., Skeiky,Y.A., Li,S.X., Kalos,M.D., Henderson,R.A., Moneill,P.D., Fanger,N., Retter,M.W., Marnerakis,M., Fanger,G.R., Vedvick,T.S., Carter,D., Watanabe,Y. and Peckham,D.W.

REFERENCE AUTHORS

```
CORIXA CORPORATION (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                   Query Match
Best Local Similarity
                                                                        527 a
                                                                                                                                                                                                                                                                                                                                                     human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
TITLE
                               source
                                                                                                                                                                                                                                                                                           DEFINITION
                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
HSU76705
                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                 RESULT 4
AX366035
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              — wang,T., Wang,A., Skeiky,Y.A., Li,S.X., Kalos,M.D., Henderson,R.A., Mcneill,P.D., Fanger,N., Retter,M.W., Marnerakis,M., Fanger,G.R., Vedvick,T.S., Carter,D., Watanabe,Y. and Peckham,D.W.
Compositions and methods for the therapy and diagnosis of lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAT 15-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang,T., Wang,A., Skeiky,Y.A., Li,S.X., Kalos,M.D., Henderson,R.A., Mcneill,P.D., Fanger,N., Retter,M.W., Marnerakis,M., Fanger,G.R., Vedvick,T.S., Carter,D., Watanabe,Y. and Peckham,D.W. Compositions and methods for the therapy and diagnosis of lung
                                                                                                                                                                                                                                                                                                                           PAT 15-FEB-2002
                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
      Compositions and methods for the therapy and diagnosis of lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 21; DB 6; Length 1743; ilarity 100.0%; Pred. No. 3.3; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1743 bp DNA Sequence 450 from Patent W00200174. AX366057.1 GI:18697500
                                                                                                                                                                                                                                                                                                                                DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent: WO 0200174-A 450 03-JAN-2002;
                                    Parent: WO 0200174-A 347 03-JAN-2002;
CORIXA CORPORATION (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent: WO 0200174-A 447 03-JAN-2002;
CORIXA CORPORATION (US)
                                                                                                                          391 t
                                                                                                                                                                                                                                                                                                                              AX366054 1743 bp 1 Sequence 447 from Patent WO0200174. AX366054.1 GI:18697498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
418 g 392
                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
| 417 g 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .1743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         527 a
                                                                                                                               526 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     uman.
                               cancer
                                                                                                                                                                                                                                                                                                                                                                                                          human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                      RESULT 2
AX366054
LOCUS
DEFINITION
                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
AX366057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                       FEATURES
               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                            ద
                                                                                                                                                                                                                                   8
```

```
4155 bp mRNA linear PRI 26-JAN-1999
Human putative RNA binding protein Kocl mRNA, complete cds.
U76705.1 GI:4098296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang,T., Wang,A., Skeiky,Y.A., Li,S.X., Kalos,M.D., Henderson,R.A., Mcneill,P.D., Fanger,N., Retter,M.W., Marnerakis,M., Fanger,G.R., Vedvick,T.S., Carter,D., Watanabe,Y. and Peckham,D.W. Compositions and methods for the therapy and diagnosis of lung
                                                                                                                                                                                                                                                                                                                                                                                                     linear PAT 15-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota in Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Mtheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 4155)

1 (bases 1 to 4155)

Mucller-Pillasch, F., Lacher, U. and Wallrapp, C.

Direct Submission
Submitted (30-0CT-1996) Innere Medizin I, University of Ulm, Robert-Roch-Str.8, Ulm 89081, Germany

1. 4155

/ Organism="Homo sapiens"
/ db xref=""Homo sapiens"
/ craniata; Homo sapiens"
/ craniata; Homo sapiens"
/ craniata; Homo sapiens"
                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 21; DB 6; Length 1764;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 21; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                      6; Length 1743;
                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            DNA
                                                                                                                                                    100.0%; Score 21; DB 6
100.0%; Pred. No. 3.3;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent: WO 0200174-A 428 03-JAN-2002;
CORIXA CORPORATION (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           394 t
                                                                                        ų
                                                                                                                                                                                                                                                                                                                                                                                                          AX366035 1764 bp D Sequence 428 from Patent WO0200174. AX366035
                                                                                        392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. 1743
/organism="Homo sapiens"
/db_xref="taxon:9606"
106 c 418 g 39
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AX366035.1 GI:18697484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 GAAAGTATCTTCAAGGACGCC 96
                                                                                                                                                                                                                                                                                         daaagrarcricaaggacgcc 75
                                                                                                                                                                                                                                                   1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .1764
                                                                                                                                                                                                        21; Conservative
```

University

Sas

```
/note="binds multiple sites in IGF-II mRNA 5'UTR; identical to KH-domain containing protein overexpressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / translation="MONGLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDC
PDESWALKAF BELGGKTELHGKPIEVBHSVPKRGYRIRKLGIPRIPPHLGWEVLDSLLV
QYGGVVESCEGONYDESTAVNKYYSSKOGARQALDKLNGFQLENFTLKVAY
QYGVVESCEGONYDESTAVNKYYSSKOGSPGSVSKQKPCDLPLRLLVPTGFVGAIIGKEGATI
RUTKQTQSKTUVHRKRANAEKSITILSFPEGTSAACKSILBIMHRARQDIKFTEE
IPLKILAHNNFVGRLIGKEGRHKKIEQDTDTKITISPPEGTSAACKSILBIMHRARQDIKFTEE
TCAKAEEEIMKKIRESYENDIASMNLQAHLIPGLNLNALGLFPPFTSGMPPPTSGPPSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeutic screening using signature sets Patent: WO 0194629-A 3742 13-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MTPPY PQFEQSETETVHLF1 PALSVGAI IGKQGQH1KQLSRFAGASIKI APAEAPDAK
VRMVI ITGPPEAQFKAQGR1YGKI KEENFVSPKEEVKLEAHIRVPSFAAGRVIGKGGK
TVNELQNLSSAEVVVPRDQTPDENDQVVVKI TGHFYACQVAQRKI QEILTQVKQHQQQ
                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. [1 (bases I to 4171)]
Nieleen, J., Christiansen, J., Lykke-Andersen, J., Johnsen, A.H., Wewer, U.M. and Nielsen, F.C.
A family of insulin-like growth factor II mRNA-binding proteins represses translation in late development
Mol. Cell. Biol. 19 (2), 1262-1270 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                             2 (bases 1 to 4171)
Nielben, J., Christiansen, J., Lykke-Andersen, J., Johnsen, A.H.,
Wewer, U.M. and Nielsen, F.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                        Submitted (30-DEC-1998) Institute of Molecular Biology, Ur of Copenhagen, Soelvgade 83H, Copenhagen DK-1307, Denmark Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 4171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product="IGF-II mRNA-binding protein 3"
protein id="AAD09828.1"
db_xref="GI:4191612"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 21; DB 9; 100.0%; Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3742 from Patent W00194629.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  853 g 1199 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
1. .4171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAAGTATCTTCAAGGACGCC 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AX333233.1 GI:18123867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KALQSGPPQSRRK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      267. .2006
/gene="IMP-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="IMP-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer (koc)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  822 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 21, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .. .4171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1292 a
  SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                             MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    321
                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                         AUTHORS
                                                                                                  REFERENCE
                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
AX333233
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOS
                                                                                                                                                                                                                                                                                                                                                                                                                                           PEATURES
                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                             /translation="MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDC
PDESWALKAIEALSGKIELHGKPIEVEHSVPKRQRIRKLQIRNIPPHLQWEVLDSLLV
YGVUSEGOVNTDSETAVVNVTYSSKOQARQALDKLAGFOLENFTLKVAYIPDEWAA
QONPLQQPRGRAGGGSSRQGSPSOVSKQKPCDLPIRLLVPTQFVGAIIGKEGATI
RNITKOTQSKIDVHRENAGAAEKSITILSTPEGTSAACKSILEIMHKEAQDIKFTEE
IPLKILAHNNFVGRLIGKEGRNLKKIEQDTDTKITISPLQELTLYNPERTITYKGNVE
TCAKKAEEEIMKKIRESYSNDIASMNLQAHLIPGLNLNALGLFPPTSGMPPTSGPPSA
                                                                                                                                                                                                                                                                                                                                                                                                                                    MTPPYPQFEQSETETVHQFIPALSVGAIIGKQGQHIKQLSRFAGASIKTAPAEAPDAK
VRWVIITGPPEAQFKAQGRIYGKIKEENFVSPKEEVKLEAHIRVPSFAAGRVIGKGGK
TWIELQNLSSAEVVVPRDQTPDENDQVVVKITGHFYACQVAQRKIQEILTQVKQHQQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAT 17-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF117108 4171 bp mRNA linear PRI 26-JAN-1999
Homo sapiens IGF-II mRNA-binding protein 3 (IMP-3) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen, Y.-T., Gure, A., Tsang, S., Stockert, E., Jager, E., Alexander, K. and Old, L.J.

and Old, L.J.

the antigen ucleic acid molecule encoding cancer associated antigen, the antigen itself, and uses thereof

Patent: US 6297364-A 402-CCT-2001;

Location/Qualifiers
                                                                                           /function="putative RNA binding protein"
/note="Kh-domain containing protein; overexpressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

100.0%; Score 21; DB 9; Length 4155;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 21; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 21; DB 6; Length 4159; 100.0%; Pred. No. 3.3; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      851 g 1181 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1181 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AR171863 4159 bp
Sequence 4 from patent US 6297364.
AR171863
                                                                                                                                                                                                                  /protein_id="AAD09223.1"
/db_xref="G1:4098297"
                                                type="pancreag"
                         cell line="Patu89889"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="unknown"
830 c 851 g
                                                                                                                                                                    codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305 GAAAGTATCTTCAAGGACGCC 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AR171863.1 GI:17910813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            305 GAAAGTATCTTCAAGGACGCC 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KALQSGPPQSRRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAAAGTATCTTCAAGGACGCC 21
/map="7p11.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:4191611
                                             /tissue_typ
251. .1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      830 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .4159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF117108
AF117108.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
```

RESULT 6
AR171863
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

g ð

BASE COUNT ORIGIN

Bource

JOURNAL

TITLE

FEATURES

REFERENCE AUTHORS BASE COUNT ORIGIN

LOCUS

RESULT 7 AF117108

ઠે 유 ACCESSION VERSION KEYWORDS

ö

Gape

ö

PAT 09-JAN-2002

Query Match

Matches

ઠે

BASE COUNT ORIGIN

FEATURES

DEFINITION ACCESSION VERSION

RESULT 9 AX365782

LOCUS

SOURCE ORGANISM

KEYWORDS

REFERENCE AUTHORS

```
OYGVVESCEQNNTDSETAVNNVTYSKDQARQALDKINGFQLENFTLKVAYIPDEMAA
QONPLQQPRGRRGLGQRGSSRQGSPGSVSKQKPCDLPLRLLVPTQFVGAIIGKEGATI
RNITKQTQSKLDVHRKENAAARKSITILSFPEGTSAACKSILEIMHKRAQDIKFTEE
IPLKILAHNNFVGRLIGKEGRNLKKIEQDTDTKITISPLQELTLXNPERTITVKGNVE
TCAKAEDEIMKKIESSYENDIASMNLQAHLIPGLNLNALGLFPPTSGMPPFTSGPPSA
MTPPYPQFEQSETETVHQFIPALSVGAIIGKQGQHIKQLSRFAGASIKIAPAEAPDAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVNELQNLSSAEVVVPRDQTPDENDQVVVKITGHPYACQVAQRKIQEILTQVKQHQQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VRMVI ITGPPEAQFKAQGRI YGKIKEENFVSPKEEVKLEAHIRVPSFAAGRVIGKGGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MNKLYIGNLSENAAPSDLESIPKDAKIPVSGPFLVKTGYAFVDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
              Mueller-Pillasch, F., Lacher, U., Wallrapp, C., Micha, A.,
Zimmerhackl, F., Hameister, H., Varga, G., Friess, H., Buchler, M.,
Beger, H.G., Vila, M.R., Adler, G. and Gress, T.M.
Direct Submission
Submitted (11-ARR-1997) Medizinische Klinik, Internal Medicine I,
Robert-Koch-Str. B, Ulm 89081, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDESWALKAIEALSGKIELHGKPIEVEHSVPKRQRIRKLQIRNIPPHLQWEVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                     Function="possible proliferation of cancer tissues" note="KH-domain containing protein overexpressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mueller, F., Gress, T. and Adler, G.
Medicament comprising a dna sequence, which codes for the
rna-binding koc protein, and comprising a koc protein or e
sequence of the koc promoter
Patent: WO 0220036-A 114-MAR-2002;
Mueller, Friederike (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 4181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product="putative RNA binding protein KOC"
protein id="AAC35208.1"
db_xref="GI:2105469"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
100.0%; Score 21; DB 9;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 21; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="unnamed protein product"
                                                                                                                                                                                                                                                                /map="7p11.5"
/cell line="PaTu8988t"
/cell_type="pancreatic cancer"
|...181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1181 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4602 bp
Sequence 1 from Patent WO0220036.
AX397963.
AX397963.1 GI:21260818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .4602
/organism="Homo sapiens"
/db_xref="taxon:9606"
672. .2411
                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  מ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 GAAAGTATCTTCAAGGACGCC 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KALQSGPPQSRRK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                         gene="koc"
                                                                                                                                                                                                                                                                                                                                                                                                                  gene="koc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  830 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
AX397963
LOCUS
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEATURES
                                                                                                                                                                FEATURES
                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.

Homo sapiens.

Homo sapiens

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Bukaryota, Metazoa, Chordata, Catarrhini, Hominidae, Homo.

Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

Muellor-Pillasch, P., Lacher, U., Wallrapp, C., Micha, A.,

Zimmerhacki, F., Hameister, H., Varga, G., Friess, H., Buchler, M.,

Beger, H.G., Vila, M.R., Adler, G. and Gress, T.M.

Cloning of a gene highly overexpressed in cancer coding for a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSU97188 4181 bp mRNA linear PRI 11-SEP-1998
Homo sapiens putative RNA binding protein KOC (koc) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang,T., Wang,A., Skeiky,Y.A., Li,S.X., Kalos,M.D., Henderson,R.A., Mcneill,P.D., Fanger,N., Retter,M.W., Marnerakis,M., Fanger,G.R., Vedvick,T.S., Carter,D., Watanabe,Y. and Peckham,D.W. Compositions and methods for the therapy and diagnosis of lung
                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                               PAT 15-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 100.0%; Score 21; DB 6; Length 4181; Il Similarity 100.0%; Pred. No. 3.3; 21; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                          6; Length 4181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 others
                                                                                                                           16 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA
                                                                                                                                                                                          ch 100.0%; Score 21; DB 6
1 Similarity 100.0%; Pred. No. 3.3;
21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent: WO 0200174-A 175 03-JAN-2002;
CORIXA CORPORATION (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1181 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AX365782 4181 bp C
Sequence 175 from Patent WO0200174.
AX365782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oncogene 14 (22), 2729-2733 (1997) 97322117 917871
                                                                                                                           1181
                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
_830 c 851 g 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
830 c 851 g 1181
         Avalon Pharmaceuticals (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 GAAAGTATCTTCAAGGACGCC 325
                                                                                                                                                                                                                                                                                                                   305 GAAAGTATCTTCAAGGACGCC 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AX365782.1 GI:18697320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                    1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U97188.1 GI:2105468
                                                     1. .4181
                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ಹ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human.
```

source

FEATURES

JOURNAL

TITLE

BASE COUNT ORIGIN

PAT 27-MAY-2002

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

JOURNAL MEDLINE PUBMED

TITLE

DEFINITION

ACCESSION

RESULT 10 HSU97188

ઠે 셤

Gaps

; 0

1463

BASE COUNT ORIGIN

```
sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence ampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                          Contact: sequence submissions@genome.wi.mit.edu Project Information Center project name: L13138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 768: contig of 768 bp in length 769 868: gap of 100 bp 869 1597: contig of 729 bp in length 1598 1697: gap of 100 bp 2453 2552: gap of 100 bp 2553 3294: contig of 755 bp in length 2553 3294: contig of 742 bp in length 3295 3394: contig of 742 bp in length 3295 3394: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9203 9302: gap of 100 bp 10050: contig of 748 bp in length 10051 10150: gap of 100 bp 10151 10869: contig of 718 bp in length 10869 10968: gap of 100 bp 101719 11718: contig of 750 bp in length 11719: last of 750 bp in length 11719: contig of 723 bp in length 12542 12641: gap of 100 bp 12642 13641: gap of 100 bp 12642 1349: contig of 708 bp in length 12642 1349: contig of 708 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150 13459; gap of 100 bp in length 151 13499; gap of 100 bp 175 14996; contig of 725 bp in length 175 14996; contig of 725 bp in length 175 13996; contig of 731 bp in length 18677; contig of 731 bp in length 18677; contig of 730 bp in length 178 16777; contig of 750 bp in length 179 17596; gap of 100 bp 17496; contig of 750 bp in length 17496; contig of 746 bp in length 17596; gap of 100 bp 1842; gap of 100 bp 19842; gap of 100 bp 1993; contig of 751 bp in length 19193; contig of 751 bp in length 19193; contig of 751 bp in length 154 20144; gap of 100 bp 100 bp 155 20144; gap of 100 bp 100 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 bp
of 755 bp in length
of 742 bp in length
100 bp
of 757 bp in length
100 bp
of 744 bp in length
100 bp
of 753 bp in length
100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 bp
of 742 bp in length
100 bp
of 730 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 bp .
of 741 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         p of 100 bp contig of 743 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15: gap of 100 bp 22547: contig of 732 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47: gap of 100 bp 23401: contig of 754 bp in length
                                                                                                                                                                                                                                              NOTE: This record contains 61 individual
                           Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 7631: gap of 100
8361: contig of 7
8461: gap of 100
2 9202: contig of 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9202: contig of 7
02: gap of 100
10050: contig of 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5948: gap of 10
6689: contig of
6789: gap of 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5095: gap of 10
5848: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7531: contig of
                                                                                                                                                                            Center clone name: 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ______gap_of
20872: ______
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          con.
. gap of 21715:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4251: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20972:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22647:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5849
5949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8362 8
8462
9203 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7532
7632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signature, B. Lintcon, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barran, B., Lintcon, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Bastien, Y., Bogualavkiy, L., Boukhgalter, B., Brown, A., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Hagos, B., Haford, A., Horton, L., Hulme, W., Illev, I., Obbnson, R., Lakogua, M., Lakogua, W., Illev, I., Obbnson, R., Lehoczky, J., Levine, R., Lakogua, K., Lamazares, R., Landers, T., Marthews, C., McZurthy, M., Matthews, C., McZurthy, M., Mackan, P., McEwan, P., McEwan, P., McEwan, P., McPheeters, W. Matthews, C., McZurthy, M., Meswan, P., McRen, P., O'Connor, T., O'Donnell, P., O'Neil, D., O'Neil, D., O'Connor, T., O'Donnell, P., O'Neil, D., O'Neil, D., O'Neil, D., Raymond, C., Retta, R., Ribback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schupack, R., Schupack, R., Schupack, R., Schupack, R., Schupack, R., Schupack, R., Stojanovic, N., Trayers, M., Trayers, M.
                                                                                                 PDESWALKAIEALGKIELHGKFIEVPERGYPRKORIRKLOINNIPPHLOWEVLDSLIV
OVGVVEGCONTDSETAVAVNTYSSKOQARQALDKLINGFQLENFTLKVAYIPDEMAA
OVGVVEGCORGORGSSROGSPGSVSKOKFODLPLRLLVPPOFVCHOJ
RNITKOTOSKIDVHRENAGARENSTTILSTPEGTSAACKSILEIMHREAQDIKFTEE
PLKILAHNNPVGRLICKEGRNLKKIEQDTDTKITISPLQELTLYNPERTITVKGNVE
TCAKAEEEIMKXIRESYEDNIAMNLOAHLIPUNANLGIPPTSGHPPFSGPPSA
MTPPYPOPEGSFTFTTHOFIPALSVGAIIGKGGONIKQLSRPAGASIKIAPABABAK
VRWVIITGPPEAQFKAGGRIYGKIKEENPVSPREEVKLAAHIRVPSSPAGRVIGKGGGY
/proteIn_id="CAD32603.1"
|db_xref="GI:21260819"
|translation="MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTG 13-APR-2001
LOW-PASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 51119)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 15, clone RP11-494F2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (11-MAR-2001) Whitehead Institute/MIT Center for Genome Submitted (11-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 13, 2001 this sequence version replaced g1:13273446. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 21; DB 6; Length 4602; 100.0%; Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens chromosome 15 clone RP11-494F2.map 15, SECUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     918 g 1298 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   726 GAAGTATCTTCAAGGACGCC 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC090865.2 GI:13621281
HTG; HTGS_PHASE0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  KALQSGPPQSRRK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 51119)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     907 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Warches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ಥ
```

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS

TITLE JOURNAL COMMENT

LOCUS DEFINITION

ACCESSION

RESULT 12 AC090865

요

```
23402 23501; gap of 100 bp 10 length 24256 2435; contig of 745 bp in length 24256 2435; contig of 745 bp in length 25322 2524; gap of 2539 contig of 724 bp in length 25322 2524; gap of 2539 contig of 724 bp in length 25323 2652; contig of 724 bp in length 25323 2652; gap of 674 bp in length 25324 27639; gap off 674 bp in length 25324 27639; gap off 674 bp in length 25329 2327; gap off 676 bp in length 25329 2327; gap off 676 bp in length 23329 2323; gap off 676 bp in length 2329 2329; gap off 772 bp in length 2329 2329; gap off 772 bp in length 2329 2329; gap off 100 bp in length 2329; gap off 100 bp in length
```

```
Direct Submission
Submitted (21-FRB-2002) Department of Genetics, Washington
Submitted (21-FRB-2002) Department of Genetics, Missouri 63108, USA
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Jan 6, 2011s sequence version replaced gi:17298647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (06-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444.Forest Park Parkway, St. Louis,
06 3108, USA
(bases 1 to 54379)
Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (10-SEP-2000) Genome Sequencing Center, Washington
Submitted (10-SEP-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (Dases 1 to 54379)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                              PRI 21-FEB-2002
                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 54379)
Sulficon, J. B. and Waterston, R.
                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                               ACU79780 54379 bp DNA linear PRI 21-FE
Homo sapiens BAC clone RP11-379L16 from 7, complete sequence.
AC079780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                         ö
                                                                               Swearengen, S., Meyer, R. and Cotton, M. The sequence of Homo sapiens BAC clone RP11-379L16 Unpublished (2001)
                      6735 others
/clone lib="RPCI-11 Human Male BAC"
12444 a 10521 c 9576 g 11843 t 6735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ....---- Summary Statistics
Center project name: H_NH0379L16
                                                                                                                                                                                             DD 28678 GAAAGTATCTTCAAGGACGCC 28698
                                                                                                                                                                                                                                                                                                                                                                                  AC079780.6 GI:18072220
                                                                                                                                                                          1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 (bases 1 to 54379)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 54379)
                                                                                          Query Match
Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99063792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9847074
                                                                                                                                                                                                                                                                                                                         LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                    RESULT 13
AC079780/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
```

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

FEATURES

```
1775 ... 9981

17pt family="Alu"

1859 ... 9081

17pt family="(A)n"

1106 ... 9390

17pt family="Alu"

11078 ... 10478

11079 ... 10478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
'note="match to EST BF825880 (NID:g12168647)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
               335. .5644
/note="match to EST BE149137 (NID:g8611874)"
                                                                                                             5780 . 5810
'note="match to EST BE149137 (NID:98611874)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="Alu"
12247. .13341
13448. .13617
incte="match to EST AA301911 (NID:g1954244)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 21; DB 9; Length 54379; llarity -100.0%; Pred. No. 3.5; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                    /rpt_family="Alu"
7989_ .8031
/rpt_family="Ar_rich"
8775_ .9081
/rpt_family="Alu"
                                   5515. .5592
/rpt_family="Alu"
5609. .5920
/rpt_family="Alu"
5780. .5810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rpt_family="AT_rich"
2739. .12937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="(TTTG)n"
2938. .13246
                                                                                                                                      /rpt_family="Alu"
13849. .13892
/rpt_family="(T)n"
                                                                                                                                                                                                                                                                                                                    rpt_family="Alu"
782. .8020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="L2"
10464. .10592
/rpt_family="L1"
10593. .10898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2739. .12937 --
rpt family="Alu"
2932. .12965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 family="Alu"

    .11668
    family="L1"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . .11965
family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .0379. .10454
rpt_family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 family="L1"
3. .11512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rpt_family="L1"
2007. .12320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .13836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rpt_fa
1238.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rpt_f
1669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rpt_f
1966.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rpt_f2292.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 21; Conserv
                                            repeat_region
                                                                            repeat_region
                                                                                                                                         repeat_region
                                                                                                                                                                          repeat_region
                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                      repeat_region
             misc_feature
                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
        The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov/ or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                   The clone sequenced to the left is GS1-117B4, 2000 bp overlap, the clone sequenced to the right is GS1-13M19, 2000 bp overlap. Actual start of this clone is at base position 25835 of GS1-117B4, actual end is at base position 49313 of GS1-13M19.
                                                                                                                                                                      The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genemics 51:1-8. The clone may be obtained either from and coworkers at http://www.resgen.com) or Pieter de Jong VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                   Polymorphisms have been identified between AC023105 and AC079780.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="match to EST BG003407 (NID:g12443713)"
                                                                                                                                                                                                                                                                                                                      NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .54379
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1802. .1840
/rpc_family="(TAAA)n"
2087. .2289
/rpc_family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2895. .2939
/rpt_family="Alu"
2927. .2949
/rpt_family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rpt_family="AT_rich"
280. .3575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="RP11-379L16"
clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1150. .1454
/rpt_family="Alu"
1516. .1828
/rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="Alu"
2895. .2010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="Alu"
4603. .4759
/rpt_family="Alu"
5152. .5722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rpt_family="Alu"
2. .370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'rpt_family="(A)n"
308. .460?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pt_family="Alu"
54. .357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rpt_family="Alu"
                                                                                                                                                         SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
```

FEATURES

ö

RESULT 14 AC090245/c LOCUS DEFINITION

ŝ

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS

```
19779
18488
18587: General of 100 bp
18588
19297: contig of 710 bp in length
19298
19397: app of 100 bp
20106
20206
20301: contig of 708 bp in length
20306
20305: gap of 100 bp
2031
21030: contig of 708 bp in length
2031
21330: app of 100 bp
21331
22546: contig of 720 bp in length
21731
21830: app of 100 bp
22647
22647
22647
2373: contig of 716 bp in length
22547
22646: gap of 100 bp
2347
23482: contig of 716 bp in length
2347
24183
24283: contig of 711 bp in length
24183
24283: gap of 100 bp
24483
24283: gap of 100 bp
24283: contig of 711 bp in length
24283: contig of 700 bp
24283: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10436 10435; contrig of 704 bp in tengent 10536 11239; contrig of 704 bp in length 11240 11339; gap of 100 bp in length 11240 11339; gap of 100 bp in length 12038 12137; gap of 100 bp in length 12038 12137; gap of 100 bp in length 12823 12322; gap of 100 bp in length 12823 12322; gap of 717 bp in length 13640 13739; gap of 100 bp in length 14450 14549; gap of 100 bp in length 14550 15569; contig of 710 bp in length 15370 1569; gap of 100 bp in length 15370 1569; gap of 100 bp in length 15370 15689; contig of 720 bp in length 16887 16886; contig of 706 bp in length 16887 16886; contig of 706 bp in length 16887 16986; gap of 100 bp 16887 16986; contig of 692 bp in length 16779 17778; gap of 100 bp 16887 16986; contig of 692 bp in length 17779 18487; contig of 706 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28274: gap of 100 bp
28993: contig of 719 bp in length
29093: gap of 100 bp
29916: contig of 723 bp in length
29916: gap of 100 bp
30632: contig of 716 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25851: gap of 100 bp
26541: contig of 690 bp in length
26641: gap of 100 bp
27366: contig of 725 bp in length
27466: gap of 100 bp
28174: contig of 708 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 bp
of 719 bp in length
100 bp
of 716 bp in length
                                100 bp
of 701 bp in length
100 bp
of 723 bp in length
                                                                                                                                                                                                                                                                          100 bp
f 707 bp in length
                                                                                                                                                                                                                                                                                                                                           00 bp
703 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 bp
f 706 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0 bp
696 bp in length
                                                                                                                                                       100 bp
f 714 bp in length
                                                                                                                                                                                                                     100 bp
f 713 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                       100 bp
f 700 bp in length
of 720 bp in length
                                                                                                                                                                                                                                                                                                                                                  00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100
                                                                                                                                                                                                                                                                                                                                                                                                                       7198: contig of 7
9 7298: gap of 100
8004: contig of 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27466: gap of 1
28174: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9619: contig of
9719: gap of
10435: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig of
                                                                                                                                contig of
                                                                                                                                                                                        contig of
                                                                                                                                                                                                                                                      contig of
                                                                                                                                                                                                                                                                                                                 contig of
                                                                                                                                                                                                                                                                                                                                                                                contig of
                                                                 contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1053c
11240 11339: gap --
11340 12037: conti
12038 12137: gap of
12822: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28994 29093: gap of 29094 29816: con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8104: gap of
8800: co
                                                                                                                                                                                                                                                                                                                                                                                                                 6498: gap of
7198: co
                                                                                                  2438: gap of
3161: co
                                                                                                                                                                                                                            4075: gap of
4788: co
                                                                                                                                                                                                                                                                                             gap of
                                                                                                                                                                                                                                                                                                                                                     5695: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8900: gap of
9619: co
                                                                                                                                                             3261: gap of
3975: co
                                1637: gap
2338:
                                                                                                                                                                                                                                                                                                                                                                                   6398:
                                                                                                                                                                                                                                                                                                                        5595:
                                                                                                                                                                                                                                                                                       4888:
                                                                                                                                   2439
3162
3262
3976
4076
                                                                                                                                                                                                                                                                                                                                                     5596
5696
6399
                                                                                                                                                                                                                                                                                                                        4889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L Unpublished
L Unpublished
L Unpublished
L Unton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,
Barran, N., Bastlen, V., Choepel, Y., Colangelo, M., Collins, S.,
Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S.,
Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
Collymore, S., Farreira, P., Fitzhugh, W., Gage, D., Galagan, J.,
Dodge, S., Raford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
Jones, C., Kartasas, A., LaRocque, K., Lamarares, R., Landers, T.,
Lehoczky, J., Levine, R., Liu, G., Maclean, C., Macdonald, P.,
Marquis, N., Matthews, C., McCarthy, M., NoEwan, P., McGernan, K.,
Murphy, T., Matthews, C., McCarthy, M., Morbau, P., McGernan, K.,
Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H.,
O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,
Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Rotetra, R.,
Rieback, M., Kiley, R., Rise, C., Schupback, R., Seaman, S., Severy, P.,
Sougnez, C., Spencer, B., Stange-Thomann, N., Scolanovi, J.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Travers, M., Travis, N., Trigilio, J., Vaosiliev, H., Viel, R., Vo, A.,
Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J.,
Zambek, L., Zimmer, A. and Zody, M.
Direct Submission

Native of the sequence version replaced gi:12957879.
All repeats were identified using RepeatMasker:
Smit, A.F. A. & Green, P. (1996-1997)
Smit, A.F. A. & Green, P. (1996-1997)
Corners, Mathemene washington-edu/RM/RepeatMasker:
Corners, Math. Walley
Corners, Mat
                                                                                                                                                                                                                                         57261 bp DNA linear HTG 17-MAR-2001
Homo sapiens chromosome 18 clone RP11-888112 map 18, LOW-PASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: This record contains 71 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L12326
Center clone name: 888_I_12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 717: contig of 717 bp in length 718 817: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birren, B., Linton, L., Nusbaum, C. and Lander, B. domo sapiens chromosome 18, clone RP11-888I12 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code: WIBR
Web site: http://www-seq.wi.mit.edu
                                                                                                                      Db 34372 GAAAGTATCTTCAAGGACGCC 34352
                                                                                                                                                                                                                                                                                                                                                                                                   AC090245.2 GI:13374670
HTG; HTGS_PHASE0.
Homo sapiens.
                                                                           2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 57261)
                                                                        1 GAAAGTATCTTCAAGGACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                             AC090245
```

TITLE JOURNAL

COMMENT

```
95 35594; gap of 100 bp 11 tengen 113 3412; gap of 100 bp 113 37086; contig of 718 bp in length 113 37086; gap of 100 bp 
33 30732: gap of 100 bp 1440: contig of 708 bp in length 1540: gap of 100 bp 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77: contig of 713 bp in length gap of 100 bp 94: contig of 717 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          p of 100 bp contig of 711 bp in length p of 113 bp in length contig of 713 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54931: gap of 100 bp 55624: contig of 693 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig of 724 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94: gap of 100 bp 52402: contig of 708 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54126: gap of 100 bp 54831: contig of 705 bp in length
                                                                                                                                                                                                                                                                                                                                                                                      34677: c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        con,
... gap of
51594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    con.
.. gap of
53213:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53313: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34777:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52502:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9451
```

Query Match
100.0%; Score 21; DB 2; Length 57261;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps

ö

 Oy
 1 GAAAGTATCTTCAAGGACGCC 21

 Db
 28686 GAAAGTATCTTCAAGGACGCC 28666

PRI 27-FEB-2002 Direct Submission
Submitted (04-JUL-2001) Genome Sequencing Center, Washington
Miversity School of Medicine, 4444 Forest Park Parkway, St. Louis,
Mo 63108, USA
4 (bases 1 to 176547)
Materston, H.H.
Direct Submission
Submitted (23-FBB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 176547) Direct Submission Submitted (27-FEB-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Feb 23, 2002 this sequence version replaced gi:16259201. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. AC092447 Homo sapiens BAC clone RP11-760D2 from 7, complete sequence. AC092447 Center: Washington University Genome Sequencing Center Center code: WUGSC 2 (bases 1 to 176547)
"Armstrong,J. and Cotton,M.
The sequence of Homo sapiens BAC clone RP11-760D2
"Mupublished (2001)
3 (bases 1 to 176547)
Waterston,R.H. Web site: http://genome.wustl.edu/gsc Contact: sapiens@watson.wustl.edu -------- Summary Statistics 1 (bases 1 to 176547)
Sulston,J.B. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998) Center project name: H\_NH0760D02 ---- Genome Center AC092447.5 GI:18873962 sapiens Homo saplens Waterston, R. HTG ACCESSION VERSION KEYWORDS SOURCE ORGANISM LOCUS REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL TITLE JOURNAL REFERENCE AUTHORS JOURNAL COMMENT

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

## MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nh.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu/gsc

SOURCE INFORMATION: The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E.

```
misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                             NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP13-492C18; the clone sequenced to the right is RP11-10F11, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-760D2; actual end is at base position 1 of RP11-10F11.
                                                                                                                                                                                          The region from 20341 to 20385 is covered only by a pcr product from clone DNA. An unresolved simple sequence repeats exists and between 84203 and 84724. Polymorphisms exists between AC024199 and AC092447. Data from AC024199 and AC092447.
Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="match to EST A1334287 (NID:g4070846) gq25e08.x1" 4411. 14446
                                                                                                                                                                                                                                                                                                                                                                                                                                       rpt_family="L1"

1210_ .2483

rpt_family="Alu"

7795_ .3012

700te="match to EST BF894500 (NID:g12285959)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF895059 (NID:g12286518)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4411. .14446
note="similar to Homo sapiens BST BF979990
(NID:g12347205)"
                                                                                                                                                                                                                                                                                                                  1. .176547
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               799. .2962
note="match to EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="Alu"
10336. . inco.
                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                'clone="RP11-760D2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="L1"
6528. .6825
/rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1975. .12282
rpt family="Alu"
2457. .12765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rpt family="Alu"
4411. .14448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3/95..4263
/rpt_family="L1"
4259..454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4259. .4542
/rpt_family="L1"
4548. .4740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / 2002. .3388
/rpt_family="L2"
3419. .352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       380. .8686
rpt_family="Alu"
924. .9225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . .5046
_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rpt_family="Alu"
838. .10125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           537. .3794
rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rpt_family="L1"
537. .3794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . .4748
family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                      FEATURES
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens EST AA669082 (NID:92630581)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="Alu"
16113. .16529
1672p_family="L1"
16530. .16941
/note="similar to Homo sapiens EST AA446576 (NID:g2159241)
zw84d02.s1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens EST AI744560 (NID:95112848)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  i6912. .17332
/note="similar to Homo sapiens BST AA446703 (NID:g2159368)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 176547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="match to EST BG479148 (NID:gl3411427)"
71135. 17383
'note="match to EST BG773852 (NID:gl4044151)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18142. .18846
/rpt_family="ERV1"
18530. .18619
/note="match to EST BF894500 (NID:g12285959)
19083. .19168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17144. 17383
Anote="similar to Homo sapiens EST BG480641
(NID:913412920)"
14412. .14455
/note="eimilar to Homo sapiens EST BE879245
(NID:g10328021)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE622588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE966979
                                                                                                                                     sapiens EST AL520426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16586. 17133
Morte="Waimlar to Homo sapiens EST (NID:99893515)"
16610. 17149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 21; DB 9;
100.0%; Pred. No. 3.6;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="L1"
17856. 18132
17826. 17839
17826. 17839
                                                                      /note="similar to Homo s. (NID:g12783919)"
14530, 114520, 114520, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 114530, 1145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16541. .17068
note="similar to Homo
(NID:911772953)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="similar to Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                    2. .16112
family="Alu"
3. .16529
                                                                                                                                                                                                                        /rpt_family="L1"
14609. 14910
/rpt_family="Alu"
14911. 15079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DD 167744 GAAAGTATCTTCAAGGACGCC 167764
                                                                                                                                                                                                                                                                                                           /rpt family="L1"
/rpt family="L1"
/s062. 1501
                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="L1"
5812. .16112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .17383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .17822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ab92h09.81"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            wg09g02.x1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        750c07.rl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              zw84d02.rl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .7383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                         misc_feature
```

Search completed: April 18, 2003, 06:15:49 Job time : 345.727 secs

```
April 18, 2003, 04:12:35 ; Search time 93.5455 Seconds (without alignments) 505.551 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | SIDS2/gcgdata/geneseq_geneseq_nemb_/Na1990.DAT: |
| SIDS2/gcgdata/geneseq_geneseq_nemb_/Na1990.DAT: |
| SIDS2/gcgdata/geneseq_geneseq_nemb_/Na1991.DAT: |
| SIDS2/gcgdata/geneseq_geneseq_nemb_/Na1993.DAT: |
| SIDS2/gcgdata/geneseq_geneseq_nemb_/Na1993.DAT: |
| SIDS2/gcgdata/geneseq_geneseq_nemb_/Na1995.DAT: |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | SIDS2/gcgdata/geneseq_geneseq_embl/NA1981.DAT:
| SIDS2/gcgdata/geneseq_geneseq_embl/NA1981.DAT:
| SIDS2/gcgdata/geneseq_geneseq_embl/NA1981.DAT:
| SIDS2/gcgdata/geneseq_geneseq_embl/NA1981.DAT:
| SIDS2/gcgdata/geneseq_geneseq_embl/NA1985.DAT:
| SIDS2/gcgdata/geneseq_geneseq_embl/NA1985.DAT:
| SIDS2/gcgdata/geneseq_geneseq_embl/NA1985.DAT:
| SIDS2/gcgdata/geneseq_geneseq_embl/NA1981.DAT:
| SIDS2/gcgdata/geneseq_geneseq_embl/NA1989.DAT:
| SIDS2/gcgdata/geneseq_geneseq_geneseq_embl/NA1989.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:
|SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:
|SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999_DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000_DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <sup>7</sup>gcgdata/geneseq/geneseqn-emb1/NA1980.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4370478
GenCore version 5.1.4 p5_4578.
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2185239 seqs, 1125999159 residues
                                                                                                                                                                                  OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 gaaagtatcttcaaggacgcc 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N_Geneseq_101002:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-270-437D-9
21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                         Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Regult NO.11 20 20 20 40 70 70 80	Score 21 21 21 21 21 21 21 21	Match Match 100.0 100.0 100.0 100.0	Te Match Length DB I Match Len	DB 22 24 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	SUMMARIES  ID  AAZ36155  AAZ36155  AAG6035  ABL49297  ABL49299  ABL49283  AAL49283  AAL49283	Description PCR primer for DNA Human lung tumour BNA encoding cance
O	21	100.0	4181	24	ABL65405	human lung cancer- Lung cancer relate

The state of the s	Himan KOC DAR HO	ã	encoding	Human Osteoblast d	Drosophila melano			Drogophila melano		s ec			æ		brain expre	bone		#22319 used	qenome	Human breast cell	foetal	#1856 £	n brain	bone m				Human genome-deriv	Gene #2878 used to	_	Probe #7227 for ge	brain expre	bone	#677	#9242
ABT.49119	ABA99958	AAS86150	AAS76779	ABQ88221	ABL13727	ABL20653	AAH14309	ABL13726	ABL13722	ABL20652	ABL12304	ABL11528	ABA73205	ABA38638	AAK21640	AAK47805	AAI26041	AAI53633	ABS21812	ABA43210	ABA53638	ABA23390	AAK01900	AAK27357	AAI11930	AAI33261	AAI01867	ABS01870	ABN96380	ABA60667	ABA28761	AAK08949	AAK34840	AAI16846	AA140556
24	24	23								23			22	22	22	22	55	22	24	22	22	22	22	22	22	22	22	24	24	22	22	22	22	22	22
4181	4601	4264	1985	7661	557	1421	1920	2557	2645	3541	6015	6747	359	359	359	359	359	359	359	476	476	476	476	476	476	476	476	476	479	597	597	597	597	597	597
100.0	100.0	95.2	84.8	80.0	78.1	78.1	78.1	78.1	78.1	78.1	78.1	78.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	17.1
21	21	20	17.8	16.8	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.2	16.2	16.2	16.2	16.2	16.2	16.2	16.2	16.2	16.2	16.2	16.2	16.2	9	16.2	16.2	16.2	16.2	16.2	ø	16.2	9	16.2
10	11	12	13	c 14	-	-			ი 19		21	22				c 56				30	31	32	33	J. 6	35	3.6	37	80 6	•	•	•	•	c 43	•	•

## ALIGNMENTS

AAZ3615

Cancer associated antigen; KOC-1; cancer; vaccine; CT7; PCR primer; ss. PCR primer for DNA encoding cancer associated antigen KOC-1. AAZ36155 standard; DNA; 21 BP. 11-FEB-2000 (first entry) Homo sapiens. Synthetic. 

instant WO9954738-A1.

28-OCT-1999.

(LUDW-) LUDWIG INST CANCER RES. 99WO-US05766 98US-0061709 17-APR-1998; 16-MAR-1999;

old LJ; Knuth A, Jager E, Gure A, Tsang S, Stockert E, WPI; 2000-013284/01. Chen Y,

Nucleotides representing cancer-associated genes, used to develop products for the diagnosis, monitoring and treatment of cancers

Claim 108; Page 13; 44pp; English

```
This invention describes a novel isolated polypeptide (I) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polynucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention
                                 pCR primers AA236155-56 were used to amplify a cancer associated antigen gene designated KOC-1. The specification also describes a cancer associated antigen designated CT7. The CT7 polymucleotide was isolated from SK-MEL-37 melanoma cells. The polypeptide has some homology with MAGB-10, limited to about 210 carboxy terminal amino acids. The amino terminal of the protein has a repetitive pattern, with repeats rich in the peptide given in AAV43877. The CT7 polypeptide can be processed to peptides which provoke lysis by cytolytic T cells. The polymucleotides and polypeptides can be used for treating a cancerous condition and screening for or diagnosing cancerous conditions. The cancer associated antigens can be used as an immunogenic or vaccine composition with an adjuvant, e.g. a cytokine, a saponin, or granulocyte macrophage-colony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated polypeptide comprising an immunogenic portion of a lung tumor protein is used for detecting and monitoring progression of lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapy; treatment; human; tumor; immunogenic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 21; DB 21; Length 21; 100.0%; Pred. No. 0.26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human lung cancer-associated cDNA antigen L523S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21 BP; 7 A; 5 C; 5 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1a; Page 258-259; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; FAC. 0; W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC66035 standard; cDNA; 1740 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-APR-1999; 99US-0285479.
17-DEC-1999; 99US-0466396.
30-DEC-1999; 99US-046496.
10-JAN-2000; 2000US-0480884.
22-FEB-2000; 2000US-0510376.
                                                                                                                                                                                                                                                                                                                                                                                                                                            adjuvant, e.g. a cytokine, a stimulating factor (GM-CSF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-APR-2000; 2000WO-US08896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lung cancer; therapy; to vaccine; detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000-628399/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAB11365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200061612-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC66035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AACGG035
AACGG035
AACGG035
AACGG035
AACGG035
AACAGG035
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠ
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes human lung tumour proteins. Human lung tumour proteins and polymuclectides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polymucleotides, antibodies, tusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABL48959 to ABL43300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polynucleotides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polynucleotides encoding lung tumor polypeptides, useful for treating lung cancer or stimulating an immune response -
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Henderson RA;
                                                                                                                                                                          ó
                                                                                                                                        100.0%; Score 21; DB 21; Length 1740; 100.0%; Pred. No. 0.55;
                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1740 BP; 526 A; 406 C; 417 G; 391 T; 0 other;
                                                                                                                Sequence 1740 BP; 526 A; 406 C; 417 G; 391 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                            Human lung tumour L523S cDNA sequence SEQ ID NO:347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang A, Skeiky YAW, Li SX, Kalos MD,
PD, Panger N, Retter MW, Marnerakis M,
PS, Carter D, Watanabe Y, Peckham DW;
                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 330; 374pp; English.
                                                                                                                                                                                                                                                                                                                      ABL49254 standard; cDNA; 1740 BP
                                                                                                                                                                                 ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-AUG-2000; 2000US-0630940.
21-AUG-2000; 2000US-0643597.
15-SEP-2000; 2000US-0662786.
09-000; 2000US-0685696.
12-DEC-2000; 2000US-0735705.
07-MAY-2001; 2001US-0850716.
                                                                                                                                                                                                              21
                                                                                                                                                                                                                                         GAAAGTATCTTCAAGGACGCC 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUN-2001; 2001WO-US21065.
                                                                                                                                                                                                              GAAAGTATCTTCAAGGACGCC
                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PD, Fanger N,
TS, Carter D,
                                                                                      development of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-090513/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CORI-) CORIXA CORP.
                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immune response; 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; ABB74997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200200174-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JUN-2000;
02-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JAN-2002.
                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                        ABL49254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang T,
McNeill
                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vedvick
                                                                                                                                                                     Local
                                                                                                                                                                       Best Loca
Matches
                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                            RESULT 3
                                                                                                                                                                                                                                                                                                              ABL49254
                                                                                                                                                                                                                                                                                                                           888888888
```

ö

Gaps ö 3

ö

Gaps

ö

Indels

us-09-270-437d-9.rng

```
Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polynucleotides encoding lung tumor polypeptides, useful for treating lung cancer or stimulating an immune response -
                                                                                                                                                                           Human lung tumour L523S recombinant polynucleotide SEQ ID NO:447;
      24; Length 1740;
 100.0%; Score 21; DB 24; I
ilarity 100.0%; Pred. No. 0.55;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                   Skeiky YAW, Li SX, Kalos MD, )
er N, Retter MW, Marnerakis M,
er D, Watanabe Y, Peckham DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 367; 374pp; English.
                                                                                                                  BP.
                                                                                                              ABL49297 standard; cDNA; 1743
                                                               75
                                          GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                               28-JUN-2000, 2000US-0606421.
02-AUG-2000, 2000US-0630940.
21-AUG-2000, 2000US-064597.
15-SEP-2000, 2000US-0662786.
09-OCT-2000, 2000US-0685696.
12-DEC-2000; 2000US-0685696.
                                                         SS GAAGTATCTTCAAGGACGCC
                                                                                                                                                                                                                                                                                           28-JUN-2001; 2001WO-US21065
                                                                                                                                                                                                                                                                                                                                                                                                                   Wang T, Wang A, Skel)
McNeill PD, Fanger N,
Vedvick TS, Carter D,
Query Match
Best Local Similarity
Matches 21, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-090513/12.
                                                                                                                                                                                                            immune response; ss
                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; ABB75053
                                                                                                                                                                                                                                                 WO200200174-A2
                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                         01-MAY-2002
                                                                                                                                                                                                                                                                       03-JAN-2002
                                                                                                                                     ABL49297;
                                                                                                     ABL49297
                                                                                             RESULT
                                                            g
                                                                                                                ઠે
```

The present invention describes human lung tumour proteins. Human lung tumour proteins and polynucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present

Fanger GR; Henderson

ö

Sequence 1743 BP; 527 A; 406 C; 418 G; 392 T; 0 other;

Gaps ô 100.0%; Score 21; DB 24; Length 1743; 100.0%; Pred. No. 0.55; 1.ve 0; Mismatches 0; Indels 0. 100.0%; Fr. 0; Conservative Local Similarity les 21, Conserv Query Match Best Loca Matches

55 GAAAGTATCTTCAAGGACGCC 75 GAAAGTATCTTCAAGGACGCC 21 н

ઠે g Human lung tumour L523S recombinant polynucleotide SEQ ID NO:428.

(first entry)

01-MAY-2002

ABL49283;

ABL49283 11D ABL4 XX AC ABL4 XX DT 01-M XX

멾.

ABL49283 standard; cDNA; 1764

RESULT

; 0

```
The present invention describes human lung tumour proteins. Human lung tumour proteins and polynuclectides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
                                                                                                                              tumour; lung cancer; cytostatic; immunostimulant; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polynucleotides encoding lung tumor polypeptides, useful for treating lung cancer or stimulating an immune response -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                 Human lung tumour 15238 recombinant polynucleotide SEQ ID NO:450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fanger GR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 100.0%; Score 21; DB 24; Length 1743; 1 Similarity 100.0%; Pred. No. 0.55; 21; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1743 BP; 527 A; 406 C; 418 G; 392 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                            g A, Skeiky YAW, Li SX, Kalos MD,
Fanger N, Retter MW, Marnerakis M,
Carter D, Watanabe Y, Peckham DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 370; 374pp; English.
            ABL49299 standard; cDNA; 1743 BP.
                                                                                                                                                                                                                                                                                                       02-AUG-2000; 2000US-0630940.
21-AUG-2000; 2000US-0643597.
15-SEP-2000; 2000US-0662786.
09-07-2000; 2000US-0685696.
12-DEC-2000; 2000US-0735705.
07-MAY-2001; 2001US-0850716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 GAAAGTATCTTCAAGGACGCC 75
                                                                                                                                                                                                                                                                28-JUN-2001; 2001WO-US21065.
                                                                                                                                                                                                                                                                                            28-JUN-2000; 2000US-0606421
                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAAAGTATCTTCAAGGACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-090513/12.
P-PSDB; ABB75054.
                                                                                                                                Human; lung tumour; immune response; ss
                                                                                                                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang A,
                                                                                                                                                                                                      WO200200174-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang T, Wang
McNeill PD,
Vedvick TS,
                                                                    01-MAY-2002
                                                                                                                                                                                                                                  03-JAN-2002,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nvention.
                                          ABL49299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
ABL49299
            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

Old LJ;

Knuth A,

Jager E,

Tsang S, Stockert E,

```
Nucleotides representing cancer-associated genes, used to develop products for the diagnosis, monitoring and treatment of cancers
                                                                                                                                                                                                                                      Claim 88; Page 39-40; 44pp; English
                                                                       (LUDW-) LUDWIG INST CANCER RES
99WO-US05766
                                98US-0061709
                                                                                                                                               WPI; 2000-013284/01
                                                                                                              Gure A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-FEB-2001
 16-MAR-1999;
                                        17-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC65900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC65900
   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes human lung tumour proteins. Human lung tumour proteins and polynuclectides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
                   Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine; immune response; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynucleotides encoding lung tumor polypeptides, useful for treating
lung cancer or stimulating an immune response -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                 Henderson RA;
Fanger GR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 100.0%; Score 21; DB 24; Length 1764; Best Local Similarity 100.0%; Pred. No. 0.55; 9; Indels 0; Matches 21; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cancer associated antigen; KOC-1; cancer; vaccine; CT7; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1764 BP; 534 A; 417 C; 419 G; 394 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                               Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, McMeill PD, Fanger N, Retter MW, Marnerakis M, Vedvick IS, Carter D, Watanabe Y, Peckham DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding cancer associated antigen KOC-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 355-356; 374pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ36150 standard; DNA; 4159 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JUN-2000; 2000US-0606421.
02-AUG-2000; 2000US-0630940.
21-AUG-2000; 2000US-0643597.
15-SEP-2000; 2000US-0662786.
09-QCT-2000; 2000US-0685696.
12-DEC-2000; 2000US-0735705.
07-MAY-2001; 2001US-0950716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAAAGTATCTTCAAGGACGCC
                                                                                                                                                                                                   28-JUN-2001; 2001WO-US21065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-090513/12.
P-PSDB; ABB75048.
                                                                                                                                                                                                                                                                                                                                                                                    (CORI-) CORIXA CORP
                                                                                                                            WO200200174-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-FEB-2000
                                                                                             Homo sapiens.
                                                                                                                                                                  03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ36150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
```

```
The present sequence represents a cancer associated antigen gene designated KOC-1. The specification also describes a cancer associated antigen designated CT7. The CT7 polymucleotide was isolated from antigen designated CT7. The CT7 polymucleotide was isolated from SK-MEL-37 melanoma cells. The polypeptide has some homology with mager-10, limited to about 210 carboxy terminal amino acids. The amino series, proline, glutamine and leucine, and an almost invariable core of serine, proline, glutamine and leucine, and an almost invariable core of the peptide given in AAY43877. The CT7 polypeptide can be processed to and polypeptides can be used for treating a cancerous condition and and application with an attigens can be used as an immunogenic or vaccine composition with an attigens can be used as an immunogenic or vaccine composition with an adjuvant, e.g. a cytokine, a saponin, or granulocyte macrophage-colony stimulating factor (GM-CSF).
                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                               Length 4159;
                                                                                                                                                                                                                                                                                         Sequence 4159 BP; 1281 A; 830 C; 851 G; 1181 T; 16 other;
                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                 100.0%; Score 21; DB 21; 100.0%; Pred. No. 0.63;
                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human lung cancer-associated cDNA L523S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC65900 standard; cDNA; 4181 BP.
                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 GAAAGTATCTTCAAGGACGCC 325
                                                                                                                                                                                                                                                                                                                                                                                                                   21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-APR-1999; 99US-0285479.
17-DEC-1999; 99US-0466396.
30-DEC-1999; 99US-0476496.
10-JAN-2000; 2000US-0480884.
22-FEB-2000; 2000US-0510376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-APR-2000; 2000WO-US08896
                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAAAGTATCTTCAAGGACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                         vaccine; detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-628399/60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORI-) CORIXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fan L:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang T,
```

WO9954738-A1 Homo sapiens

XBXBXBXBXBXBX

g

ò

28-OCT-1999

```
This invention describes a novel isolated polypeptide (I) which which which have cytostatic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polynucleotides are used in compositions and vaccines to inhibit the development of cancer, can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the are treated with P2, polynucleotides encoding P2 or antigen presenting development of cancer.
                         Isolated polypeptide comprising an immunogenic portion of a lung tumor protein is used for detecting and monitoring progression of lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
gene; ds.
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                  100.0%; Score 21; DB 21; Length 4181;
100.0%; Pred. No. 0.63;
.ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                       Sequence 4181 BP; 1303 A; 830 C; 851 G; 1181 T; 16 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lung cancer related gene sequence SEQ ID NO:3742.
                                                                             Claim 1a, Page 184-186; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL65405 standard; DNA; 4181 BP
                                                                                                                                                                                                                                                                                                                                                                            305 GAAAGTATCTTCAAGGACGCC 325
                                                                                                                                                                                                                                                                                                                                                         1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUN-2000; 20000S-2093151P.
18-SEP-2000; 2000US-231313P.
20-SEP-2000; 2000US-231617P.
20-SEP-2000; 2000US-234034P.
20-SEP-2000; 2000US-234034P.
22-SEP-2000; 2000US-234052P.
22-SEP-2000; 2000US-234569P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2001, 2001WO-US10838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUN-2000; 2000US-209473P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-234567P
2000US-234923P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-234924P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-235082P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-235134P
2000US-235280P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-235077P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-235637P
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
....hes 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
 P-PSDB; AAB11328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200194629-A2
                                                        in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-SEP-2000; 25-SEP-2000; 25-SEP-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL65405;
                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL65405
ID ABL6
                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
ò
```

```
The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene [1] of a signature gene set, where [1] comprises a sequence (S) selected from 847 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytoscatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical result of M1, and the data is sufficient to convey the chemical cancer and/or properties of the agent. M1 can be used in the conveythement of cancer such as colon, breast, stomach, lung, thyroid, cosephageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating ductal cancer, carcinoma, papillary carcinoma and Wilm's tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Horrigan S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 21; DB 24; Length 4181; 100.0%; Pred. No. 0.63; cive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Endress G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4181 BP; 1303 A; 830 C; 851 G; 1181 T; 16 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ebner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID 3742; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Carter KC,
                                                                2000US-236034P
2000US-236034P
2000US-236110P
2000US-236111P
2000US-236891P
2000US-236891P
2000US-23691P
                                                                                                                                                                                  2000US-237173P.
2000US-237278P.
2000US-237294P.
2000US-237295P.
2000US-237316P.
                                                                                                                                                                                                                                                                                                                     03-0CT-2000; 2000US-237666P.
03-0CT-2000; 2000US-23760BP.
01-NOV-2000; 2000US-244867P.
01-NOV-2000; 2000US-245084P.
                                                                                                                                                                                                                                                                        2000US-237425P.
                                                                                                                                                                                                                                                                                        03-OCT-2000; 2000US-237598P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Augustus M,
Weaver Z;
                                                                                                                                                                                                                                                                                                                                                                                                          (AVAL-) AVALON PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-188264/24.
                                                                28-SEP-2000; 28-SEP-2000; 28-SEP-2000; 2
                                                                                                                28-SEP-2000;
29-SEP-2000;
29-SEP-2000;
                                                                                                                                                                                                                 02-OCT-2000; 2
02-OCT-2000; 2
02-OCT-2000; 2
                                28-SEP-2000;
                                                                                                                                                                  02-OCT-2000;
02-OCT-2000;
                                                                                                                                                                                                                                                                      03-OCT-2000;
                                                                                                                                                                                                    02-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Young PE, 1
Soppet DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
```

Gaps

ö

305 GAAAGTATCTTCAAGGACGCC 325

셤 ઠે

1 GAAAGTATCTTCAAGGACGCC 21

Matches

ABL49119
ID ABL49119 standard; cDNA; 4181
XX
AC ABL49119;
XX
XX
DT 01-MAY-2002 (first entry)

RESULT 10

01-MAY-2002 (first entry)

27-SEP-2000; 2000US-235720P

```
The present invention describes human lung tumour proteins. Human lung tumour proteins and polynuclectides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynuclectides, antibodies, tusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KOC; promoter; human; cytostatic; dermatological; vulnerary; tumour; chemocherapy; allogenic bone marrow transplant; pancreatic carctinoma; domain-containing protein overexpressed in cancer; immunostimulant; gene therapy; chronic pancreatitis; pluripotency; adjing; wound healing; radiation therapy; skin regeneration; cell differentiation; cancer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polynucleotides encoding lung tumor polypeptides, useful for treating
lung cancer or stimulating an immune response -
                                    Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
                                                                                                                                                                                                                                                                                                                                                                               Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson Ri
McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;
Vedvick TS, Carter D, Watanabe Y, Peckham DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4181 BP; 1303 A; 830 C; 851 G; 1181 T; 16 other;
      Human lung tumour L523S cDNA sequence SEQ ID NO:175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 266-267; 374pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABA99958 standard; DNA; 4601 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 GAAAGTATCTTCAAGGACGCC 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                      21-AUG-2000; 2000US-0643597.
15-SEP-2000; 2000US-0662786.
09-0CT-2000; 2000US-0685696.
12-DEC-2000; 2000US-0737005.
07-MAY-2001; 2001US-0850716.
                                                                                                                                                                                                                                          2000US-0630940.
2000US-0643597.
                                                                                                                                                                                        28-JUN-2001; 2001WO-US21065
                                                                                                                                                                                                                         2000US-0606421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
Les 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-090513/12.
                                                                                                                                                                                                                                                                                                                                                         (CORI-) CORIXA CORP.
                                                              immune response; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; ABB74960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human KOC DNA
                                                                                                                              WO200200174-A2
                                                                                                Homo sapiens.
                                                                                                                                                                                                                           28-JUN-2000;
                                                                                                                                                                                                                                              02-AUG-2000;
                                                                                                                                                              03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABA99958;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABA99958
ò
```

Henderson RA;

```
This invention describes a novel KOC (KH domain-containing protein overexpressed in cancer) promoter. The products of the invention have overexpressed in cancer) promoter. The products of the invention have cytostatic, dermatological, vulnerary and immunostimulant activity, are capable of modulating activity/expression of the KOC protein and can be used for gene therapy. The KOC promoter is also useful (i) for diagnosis used for gene therapy. The KOC promoter is also useful (i) for diagnosis of tumours that express KOC, particularly for differentiating between of themote panceatic carcinoma; (ii) to detect chronic panceatists and panceatic carcinoma; (iii) to detect cond (iii) to evaluate treatments; (iv) to impart pluripotency to cells; and (iii) to evaluate treatments; (iv) to impart pluripotency to cells; (v) to prepare tissues or organs (by differentiation of seem cells; (v) to prepare tissues or organs (by differentiation of seem cells; (vii) to improve ex vivo populations); (vi) in high-dose chemotherapy; (vi) to improve aging processes; (x) as prophylactic agents during chemotherapy/radiation processes; (x) as prophylactic agents during chemotherapy/radiation chemotherapy; (xi) to regenerate skin defects and accelerate wound healing, thoughing for cosmeller purposes; and (xi) to immunise against malignant chemotherapy; (xi) to regenerate skin defects and accelerate wound healing, thoughting for cosmeller precursor stages. The promoter can also be used (i) for the compare of feel differentiation of cells and tissues; (ii) to detect the degree of (ed) differentiation of cells and tissues; (ii) and (iv)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in gene therapy of cancer (for controlling protein expression); and (iv) to identify compounds, potentially useful in cancer treatment, that bind to the promoter and modulate its activity. The promoter makes possible generation of stem cells of any selected type. Since expression of KOC is not sensitive to other physiological states, e.g. inflammation, it represents a tumour marker with 100% sensitivity and specificity. This sequence represents the human KOC gene described in the disclosure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                  New promoter of the KOC gene, useful for diagnosis and treatment of cancer, for inducing cellular dedifferentiation and for identifying modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 21; DB 24; Length 4601;
100.0%; Pred. No. 0.64;
iive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4601 BP; 1462 A; 906 C; 918 G; 1298 T; 17 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding novel human diagnostic protein #21954.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS86150 standard; cDNA; 4264 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Fig la-b; 74pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            725 GAAAGTATCTTCAAGGACGCC 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                     Adler G;
                                                                                                                           01-AUG-2001; 2001WO-DE02948
                                                                                                                                                                     06-SEP-2000; 2000DE-1043964
14-FEB-2001; 2001DE-1006829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
Matches 21, Conservative
                                                                                                                                                                                                                                                                                     Mueller F, Gress T,
                                                                                                                                                                                                                                                                                                                               WPI; 2002-292230/33
                                                                                                                                                                                                                                        (MUEL/) MUELLER F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the invention
                                        WO200220036-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-FEB-2002
Homo sapiens.
                                                                                     14-MAR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS86150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠ
```

ö

ö

Gaps 0

100.0%; Score 21; DB 24; Length 4181; 100.0%; Pred. No. 0.63; ative 0; Mismatches 0; Indels 0;

```
The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence: tags for identifying expressed genes. (I) is useful in gene therapy techniques (I) creatore normal activity of (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as imaging of sites expressing (II) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. (IT) and its binding partners are useful in medical disorders involving aberrant protein expression or biological activity. (IT) expression of a (II) are useful in medical disorders involving aberrant protein expression or biological activity. (IT) expression or biological activity. (IT) expression or biological activity. (IT) and into activity of agenetic alsorders or other traits to assess biodiversity amino acid sequences of the invention.

CC and to produce other types of data and products dependent on DNA and diagnostic coding sequences of the invention.

CC diagnostic coding sequences of the invention.

CC diagnostic coding sequences of the invention.

CC Specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
food supplement, medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.2%; Score 20; DB 23; Length 4264;
100.0%; Pred. No. 2.1;
Live 0; Mismatches 0; Indels c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4264 BP; 1301 A; 854 C; 881 G; 1228 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 Similarity 100.0%; Pred. No. 2.1
20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID No 21954; 103pp; English.
                                                                                                                                                                                                                                                                                                                      Tang YT;
                                                                                                                                                                 30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                         31-MAR-2000; 2000US-0540217, 23-AUG-2000; 2000US-0649167,
                                                                                                                                                                                                                                                                                                             Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; ABG21963
                                                                                WO200175067-A2.
                                             Homo sapiens
                                                                                                                            11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
  ઠે
```

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess

Tang YT;

WPI; 2001-639362/73. P-PSDB; ABG12592. Drmanac RT, Liu C, (HYSE-) HYSEQ INC.

30-MAR-2001; 2001WO-US08631.

WO200175067-A2 Homo sapiens.

11-OCT-2001

31-MAR-2000; 2000US-0540217. 23-AUG-2000; 2000US-0649167.

Claim 1; SEQ ID No 12583; 103pp; English.

biodiversity

```
18-SEP-2002
                                                                                                                                                                                                                                             ABQ88221;
Query Match
                    Best Loca
Matches
                                                                                                                                                                    RESULT 14
                                                                                                                                                                                        ABQ88221,
                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                           Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement; medical imaging; diagnostic, genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                     DNA encoding novel human diagnostic protein #12583.
                                                                                                                                                                                                                       AAS76779 standard; cDNA; 1985 BP.
                                                                                                                          398 AAAGTATCTTCAAGGACGCC 417
                                                                                      2 AAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                 13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                               AAS76779;
```

a

```
The invention relates to isolated polynucleotide (I) and

CC polypeptide (II) sequences. (I) is useful as hybridisation probes,

CC polymerase chain reaction (PER) primers, oligomers, and for chromosome

CC and gene mapping, and in recombinant production of (II). The

polynucleotides are also used in diagnostics as expressed sequence tags

CC in restore normal activity of (II) is useful in gene therapy techniques

CC or restore normal activity of (II) or to treat disease states involving

CC or supplement. (II) and its binding partners are useful in medical

maging of sites expressing (II). (I) and (II) are useful in medical

imaging of sites expressing (II). (I) and (II) are useful in medical

ca food supplement. (II) and its binding partners are useful in medical

imaging of sites expressing (II). (I) and (II) are useful in medical

collected involving aberrant protein expression or biological activity.

CC disorders involving aberrant protein expression or biological activity.

CC and to produce other types of data and products dependent on DNA and

diagnostics, forensics, gene mapping, identification of mutations

CC and to produce other types of data and products dependent on DNA and

diagnostic coding sequences of the invention.

CC and to but was obtained in electronic format directly from WIPO

or of the publication, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; osteoblast; stem cell differentiation; bone tissue deposition; osteoporosis; osteopathic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 84.8%; Score 17.8; DB 23; Length 1985; 1 Similarity 90.5%; Pred. No. 26; 19; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human osteoblast differentiation related cDNA SEQ ID NO 128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1985 BP; 611 A; 472 C; 460 G; 441 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3221/c
ABQ88221 standard; cDNA; 7661 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 GAAGGTATCTTGAAGGACGCC 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
```

WO200250301-A2

```
monitoring the monitoring treatment of the conditions cited in (b), or monitoring treatment of bone tissue deposition.

Specific conditions include postmenopausal osteoporosis, glucocorticoid osteoporosis or male osteoporosis, osteoporosis, osteoporosis, determined and or male osteoporosis, and osteoporosis, skeletal disease linked to breast cancer, mastocytosis, osteoporosis), skeletal disease linked to breast cancer, mastocytosis, osteoplast differentiation associated CDNA marker of the invention. Osteoplast differentiation associated CDNA marker of the invention. Note: The sequence data for this patent did not form part of the printed appetitication, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                    Use of genes and their expression profiles associated with osteoblast differentiation for screening modulators bone formation, for diagnosing or treating e.g. osteoporosis, or as markers for the differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to genes and their expression profiles are used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  screening modulators of precursor stem cell differentiation into soblasts, or bone tissue deposition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (b) diagnosing abnormal deposition of bone tissue, abnormal rate of osteoblast formation or osteoporosis; or
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 128; 78pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                Axelrod DW, Cook JS,
                                                                     18-DEC-2001; 2001WO-US48276.
                                                                                                             18-DEC-2000; 2000US-255882P.
24-APR-2001; 2001US-285691P.
                                                                                                                                                                       (GENE-) GENE LOGIC INC.
(PROC ) PROCTER & GAMBLE CO.
                                                                                                                                                                                                                                                                                             WPI; 2002-557663/59.
                                      27-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                  process
                                                                                                                                                                                                                                        'n
```

```
ö
                                                                                          Gaps
                                        Query Match
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0;
Sequence 7661 BP; 1707 A; 1826 C; 1815 G; 2311 T; 2 other;
```

2160 AAGTCTCTTCAAGGAGGCC 2141 2 AAAGTATCTTCAAGGACGCC 21 셤 Š

1727/c ABL13727 standard; cDNA; 557 BP. (first entry) 26-MAR-2002 ABL13727; RESULT 15 ABL13727, 

Drosophila melanogaster expressed polynucleotide SEQ ID NO 35663

Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ss.

Drosophila melanogaster.

WO200171042-A2

23-MAR-2001; 2001WO-US09231.

23-MAR-2000; 2000US-191637P. 11-JUL-2000; 2000US-0614150.

(PEKE ) PE CORP NY

Myers EW; Li PWD, Adams M, Venter JC,

Houghton A;

Jaiswal N, Einstein R,

New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell WPI; 2001-656860/75 P-PSDB; ABB69624

Claim 1; SEQ ID NO 35663; 21pp + Sequence Listing; English. interactions -

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences. The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and insectioides, theractions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins 

Sequence 557 BP; 135 A; 126 C; 139 G; 157 T; 0 other;

Gaps ö 78.1%; Score 16.4; DB 23; Length 557; 94.4%; Pred. No. 1.1e+02; ive 0; Mismatches 1; Indels 0; Best Local Similarity 94.4 Matches 17; Conservative Query Match

ö

177 AGTATCTTCAAGGACACC 160 4 AGTATCTTCAAGGACGCC 21 g ð

Search completed: April 18, 2003, 05:45:16 Job time : 97.5455 secs

us-09-270-437d-9.rnf

```
Sequence 347, App Sequence 175, App Sequence 175, App Sequence 13, Appli Sequence 2, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 31, Appli Sequence 31, Appli Sequence 31, Appli Sequence 34, Appli Sequence 34, Appli Sequence 34, Appli Sequence 34, Appli Sequence 37, Appli Sequence 1126, Appli Appli
                                                                                                                                                                                                                          April 18, 2003, 04:53:41; Search time 20.5227 Seconds (without alignments) 313.809 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seguence
GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/RDCTUS_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-643-597-347
US-09-643-597-347
US-09-661-709-4
US-08-288-663A-2
US-08-288-663A-2
US-08-288-663A-2
US-08-288-663A-3
US-08-36-051B-1
US-08-36-051B-1
US-08-36-051B-3
US-09-026-601-39
US-09-026-601-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  441362 segs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                             - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 gaaagtatcttcaaggacgcc 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                           US-09-270-437D-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 
                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
                                                                                                                                                 OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Result
```

```
ö
                                                                                                    9, Appli
4, Appli
14, Appli
14, Appli
1, Appli
1, Appli
1, Appli
1, Appli
1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                    Sequence
                                   Sequence
                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 21; DB 4; Length 1740; Best Local Similarity 100.0%; Pred. No. 0.061; Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 347, Application US/09643597

Sequence 347, Application US/09643597

GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Li, Samuel X.
APPLICANT: Hang, Aijun
APPLICANT: Henderson, Robert A.
AP
                         US-09-276-531-84

US-08-818-024-2

US-08-314-775A-2

US-09-347-798-9

US-08-36-64B-4

US-08-46-047B-4

US-09-10-398-14

US-09-36-14

US-09-36-14

US-08-801-263A-1

US-08-801-263A-1

US-08-801-263A-1

US-08-801-263A-1

US-09-102-248-1

US-09-102-248-1

US-09-102-248-1

US-09-102-248-1

US-09-102-248-1

US-09-102-248-1

US-09-102-248-1

US-09-103-248-1

US-09-218-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09061709B
Patent No. 6297364
GENERAL INFORMATION:
APPLICANT: Chen, Yao-Tseng
APPLICANT: Tsang, Solam
APPLICANT: Tsang, Solam
APPLICANT: Tsang, Solam
APPLICANT: Stockert, Elisabeth
APPLICANT: Muth, Alexander
APPLICANT: Old, Lloyd J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 GAAGTATCTTCAAGGACGCC 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAAAGTATCTTCAAGGACGCC 21
  733
1083
1498
1498
1654
2175
2175
2175
2175
11663
11663
11663
11663
11663
11663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
  US-09-643-597-347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-643-597-347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 347
LENGTH: 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-061-709-4
228
333
332
333
334
444
444
444
455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

```
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S
REGISTRATION NUMBER: 34,235
                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: unsure
LOCATION: (4088)
OTHER INFORMATION: n
NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                          IAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
US-08-288-663A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof File Reperence: LUD 5538
CURRENT APPLICATION NUMBER: US/09/061,709B
CURRENT FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Score 21; DB 4; Length 4159;
Best Local Similarity 100.0%; Pred. No. 0.072;
Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MCNeill, Patricia D.
FENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FENTION: AND DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 175, Application US/09643597
Patent No. 6426072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ION: (3549)
INFORMATION: n=A, T, C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ION: (3646)
INFORMATION: n=A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: unsure
LOCATION: (3506)
OTHER INFORMATION: n=A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (3520)
OTHER INFORMATION: n=A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ION: (3538)
INFORMATION: n=A, T, C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OCATION: (3502)
THER INFORMATION: n=A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bangur, Chaitanya S.
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
                                                                                                                                                                                                                                                                                                                                                                                    305 GAAAGTATCTTCAAGGACGCC 325
                                                                                                                                                                                                                                                                                                                                                                 1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATION: (3347)
HER INFORMATION: n=A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kalos, Michael D
                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-061-709-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITLE OF INVENTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Fas
SEQ ID NO 175
LENGTH: 4181
                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                         ઠે
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 21; DB 4; Length 4181; Best Local Similarity 100.0%; Pred. No. 0.072; Matches 21; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/08288663A
; Sequence 13, Application US/08288663A
; Patent No. 5879896
; GENERAL INFORMATION:
; APPLICANT: HINUMA, Shuji
APPLICANT: HONOYA, Masaki
APPLICANT: ONDA, Haruo
TITLE OF INVENTION: HUMAN TRH RECEPTOR, ITS PRODUCTION
TITLE OF INVENTION: AND USE
NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/288,663A
FILING DATE: 09-AUG-1994
PRIOR APPLICATION 435
PRIOR APPLICATION DATA:
APPLICATION VUMBER: 198309/1993
FILING DATE: 10-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 10-AUG-1993
APPLICATION NUMBER: 286986/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 325215/1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (4115); OTHER INFORMATION: n=A,T,C or GUS-09-643-597-175
                                                                                                                                                                                                                                              LOCATION: (4056)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                             LOCATION: (4062)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (4080)
OTHER INFORMATION: n=A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305 GAAAGTATCTTCAAGGACGCC 325
                                                                          NAME/KEY: unsure
LOCATION: (3974)
OTHER INFORMATION: n=A,T,C or G
                                                                                                                                                                                              DITHER INFORMATION: n=A, T, C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n=A, I, C or
NAME/KEY: unsure
LOCATION: (3968)
OTHER INFORMATION: n=A,T,C or
```

```
75.2%; Score 15.8; DB 2; Length 1194; 89.5%; Pred. No. 30;
                                                                            2; Indels
                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: HINUMA, Shuji
APPLICANT: HOSOYA, Masaki
APPLICANT: HOSOYA, Masaki
APPLICANT: ONDA, Haruo
TITLE OF INVENTION: HUMAN TRH RECEPTOR, ITS PRODUCTION
TITLE OF INVENTION: AND USE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZUP: 02.09
ZIP: 02.09
COMPUTER READABLE FORM:
MEDIUM TYPE: Disketer
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
CORRESTING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/28,663A
FILING DATE: 09-AUG-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: 198309/1993
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: 26966/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 325215/1993
FILING DATE: 22-DEC-1993
ATTORNEY, AGENT INPORMATION:
NAMME: REGALICKT NUMBER: 34,235
REGISTRATION NUMBER: 34,235
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44612
TELECOMMUNICATION INPORMATION:
TELERHONE: 617-523-3400
TELERHONE: 617-523-5440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 75.2%; Score 15.8; Dest Local Similarity 89.5%; Pred. No. 30; Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                             US-08-288-663A-3
; Sequence 3, Application US/08288663A
; Patent No. 5879896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 1, Application US/08045806
; Patent No. 5378822
                                                                                                                                                      769 ACAGTATCTTCAAGGAAGC 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       781. ACAGTATCTTCAAGGAAGC 799
                   Query Match
Best Local Similarity 89.5'
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INPORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1228 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 130 Wat
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-288-663A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
US-08-045-806-1
                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                      DB 2; Length 936;
                                                                                                                                                                                                                                                                                                                                                    Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: HINUMA, Shuji
APPLICANT: HOSOYA, Masaki
APPLICANT: HOSOYA, Masaki
APPLICANT: ONDA, Haruo
TITLE OF INVENTION: HUMAN TRH RECEPTOR, ITS PRODUCTION
TITLE OF INVENTION: AND USE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
STREET: 130 WALER Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONTESTUDENCE ADDRESSE:
ADDRESSE:
ADDRESSE:
DIRE, BRONSTEIN, ROBERTS & CUSMAN, STREET: 130 Water Street
CITY: Boston
STATE: MA
STATE: MA
COUNTRY: USA
ZIP: O2109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/288,663A
CLASSIPICATION NUMBER: 198309/1993
FILING DATE: 09-AUG-1993
APPLICATION NUMBER: 286986/1993
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: 286986/1993
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: 32-DEC-1993
APPLICATION NUMBER: 32-DEC-1993
APPLICATION NUMBER: 32-DEC-1993
APPLICATION NUMBER: 34,235
REGISTRATION NUMBER: 34,235
REGISTRATION NUMBER: 34,235
TELEPHONE: 617-523-3400
WHELEWALICATION NUMBER: 34,235
TELEPHONE: 617-523-5440
                                                                                                                                                                                                                                                                                          75.2%; Score 15.8; DF
89.5%; Pred. No. 29;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
US-08-288-663A-2
; Sequence 2, Application US/08288663A
; Sequence 2, Application US/08288663A
                   TELECOMMUNICATION INFORMATION
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                              781 ACAGTATCTTCAAGGAAGC 799
                                                                                                  INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 936 base paire
LYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                   2 AAAGTATCTTCAAGGACGC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1194 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                         , TOPOLOGY:
US-08-288-663A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-288-663A-2
                                                                                                                                                                                                                                                                                                                                                                                                                           윱
```

ö

Gaps

ö

```
GENERAL INFORMATION:
APPLICANT: Bradfield, Christopher Alan
APPLICANT: Dolard, Alan
APPLICANT: Poland, Alan
TITLE OF INVENTION: Ah Receptor cDNA and Method of
TITLE OF INVENTION: Determining Human Risks To Environmental Pollutants
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tilton, Fallon, Lungwus & Chestnut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 3207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSES: Tilton, Fallon, Lungwus & Chestnut ADDRESSES: Tilton, Fallon, Lungwus & Chestnut STREET: 100 South Wacker Drive, Suite 960
CITY: Chicago
STREET: 11linois
COUNTRY: USA
ZIP: 60666-4002
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
ATORNEY APPLICATION DATA:
APPLICATION NUMBER: US/08/045,806
FILING DATE: 19930408
CLASSIFICATION: 435
ATORNEY ADBATT INPORMATION:
NAME: FERIFERS SUSAN B.
REGISTRATION NUMBER: 31,327
REBERRENCE/DOCKET NUMBER: 31,327
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/366,051B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Tilton, Timothy L.
REGISTRATION NUMBER: UV-9207-CIP
REGISTRATION NUMBER: 04.926
REGISTRATION INFORMATION:
TELEFONDE: (312)-456-6000
TELEFAX: (312)-456-7776
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LEMGTH: 3207 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 15.4; DB
Pred. No. 60;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08045806
Patent No. 5378822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 94.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (312)-456-7776
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       711 AAAGTATCTTCATGGAC 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 AAAGTATCTTCAAGGAC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1..2415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: 1...?
US-08-366-051B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/0836051B
Sequence 1, Application US/0836051B
Patent No. 55620B
Patent No. 55620B
GENERAL INFORMATION:
APPLICANT: Dolwick, Kristin M.
APPLICANT: Carver, Lucy A.
TITLE OF INVENTION: Engineered Cells for Detecting Agonists to the Ah
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut
                                     APPLICANT: Bradfield, Christopher Alan
APPLICANT: Bradfield, Christin Marie
APPLICANT: Doland, Alan
APPLICANT: Poland, Alan
TITLE OF INVENTION: Alan
TITLE OF INVENTION: Determining Human Risks To Environmental Pollutants
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 3207,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SECTION NUMBER: US/08/045,806
FILING DATE: 19930408
CLASSIFICATION NUMBER: US/08/045,806
FILING DATE: 19930408
CLASSIFICATION NUMBER: NU-9207
REGISTATION NUMBER: NU-9207
REFERENCE/DOCKET NUMBER: NU-9207
TELEPRATION NUMBER: 31,327
REFERENCE/OMCTION INFORMATION:
TELEPRATION NUMBER: 31,327
REFERENCE (312) -456-8000
TELEPRAX: (312) -456-8000
TELEPRAY: USCALIO
STRANDBONESS: GOUDLE
TOPOLOGY: unknown
MOMECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3: Tilton, Fallon, Lungmus & Chestnut
100 South Wacker Drive, Suite 960
                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut
STREET: 100 South Wacker Drive, Suite 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          711 AAAGTATCTTCATGGAC 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AAAGTATCTTCAAGGAC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.3
Dest Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
1..2415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 100 South
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                      60606-4002
                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                             STATE: Illinc
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , NAME/KEY:
, LOCATION:
US-08-045-806-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
US-08-366-051B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
```

Gaps

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bradfield, Christopher A. APPLICANT: Bradfield, Christopher A. APPLICANT: Carver, Lucy A. APPLICANT: Carver, Lucy A. TITLE OF INVENTION: Ah Receptor CDNAs and Genetically TITLE OF INVENTION: Engineered Cells for Detecting Agonists to the Ah TITLE OF INVENTION: Receptor CORRESPONDENCE ADDRESS: 36 CORRESPONDENCE ADDRESS: ADDRESSE: Tilton, Fallon, Lungmus & Chestnut STREET: 100 South Wacker Drive, Suite 960 CITY: Chicago STATE: Illinois COUNTRY: USA.
                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                       ö
                                                                                                                                             Query Match 73.3%; Score 15.4; DB 1; Length 5261; Best Local Similarity 94.1%; Pred. No. 66; Matches 16; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 5261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Chicago
CITY: Chicago
COUNTRY: 111inois
COUNTRY: 112inois
COUNTRY: 128
ZIP: 60606-4002
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: 18M FC. Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/366,0518
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.3%; Score 15.4; D'
94.1%; Pred. No. 66;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Tilton, Timothy L.
REGISTRATION NUMBER: 16,926
REFERENCE/BOCKET NUMBER: 16,926
TELEPHONE: (312)-456-8000
TELEPAK: (312)-456-8000
TELEPAK: (312)-456-7776
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 5261 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDENESS: double
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08366051B Patent No. 5650283 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   Db 1111 AAAGTATCTTCATGGAC 1127
                                                                                                                                                                                                                                  2 AAAGTATCTTCAAGGAC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 94.1
Matches 16, Conservative
                                                                CDS
383..2927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) NAME/KEY: CDS
; LOCATION: 383.2927
US-08-366-0518-3
TOPOLOGY: unknown MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown MOLECULE TYPE: CDNA
                                                       NAME/KEY:

LOCATION:

US-08-045-806-3
                                                                                                                                                                                                                                                                                                                                  RESULT 10
US-08-366-051B-3
                                                                                                                                                                                                                               ઠે
```

1111 AAAGTATCTTCATGGAC 1127

RESULT 11

2 AAAGTATCTTCAAGGAC 18

```
Sequence 12. Action to 10.00000001

GENERAL INFORMATION:

MONETALY: Becaling the bolymera and Balley Fungal
TITLE OF INVESTION: Rathogene Using the Polymerae Chain Reaction
CORRESSENCE OF CASSESSION TRANSMILLS FORM:

ADDRESSES No. 5138680th Carolina
CORRITATION TRANSMILLS FORM:

ADDRESSES No. 5138680th Carolina
COMPITES IN PROPERTY OF THE POWART OF T
```

```
RESULT 13
US-09-026-601-31/C
US-09-026-601-31/C
Sequence 31, Application US/09026601
Sequence 31, Application US/09026601
Sequence 31, Application US/09026601
THORNATION: Beck, James J.
APPLICANT: Beck, James J.
TITLE OF INVENTION: Pathogens Using the Polymerase Chain Reaction TITLE OF INVENTION: Pathogens Using the Polymerase Chain Reaction NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS: 41
STREET: 3054 Cornwallis Road
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6358680th Carolina
COUNTRY: ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "5' end of large subunit
rRNA gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             end of small subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/026,601
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 209.365
OTHER INFORMATION: /note= "5.88 rRNA gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Medgey J. Timothy
NAME: Medgey J. Timothy
NAME: Medgey J. Timothy
NAME: Medgey J. Timothy
NEGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1984
TELEPATION FOR SEQ 19.541-8689
INFORMATION FOR SEQ 1D NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: mucleic acid
STRANDEDNESS: aingle
TOPOLOGY: linear
MOLGCULE TYPE: aingle
TOPOLOGY: linear
MOLGCULE TYPE: BNA (genomic)
ORIGINAL SOURCE:
ORIGINAL SOURCE:
INMUSTICLE TYPE: CONTRIBUTION CENTRAL SOURCE:
INMUSTICLE TYPE: CONTRIBUTION CENTRAL SOURCE:
CICLORE: 2-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: 31..208
OTHER INFORMATION: /note= "ITS1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 366..526
OTHER INFORMATION: /note= "ITS2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: 1..30
OTHER INFORMATION: /note= "3'
OTHER INFORMATION: rRNA gene"
                                                   515 GAAAGAAGCTTCATGGACGC 496
1 GAAAGTATCTTCAAGGACGC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 527. 579
CTHER INFORMATION:
CTHER INFORMATION:
US-09-026-601-31
         ð
                                                                                    US-09-026-601-30/C

Sequence 30, Application US/09026601

Patent NO. 635680

GENERAL INFORMATION:
Patent NO. 635680

GENERAL INFORMATION:
Patent NO. 635680

TITLE OF INVENTION: Pathogens Using the Polymerase Chain Reaction NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
COUNTRY: No. 635860artis Corporation
STREET: 3044 Cormallis Road
GITY: Research Triangle Park
STATE: No. 635860art Accolina
COUNTRY: USA
ZIP: No. 635860art Carolina
COUNTRY: USA
ZIP: No. 635860art Dealer Street Carolina
COUNTRY: USA
ZIP: No. 635860art Street Stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

72.4%; Score 15.2; DB 4; Length 579;
Best Local Similarity 85.0%; Pred. No. 54;
Matches 17; Conservative 0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "5' end of large subunit
rRNA gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 1.30
OTHER INFORMATION: /note= "3' end of small subunit
OTHER INFORMATION: rRNA gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: 209.365
OTHER INFORMATION: /note= "5.88 rRNA gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Pyrenophora tritici-repentis INDIVIDUAL ISOLATE: 6715
IMMEDIATE SOURCE: CLOME: 2 and 4 (consensus)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature

JOCATION: 366.526

LOCATION: 366.526

OTHER INFORMATION: /note= "ITS2"

PRATURE:

NAME/KEY: misc_feature

JOCATION: 527..579

OTHER INFORMATION: rRNA gene"

US-09-026-601-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 31..208
OTHER INFORMATION: /note= "ITS1"
                                                                          RESULT 12
US-09-026-601-30/c
```

Gaps

0

Gaps

```
RESULT 15
US-09-026-601-34/C
| Sequence 34, Application US/09026601
| Patent No. 6358680
| GENERAL INFORMATION:
| APPLICANT: Beck, James J. TITLE OF INVENTION: Detection of Wheat and Barley Fungal TITLE OF INVENTION: Pathogens Using the Polymerase Chain Reaction CORRESPONDENCE: 41
| CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: No. 65358680artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6358680th Carolina COUNTRY: USA
                                                                                                                                                                       0
                                                                                                                 Query Match 72.4%; Score 15.2; DB 4; Length 579; Best Local Similarity 85.0%; Pred. No. 54; Matches 17; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                       3; Indels
                             /note= "5' end of large subunit rRNA gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: 1.30
OTHER INFORMATION: /note= "3' end of small subunit
OTHER INFORMATION: rRNA gene"
NAME/KEY: misc feature
LOCATION: 31..208
LOCATION: 31..208
COTHER INFORMATION: /note= "ITS1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: 209.7365
OTHER INFORMATION: /note= "5.85 rRNA gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pyrenophora tritici-repentis
INDIVIDUAL ISOLATE: 44184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:

CLASSIFICATION:
ATTORNEY/AGENT INCORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFRENCE/DOCKET NUMBER: CGC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8689
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: mucleic acid
TYPE: mucleic acid
TYPE: mucleic acid
TYPE: mucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
366..526
                        ; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-026-601-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
CLONE: 3-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Beck, James J.
TITLE OF INVENTION: Detection of Wheat and Barley Fungal
TITLE OF INVENTION: Detection of Wheat and Barley Fungal
TITLE OF INVENTION: Pathogens Using the Polymerase Chain Reaction
CORRESPONDENCES: 41
CORRESPONDENCES: 41
CORRESPONDENCES:
ADDRESSER: No. 6358660artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STREET: No. 6358680th Carolina
COUNTRY: USA
ZIP: 21709
COUNTRY: USA
ZIP: EN PC Compatible
COMPUTER: ISM PC compatible
COMPUTER: PIOPPY disk
COMPUTER: PEADALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PEATANC SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENTING SYSTEM: US/09/026,601
FILICATION NUMBER: US/09/026,601
                                                                ö
Query Match 72.4%; Score 15.2; DB 4; Length 579; Best Local Similarity 85.0%; Pred. No. 54; Matches 17; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 end of small subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 209.365
OTHER INFORMATION: /note= "5.8S rRNA gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Medigs, J. Timothy
REGISTRATION NUMBER: 32,411
REFERENCE/DOCKET NUMBER: GC 1984
TELEPHONE: 919-541-8689
TELEPHONE: 919-541-8689
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORGANISM: PYFenophora tritici-repentis
INDIVIDUAL ISOLATE: DL22
IMMEDIATE SOURCE:
MOLECULE TYPE: DNA (GENOMIC)
                                                                                                                                                                                                        RESULT 14
US-09-026-601-32/c
// Sequence 32, Application US/09026601
// Patent No. 6358680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 366..526
OTHER INFORMATION: /note= "ITS2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: misc feature
LOCATION: 31..208
OTHER INFORMATION: /note= "ITS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: 1.30
OTHER INFORMATION: /note= "3'
OTHER INFORMATION: rRNA gene"
                                                                                                                                          515 GAAAGAAGCTTCATGGACGC 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
527..579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
                                                                                             ઠે
```

```
CTHER INFORMATION: /note= "ITS2"

FEATURE:

NAME/KEY: misc_feature

CCATION: 527..579

COTHER INFORMATION: FRNA gene"

US-09-026-601-34

Query Match
Best Local Similarity 85.0%; Pred. No. 54;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps

QY 1 GAAAGTATCTTCAAGGACGC 20

QY 1 GAAAGTATCTTCAAGGACGC 496

DD 515 GAAAGACTTCATGAGGACGC 496
```

Search completed: April 18, 2003, 07:34:12 Job time : 25.5227 secs

ö

us-09-270-437d-9.rnpb

```
15.4
115.4
115.2
115.2
115.2
115.2
115.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 347, App
Sequence 447, App
Sequence 450, App
Sequence 428, App
Sequence 428, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Appliseduence 175, Appliseduence 175, Appliseduence 175, Appliseduence 175, Appliseduence 175, Appliseduence 1856, Appliseduence 1856, Appliseduence 1857, Appliseduence 662, Appliseduence 662
                                                                                                                                                                                                April 18, 2003, 06:35:31; Search time 87.1818 Seconds (without alignments) 241.975 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 797, Ap
Sequence 1678,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 347,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NBW PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USO6_NBW PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/USO6_NBW PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/USO6_NBW PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/USO8_NBW PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/USO8_NBW PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/USO8_NBW PUB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USO9_NBW PUB.seq:*

10: /cgn2_6/ptodata/1/pubpna/USO9_NBW PUB.seq:*

11: /cgn2_6/ptodata/1/pubpna/USO9_NBW PUB.seq:*

12: /cgn2_6/ptodata/1/pubpna/USO9_NBW PUB.seq:*

12: /cgn2_6/ptodata/1/pubpna/USO9_NBW PUB.seq:*

13: /cgn2_6/ptodata/1/pubpna/USO9_NBW PUB.seq:*

14: /cgn2_6/ptodata/1/pubpna/USO0_NBW PUB.seq:*
GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-735-705-347
US-09-850-716A-347
US-09-897-778-347
US-09-897-778-447
US-09-897-778-450
US-09-897-778-428
US-09-897-778-428
US-09-897-778-428
US-09-954-456-715
US-09-954-456-715
US-09-954-456-715
US-09-86-778-175
US-09-86-771-2958
US-09-86-771-1856
US-09-880-175-175
US-09-86-761-12958
US-09-86-761-12958
US-09-86-761-1227
US-09-880-1727
US-09-880-1727
US-09-880-1727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-764-864-1678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                639749 seqs, 502280978 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                        OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                      1 gaaagtatcttcaaggacgcc 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                               US-09-270-437D-9
21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
                                                                                                                                                                                                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database:
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                       Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
```

```
Sequence 1, Appli
Sequence 4800, Ap
Sequence 527, App
Sequence 215, App
Sequence 115, App
Sequence 115, App
Sequence 1020, Ap
Sequence 1020, Ap
Sequence 1120, Ap
Sequence 113, Appli
Sequence 113, Appli
Sequence 113, Appli
Sequence 394, App
Sequence 602, App
Sequence 602, App
Sequence 602, App
Sequence 9819, Ap
Sequence 9819, Ap
Sequence 9819, Ap
Sequence 2009, App
Sequence 2004, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1624, Ap
9 US-10-067-514-1

O US-09-14800

US-09-170-14900

US-09-170-149-134

US-10-044-090-527

US-10-042-111-36

US-10-042-111-36

US-10-09-15-1020

US-10-09-15-1020

US-09-933-797-113

US-09-933-797-113

US-09-933-797-1161

US-09-9864-761-1651

US-09-9864-761-2009

US-09-986-596-802

US-09-986-596-802

US-09-986-596-802

US-09-986-596-802

US-09-986-596-802

US-09-998-596-802

US-09-998-596-802

US-09-998-596-802

US-09-998-596-802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-09-949-192-14
US-10-098-841-292
US-08-781-986A-67
US-10-092-154-1624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
```

```
Gapa
                                                                    APPLICANT: Fan, Liqua
APPLICANT: Fan, Liqua
APPLICANT: Ralos, Michael D.
APPLICANT: Bangar, Gary
APPLICANT: Bangar, Gary
APPLICANT: Fangar, Gary
APPLICANT: Fangar, Gary R.
APPLICANT: Gary
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Mang, Aijun
APPLICANT: McNeill, Patricia D.
APPLICANT: Fangar, Neil
APPLICANT: Fangar, Neil
TILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
FILLE REFERENCE: 210121.455C14
CURRENT FILLNG DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SEQ ID NO 347
LENGTH: 1740

LENGTH: 1740

LENGTH: 1740

LENGTH: 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 21; DB 10; Length 1740;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 21; Conservative 0; Mismatches 0; Indels 0
Sequence 347, Application US/09735705
Patent No. US20020052329A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
CRGANISM: Homo sapiens
US-09-735-705-347
```

55 GAAGTATCTTCAAGGACGCC 75

ö

RESULT 2 US-09-850-716A-347 ; Sequence 347, Application US/09850716A

Gaps

Indels

ò g

```
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Marnerakis, Margarita
APPLICANT: Marnerakis, Thomas S.
APPLICANT: Panger, Thomas S.
APPLICANT: Garty R.
APPLICANT: Garty R.
APPLICANT: Matanabe, Yoshihiro
APPLICANT: Matanabe, Yoshihiro
APPLICANT: Penger, Nebert A.
APPLICANT: Penger, Nebert A.
APPLICANT: Penger, Nebert A.
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 21012.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: PRESECT OF WINDOWS Version 4.0
SOFTWARE: PASSECT OF WINDOWS VERSION 4.0
SSED ID NO 450:
LEMMETH A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 21; DB 10; Length 1743; ilarity 100.0%; Pred. No. 0.28; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      Score 21; DB 10; Length 1743;
Pred. No. 0.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-850-716A-428
US-09-850-716A-428
Sequence 428, Application US/09850716A
PATENT ON US200020115139A1
GENERAL INFORMATION:
APPLICANT: AAlos, Michael D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER; FILE REFRENCE: 210121.455C15
                                                      TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 450, Application US/09897778
Patent No. US20020147143A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ss daladratchrcalddacdcc 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21
                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAAAGTATCTTCAAGGACGCC 21
  Henderson, Robert A. Peckham, David W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
CORGANISM: Homo sapiens
US-09-897-778-450
                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CRGANISM: Homo sapiens
US-09-897-778-447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 21; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                   APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: McNeill, Patricia D.
APPLICANT: Retter, Mac W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF DATE: 210121.455015
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT APPLICATION NUMBER: 010-05-07
NUMBER OF SEQ ID NOS: 4400
SOFTWARE: PASKEG for Windows Version 3.0
SOFTWARE: PASKEG for Windows Version 3.0
TENTION 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 21; DB 10; Length 1740; Best Local Similarity 100.0%; Pred. No. 0.28; Matches 21; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10; Length 1740; 0.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Peckham, David W.
APPLICANT: Fanger, Neil
TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TILLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFREENCE: 210.121.455Clg 8997,778
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILLING DATE: 201-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 347
LENGTH: 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%; Pred. No. (
Matches 21; Conservative 0; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 447, Application US/09897778
Patent No. US20020147143A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 347, Application US/09897778
Patent No. US20020147143A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wang, Tongtong
APPLICANT: Warnerakis, Margarita
APPLICANT: Panger, Gary R.
APPLICANT: Panger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wang, Tongtong
APPLICANT: Marnerakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 gaaagrarctrcaaggacgcc 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Watanabe, Yoshihiro
Henderson, Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAAAGTATCTTCAAGGACGCC 21
Patent No. US20020115139A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
US-09-897-778-347
                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
CRGANISM: Homo sapiens
US-09-850-716A-347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-897-778-347
                                                                                                                                                                                                                                                                                                                                                    1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
```

ö

ö

g ઠે

```
LOCATION: (3940)
OTHER INFORMATION:
NAME/KEY: ungure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: unsure
                                                                                                                                                                           ; FEATURE:
US-09-899-651-4
                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Glen, Yao-Teeng
APPLICANT: Gure, Ali
APPLICANT: Gure, Ali
APPLICANT: Gure, Ali
APPLICANT: Tang, Solam
APPLICANT: Jager, Elke
APPLICANT: Mackert, Elke
APPLICANT: Mackert, Elke
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: Associated
TITLE OF INVENTION: Associated
TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
FILE REFERENCE: LUD 5538
CURRENT APPLICATION NUMBER: US/09/899,651
CURRENT FILING DATE: 2001-07-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: MUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEG ID NOS: 467
SOFTWARE: FastSEQ for Windows Version 4.0
SEC ID NO 428
LENGTH: 1764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                   Query Match
100.0%; Score 21; DB 10; Length 1764;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 21; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 21; DB 10; Length 1764;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 21; Conservative 0; Mismatches 0; Indels 0
CURRENT APPLICATION NUMBER: US/09/850,716A CURRENT FILING DATE: 2001-05-07 NUMBER OF SEQ ID NOS: 440 SPOTYMARE: FastSEQ for Windows Version 3.0 SEQ ID NO 428 LENGTH: 1764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 428, Application US/09897778
Patent No. US20020147143A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 4, Application US/09899651; Patent No. US20020111470A1; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                             1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                      76 GAAAGTATCTTCAAGGACGCC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 GAAGTATCTTCAAGGACGCC 96
                                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-850-716A-428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
COGANISM: Homo sapiens
US-09-897-778-428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-899-651-4
                                                                                                                                                                                                                                                                                                                                ઠ
                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
```

```
ö
                                                                                                                                                                                                                                                  Gapa
                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 21; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REPERENCE: 210.21.455C14 CURRENT APPLICATION NUMBER: US/09/735,705 CURRENT FILING DATE: 2000-12-12 NUMBER OF SEQ ID NOS: 419 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 175 LENGTH: 4181
PRIOR APPLICATION NUMBER: US/09/061,709
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 4
LENGTH: 4159
                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 175, Application US/09735705; Patent No. US20020052329A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
FEATURE:
FOOTION: (3347)
OTHER INFORMATION: n=A,T,C or G
LOCATION: (3502)
OTHER INFORMATION: n=A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang, Aijun
Skeiky, Yasir A.W.
Henderson, Robert A.
McNeill, Patricia D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang, Tongtong
Fan, Liqun
Kalos, Michael D.
Bangur, Chaitanya S.
Hosken, Wancy
Fanger, Gary R.
Li, Samuel X.
                                                                                                                                                                                                                                                                                                                     305 GAAAGTATCTTCAAGGACGCC 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (3549)
OTHER INFORMATION: n=A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (3646)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           n=A, T, C or G
                                                                                                                                                                                                                                                                                  1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (3538)
OTHER INFORMATION: n=A,T,C or NAME/KEY: ungure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (3520)
OTHER INFORMATION: n=A,T,C or
                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: uneure
LOCATION: (3506)
OTHER INFORMATION: n
NAME/KEY: uneure
```

```
Gaps
                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                        RESULT 11
US-09-850-716A-175
Squence 175, Application US/09850716A
Squence 175, Application US/09850716A
Squence 175, Application US/09850716A
SPECIAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF LUNG CANCER
TITLE REFERENCE: 210121.455015
FILE REFERENCE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARRE: FastSEQ for Windows Version 3.0
SSOFTWARE: FastSEQ for Windows Version 3.0
                                                                             Query Match
100.0%; Score 21; DB 10; Length 4181;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 21; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME, KEY: unBure
LOCATION: (3347)
OTHER INPORMATION: n=A,T,C or G
NAME, KEY: unBure
LOCATION: (3502)
OTHER INFORMATION: n=A,T,C or G
NAME, KEY: unBure
LOCATION: (3506)
OTHER INFORMATION: n=A,T,C or G
NAME, KEY: unBure
LOCATION: (3520)
OTHER INFORMATION: n=A,T,C or G
NAME, KEY: unBure
LOCATION: (3520)
OTHER INFORMATION: n=A,T,C or G
NAME, KEY: unBure
LOCATION: (3539)
OTHER INFORMATION: n=A,T,C or G
OTHER INFORMATION: 0539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HER INFORMATION: n=A, T, C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: unsure
LOCATION: (3549)
OCTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3646)
OCTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         n=A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            n=A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 n=A, T, C or G
                                                                                                                                                                                                                                                                    305 gadagrarcricaaggacgcc 325

// OTHER INFORMATION: n=a,t,g or c
US-09-954-456-715
                                                                                                                                                                                                            1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     n=A, T, C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       n=A, T, C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 n=A, T, C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (3940)
OTHER INFORMATION: n
NAME/KEY: unsure
LOCATION: (3968)
OTHER INFORMATION: n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: unsure
LOCATION: (4056)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (4036)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (3974)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: unsure
LOCATION: (3974)
                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
US-09-054-456-715
Sequence 715, Application US/09954456
Sequence 715, Application US/09954456
Sequence 715, Application US/09954456
Sequence 715, Application US/09954456
SEQUENCE 71 PROCESSE FOR THE P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10; Length 4181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 21;
illarity 100.0%; Pred. No. (
Conservative 0; Mismatche
                                                                                                                                                                                                                                                                                       LOCATION: (4056)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: ungure
LOCATION: (4062)
OTHER INFORMATION: n=A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: unsure
LOCATION: (4080)
OTHER INFORMATION: n=A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (4115)
, OTHER INFORMATION: n=A,T,C or G
US-09-735-705-175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: n=A,T,C or G NAME/KEY: unsure
                                                                                                                                                                                                      COCATION: (4036)

THER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         305 GAAAGTATCTTCAAGGACGCC 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                              n=A, T, C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 21; Conserv
                        LOCATION: (3968)
OTHER INFORMATION:
NAME/KEY: unsure
                                                                                                                  OCATION: (3974)
THER INFORMATION:
NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: unsure
LOCATION: (4088)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
```

```
Gape
                                                                            PRIOR PLICATION NUMBER: 10 60/207,456
PRIOR PRICATION NUMBER: 10 60/523,366
PRIOR PRICATION NUMBER: 10 90/523,366
PRIOR PLICATION NUMBER: 2000-00-03
PRIOR PLICATION NUMBER: 2000-10-04
PRIOR PLICATION NUMBER: 2000-10-04
PRIOR PLICATION NUMBER: PCT/US01/00667
PRIOR PLICATION NUMBER: PCT/US01/00667
PRIOR PLICATION NUMBER: PCT/US01/00667
PRIOR PLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PLICATION NUMBER: PCT/US01/00667
PRIOR PLICATION NUMBER: PCT/US01/00667
PRIOR PLICATION NUMBER: PCT/US01/00667
PRIOR PLICATION NUMBER: PCT/US01/00668
PRIOR PLICATION NUMBER: PCT/US01/00661
PRIOR PLICATION: EXPRESSED IN HELA: SIGNAL = 1.5
PURBER: INFORMATION: EXPRESSED IN HELA: SIGNAL = 1.5
PURBER: INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
PURBER: INFORMATION: PRIOR EXPRESSED IN HEART, SIGNAL = 1.5
PURBER: INFORMATION: PRIOR EXPRESSED IN HEART, SIGNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10; Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.1%; Score 16.2;
85.7%; Pred. No. 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 1856, Application US/09864761; Patent No. US20020048763A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              279 GAAAGCCTCTTCAAGGAAGCC 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-864-761-1856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Simi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
US-09-864-761-23958/c
US-09-864-761-23958/c
Sequence 23958, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
ITILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature

i LOCATION: 3347, 3502, 3506, 3520, 3538, 3549, 3646, 3940, 3968, 3974,

i LOCATION: 4036, 4056, 4062, 4080, 4088, 4115

i OTHER INFORMATION: n = A,T,C or G

US-09-897-778-175
                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                  DB 10; Length 4181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 21; DB 10; Length 4181; Best Local Similarity 100.0%; Pred. No. 0.32; Matches 21; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Watenabe, Yoshihiro
APPLICANT: Watenabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
APPLICANT: Peckham, David W.
APPLICANT: Panger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPRESENCE: 210121.455C16
CURRENT APPLICATION UNMERS: US/09/897,778
CURRENT PILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
                                                                                                                                                                                                                                                                   . 0.32;
-heg 0; Indels
                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                         Query Match
100.0%; Score 21;
Best Local Similarity 100.0%; Pred. No. (
Matches 21; Conservative 0; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 175, Application US/09897778
Patent No. US20020147143A1
GENERAL INFORMATION:
                      ; NAME/KEY: unBure
; LOCATION: (4088)
; OTHER INFORMATION: n=A,T,C or G
; LOCATION: (4115)
; OTHER INFORMATION: n=A,T,C or G
US-09-850-716A-175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, Tongtong
APPLICANT: Marnerakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                         305 GAAAGTATCTTCAAGGACGCC 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305 GAAAGTATCTTCAAGGACGCC 325
                                                                                                                                                                                                                                                                                                                                                        1 GAAAGTATCTTCAAGGACGCC 21
  n=A, T, C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-09-897-778-175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 R49047
US-09-880-107-2877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 479;
                                                                                                            APPLICANT: Scherf, Uwe APPLICANT: Scherf, Uwe Logic, Inc. TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer FILE REFERENCE: 44921-5028-000 CURRENT APPLICATION NUMBER: US/09/880,107 CURRENT FILING DATE: 2001-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 77.1%; Score 16.2; DB 10; Best Local Similarity 85.7%; Pred. No. 69; Matches 18; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR APPLICATION NUMBER: US 60/237,054
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: April 18, 2003, 10:13:04 Job time : 92.3485 secs
Sequence 2877, Application US/09880107
Patent No. US20020142981A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223 gaadgaacricaadgaagcc 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                      Vockley, Joseph G.
Scherf, Uwe
                                                      GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                   EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.1%; Score 16.2; DB 10; Length 476; 85.7%; Pred. No. 68; 3; Indels 0; ive 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLACENTA, SIGNAL = 1.6
HELA, SIGNAL = 1.6
HELA, SIGNAL = 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BONE MARROW, SIGNAL
BT474, SIGNAL = 2.1
FETAL LIVER, SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 09/7/4,203
PRIOR FILING DATE: 2001-01-29
WHEBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 1856
                APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HBL100, SIGNAL
                                                                                                                                                                                             PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-06
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/236,356
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                                                                                                                                                                          ILING DATE: 2000-09-27
PPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US01/00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G DATE: 2000-06-30
CATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION:
INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTHER INFORMATION:
COTHER INFORMATION:
US-09-864-761-1856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THER
```

셤 ò

Query Match 77.1 Best Local Similarity 85.7 Matches 18; Conservative

.. 0

Gaps

Run on:

```
April 18, 2003, 05:48:17; Search time 1155.95 Seconds (without alignments) 456.759 Million cell updates/sec
                                                                                                                                                                                                                                    GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                               24791104 segs, 12571243825 residues
                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                - nucleic search, using sw model
                                                                                                      1 gaaagtatcttcaaggacgcc 21
                                                                                                                      IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cgn2_6/ptodata/1/
                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                 US-09-270-437D-9
21
                                                                                            Perfect score:
                                                                                                                       Scoring table:
                                OM nucleic
                                                                                                                                                                                                                                              Database :
                                                                                                      Seguence:
                                                                                                                                                Searched:
```

```
/cgn2_6/ptodata/1/pna/US6000_COMB.seq:*
cgn2_6/ptodata/1/pna/US6001_COMB.seq:*
cgn2_6/ptodata/1/pna/US6001_COMB.seq:*
cgn2_6/ptodata/1/pna/US6003_COMB.seq:*
cgn2_6/ptodata/1/pna/US6004_COMB.seq:*
cgn2_6/ptodata/1/pna/US6005_COMB.seq:*
cgn2_6/ptodata/1/pna/US6005_COMB.seq:*
cgn2_6/ptodata/1/pna/US6005_COMB.seq:*
cgn2_6/ptodata/1/pna/US6001_COMB.seq:*
cgn2_6/ptodata/1/pna/US6012_COMB.seq:*
cgn2_6/ptodata/1/pna/US6012_COMB.seq:*
cgn2_6/ptodata/1/pna/US6012_COMB.seq:*
cgn2_6/ptodata/1/pna/US6012_COMB.seq:*
cgn2_6/ptodata/1/pna/US6013_COMB.seq:*
cgn2_6/ptodata/1/pna/US6023_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "G'ptodata/1/pha/US6019_COMB.seq:"
"G'ptodata/1/pha/US6010_COMB.seq:"
"G'ptodata/1/pha/US6010_COMB.seq:"
"G'ptodata/1/pha/US6011_COMB.seq:"
"G'ptodata/1/pha/US6012_COMB.seq:"
"G'ptodata/1/pha/US6013_COMB.seq:"
"G'ptodata/1/pha/US6014_COMB.seq:"
"G'ptodata/1/pha/US6016_COMB.seq:"
"G'ptodata/1/pha/US6016_COMB.seq:"
"G'ptodata/1/pha/US6012_COMB.seq:"
"G'ptodata/1/pha/US6012_COMB.seq:"
"G'ptodata/1/pha/US6022_COMB.seq:"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cgn2_6 / prodate 1 / pna / US8024_COMB.seq:*

Cgn2_6 / prodate 1 / pna / US8025_COMB.seq:*

Cgn2_6 / prodate 1 / pna / US8020_COMB.seq:*

Cgn2_6 / prodate 1 / pna / US8030_COMB.seq:*

Cgn2_6 / prodate 1 / pna / US8031_COMB.seq:*

Cgn2_6 / prodate 1 / pna / US8031_COMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Semience 13091 b			•	, מ נים נים נים				747	Semience 347 App			Semionos 247, Apr		מקע יידנ סטונסידסט	ממש יידר המונים מים מים מים מים מים מים מים מים מים מ	Sednence 347, App	Sequence 347, App	347	247	7	Sequence 347, App	Sequence 347, App	
ID	US-09-271-490-13091	US-09-925-552-13091	US-10-032-354-13091	US-09-287-618-27259	US-09-399-932-638	US-09-652-123-4489	US-09-652-123-8442	US-09-399-932-4493	PCT-US01-47576-347	US-09-542-615A-347	US-09-606-421A-347	US-09-606-421B-347	US-09-630-940A-347	US-09-630-940B-347	US-09-662-786-347	118-09-698-347	/ FC - DCD - CD - CD - CD	US-09-735-705-347	US-09-850-716-347	US-09-850-716A-347	110 000 000 011	08-09-89/-/8-34/	US-10-007-700-347	
DB DB	16	34	38	16	17	25	25	17	н	21	23	23	24	24	56	5		2	32	32		2	38	
Query Match Length DB	422	422	422	438	529	556	834	843	1740	1740	1740	1740	1740	1740	1740	1740		1740	1740	1740	1740	7	1740	
Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0		0.00	100.0	100.0	100		700.0	
Score	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21		77	21	21	נכ	1 7	77	
Result No.	1	~	m	4	ß	φ.	7	80	6	10	11	12	13	14	15	16	1.7	ì :	81	13	20	ì	17	

```
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: Homo sapiens
US-09-287-618-27259
                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-287-618-27259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
US-10-032-354-13091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 27259
LENGTH: 438
                                       SEQ ID NO 13091
LENGTH: 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
          Sequence 447, App Sequence 478, App Sequence 477, App Sequence 447, App Sequence 447, App Sequence 447, App Sequence 450, App Sequence 450, App Sequence 450, App Sequence 428, App Sequence 4, App Se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 175, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 21; DB 16; Length 422; 100.0%; Pred. No. 3.9; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
US-09-925-552-13091
US-09-925-552-13091
| Sequence 13091, Application US/09925552
| GENERAL INFORMATION:
| APPLICANT: Hyveq, Inc.
| TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
| TITLE OF INVENTION: FROM VARIOUS CDNA LIERARIES
| TITLE OF INVENTION: FROM VARIOUS CDNA LIERARIES
| TITLE OF INVENTION: SOULT OF STATE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1301, Application US/09271490
; GENERAL INFORMATION:
APPLICANT: Hyeeq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: NOW VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-767
CURRENT PFLICATION NUMBER: US/09/271,490
CURRENT FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 19424
SOFTHARE: PESELSEQ for Windows Version 3.0
: SEQ ID NO 13091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-466-396A-175
US-09-476-496A-175
US-09-480-884A-175
US-09-510-376A-175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -10-117-982-428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -US01-47576-175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -897-778-428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature; LOCATION: (1)...(422); OTHER INFORMATION: n = A,T,C or GUS-09-271-490-13091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369 GAAAGTATCTTCAAGGACGCC 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.º
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                            1000.0
1000.0
1000.0
1000.0
1000.0
                                                                                                                                                                                                                                                                                                                                                                                                                  100.0
                                              TYPE: DNA
                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
ö
                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 21; DB 16; Length 438; Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 38; Length 422; 3.9;
                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INVOKENTION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 2041.767
CURRENT APPLICATION NUMBER: US/10/032,354
CURRENT FILING DATE: 1999-03-18
NUMBER: OF SEQ ID NOS: 1999-03-18
NUMBER: OF SEQ ID NOS: 19424
SEQ ID NO 13091
LENGTH: 422
TYPE: DNA
ORGANISM: Homo sapiens
FRATURE:
FRATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(422)
COTHER INFORMATION: n = A,T,C or G
                                                                                                       Length 422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 27259, Application US/09287618

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-768
CURRENT APPLICATION NUMBER: US/09/287, 618
CURRENT FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 35865
SOFTWARE: PRECED FOR Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                  0; Indels
                                                                                                    Query Match
100.0%; Score 21; DB 34;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 21; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. 3
Matches 21; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                         Sequence 13091, Application US/10032354 GENERAL INFORMATION:
NAME/KEY: misc_feature

// LOCATION: (1)...(422)

// OTHER INFORMATION: n = A,T,C or G

US-09-925-552-13091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               369 GAAAGTATCTTCAAGGACGCC 389
                                                                                                                                                                                                                          369 GAAAGTATCTTCAAGGACGCC 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                               1 GAAAGTATCTTCAAGGACGCC 21
```

```
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REPERENCE: 1600.1186-001.
CURRENT APPLICATION NUMBER: 05/052,123
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,135
PRIOR PLING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 9796
SOFTWARE: PASESEQ for Windows Version 4.0
IENGTH: 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

JAPPLICANT: Holtzman, Douglas A.

APPLICANT: Gearing, David P.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A TITLE OF INVENTION: HUMAN BURKITT'S LYMPHOWA LIBRARY FILE REFERENCE: MIN98-47pM

CURRENT APPLICATION NUMBER: US/09/399,932

CURRENT APPLICATION NUMBER: 60/100,464

PRIOR FILING DATE: 1998-09-15

PRIOR FILING DATE: 1998-09-15

PRIOR FILING DATE: 1998-09-24

PRIOR FILING DATE: 1998-09-24

PRIOR FILING DATE: 1999-09-30

PRIOR FILING DATE: 1999-09-30

PRIOR FILING DATE: 1999-09-30

PRIOR FILING DATE: 1999-09-30

PRIOR FILING DATE: 1999-07-30

PRIOR FILING DATE: 1999-07-16

NUMBER: 60/144,447

PRIOR FILING DATE: 1999-07-16

NUMBER: FERENCE FEREN
                                                                                                    100.0%; Score 21; DB 25; Length 556; 100.0%; Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 21; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-652-123-8442
; Sequence 8442, Application US/09652123
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:

NAME/KEY: misc feature

LOCATION: (1)...(834)

OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                              409 GAAAGTATCTTCAAGGACGCC 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.(
Matches 21; Conservative
                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
                                                                                               Query Match
Best Local Similarity
Matches 21; Conserv
         US-09-652-123-4489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: Holtzman, Douglas A.

APPLICANT: Holtzman, Douglas A.

APPLICANT: Holtzman, Douglas A.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A TITLE OF INVENTION: HUMAN BURKITY'S LYMPHOMA LIBRARY

FILE REFERENCE: MIN98-47pM

CURRENT APPLICATION NUMBER: 60/100,464

PRIOR APPLICATION NUMBER: 60/100,464

PRIOR PILING DATE: 1998-09-15

PRIOR PILING DATE: 1998-09-24

PRIOR PRILOR DATE: 1998-10-20

PRIOR APPLICATION NUMBER: 60/106,456

PRIOR PILING DATE: 1999-10-30

PRIOR PILING DATE: 1999-10-30

PRIOR PILING DATE: 1999-03-30

PRIOR PILING DATE: 1999-04-30

PRIOR PILING DATE: 1999-04-30

PRIOR PILING DATE: 1999-07-16

NUMBER OF SEC ID NOS: 5743

SOCTWARE: FABSCEQ for Windows Version 3.0

LENGTH: 529

***CONTACT ON NOTE OF THE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 21; DB 17; Length 529;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: HEREROR
FILE REPERBNCE: 1600.1186-001
CURRENT APPLICATION NUMBER: US/09/652,123
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,135
PRIOR PILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 9796
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4499
LENGTH: 556
         0; Indels
    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
US-09-652-123-4489
'Sequence 4489, Application US/09652123
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 638, Application US/09399932; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , LUCATION: (1)...(529)
; OTHER INFORMATION: n = A,T,C or G
US-09-399-932-638
                                                                                                                                   388 GAAAGTATCTTCAAGGACGCC 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (1)...(556)
OTHER INFORMATION: n = A,T,C
21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
Matchea
                                                                                                                                                                   ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        쉽
```

```
Application US/09606421B
                                                                                                                                                                                                                                                                                                                                Sequence 347, Application US/09606421A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bangur, Chaitanya S.
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 GAAAGTATCTTCAAGGACGCC 75
                                                                                                                                                                                      1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                 Wang, Tongtong
Fan, Liqun
                 TYPE: DNA
CORGANISM: Homo sapiens
US-09-542-615A-347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
CRGANISM: Homo sapiens
US-09-606-421A-347
LENGIH: 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠ
                                                                                                                                                                                          ð
                                                                                                                                                                                                                                g
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 1740;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 21; Conservative 0; Mismatches 0; Indels
                                        Length 843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cai, Feng
APPLICANT: Cai, Feng
APPLICANT: Foy, Teresa M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPREBNCE: 210121.45503PC
CURRENT APPLICATION UNMBER: PCT/US01/47576
CURRENT PILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 469
SOFTWARE: PSESSEQ for Windows Version 4.0
LENGTH: 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
                                        Query Match
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 21; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                 Application PC/TUS0147576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 347, Application US/09542615A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Durham, Margarita
Fanger, Gary R.
Vedvick, Thomas S.
Carter, Darrick
Watanabe, Yoshihiro
Peckman, David W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      cNeill, Patricia D. anger, Neil
                                                                                                                                                                        388 GAAAGTATCTTCAAGGACGCC 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 GAAGTATCTTCAAGGACGCC 75
                                                                                                                                                                                                                                                                                                                                                                                          keiky, Yasir A.W.
i, Samual X.
                                                                                                                                                                                                                                                                                                                       Corixa Corporation
Wang, Tongtong
Wang, Aijun
                                                                                                                                                                                                                                                                                                                                                                                                                                  Kalos, Michael D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      etter, Marc W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
PCT-US01-47576-347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang, Tonger
Fan, Liqun
        US-09-399-932-4493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

```
Gaps
                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 21; DB 23; Length 1740; Best Local Similarity 100.0%; Pred. No. 5.2; Matches 21; Conservative 0; Mismatches 0; Indels 0;
DB 21; Length 1740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421A
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 354
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 347
LENGTH: 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ID METHODS FOR THE THERAPY OF LUNG CANCER
                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CA.
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 347
Query Match 100.0%; Score 21; Best Local Similarity 100:0%; Pred. No. Matches 21; Conservative 0; Mismatch
```

```
Wang, Tongtong
Fan, Liqun
              ; ORGANISM: Homo sapiens
US-09-630-940B-347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
CORGANISM: Homo Bapiens
US-09-662-786-347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang, Aijun
                                                                                                                                                                                                                                                                         JS-09-662-786-347
                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                         Score 21; DB 23; Length 1740;
Pred. No. 5.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 24; Length 1740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MCNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: 210121.455C10
CURRENT APPLICATION NUMBER: US/09/630,940A
CURRENT FILING DATE: 2000-08-02
NUMBER OF SEQ ID NOS: 367
SOFTWARE: PRELSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Particia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPERENCE: 210121.455C10
CURRENT APPLICATION NUMBER: US/09/630,940B
CURRENT FILING DATE: 2000-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .2;
a 0; Indels
                                                                                     Indels
                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 21;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 367
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                            Sequence 347, Application US/09630940A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 347, Application US/09630940B
                                                                                   ö
                                                                                                                                                                                                                                                                                                                                      Kalos, Michael D.
Bangur, Chaitanya S.
Hosken, Nancy
Panger, Gary R.
Li, Samuel X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bangur, Chaitanya S.
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
                                   Query Match
Best Local Similarity 100.0%;
Matches 21, Conservative 0,
                                                                                                                                                  55 GAAGTATCTTCAAGGACGCC 75
                                                                                                                  1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Henderson, Robert A
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Skeiky, Yasir A.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang, Aijun
Skeiky, Yasir A.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kalos, Michael D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-630-940A-347
US-09-606-421B-347
                                                                                                                                                                                                                                     US-09-630-940A-347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-09-630-940B-347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT
                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
    DB 24; Length 1740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MCNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121, 4855C12
                                            0; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 26;
                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/662,786
CURRENT FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 381
SSOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 100.0%; Pred. No. 5
Matches 21; Conservative 0; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: April 18, 2003, 09:35:40 Job time : 1159.95 secs
                                                                                                                                                                                                                             Sequence 347, Application US/09662786 GENERAL INFORMATION:
Query Match
Best Local Similarity 100.0%;
Matches 21; Conservative 0;
                                                                               1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                     55 GAAAGTATCTTCAAGGACGCC 75
                                                                                                                                                                                                                                                                                                                    Kalos, Michael D.
```

				#1-	
	• •	•			
	* .		$oldsymbol{s}^{i}$ .	•	
			4 · · · · · · · · · · · · · · · · · · ·		
		•			
	en e				
			•		
		•			
i grande et de la companya de la com				•	
•	•				
				•	
		•			
	AA A				$\frac{1}{2} \left( \frac{1}{2} \right) \right) \right) \right) \right)}{1} \right) \right) \right)} \right) \right)} \right)} \right)} \right)} \right)} \right)} \right$
•					
and the second second				ar i	
					V Comment
	[현실 : 100 전 1 전 1 전 2 전 2 전 2 전 2 전 2 전 2 전 2 전 2	and the second s	en fragen i verskriver i i i france frage St		
					e Wig
•					
				100	
				en de la companya de La companya de la co	
				· · · · · · · · · · · · · · · · · · ·	

```
Sequence 9, Appli
Sequence 44306, A
Sequence 44306, A
Sequence 478, App
Sequence 478, App
Sequence 478, App
Sequence 447, App
Sequence 450, App
Sequence 450, App
Sequence 44307, A
Sequence 44307, A
Sequence 44307, A
Sequence 44305, A
Sequence 47305, A
Sequence 155, Appl
Sequence 155, Appl
Sequence 155, Appl
Sequence 15307, A
                                                                             April 18, 2003, 06:35:28; Search time 234.023 Seconds (without alignments) 400.770 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                   Pending Patents NA New:*

1. /cgn2 6/ptodata71/pna/PcT NEW COMB.seq:*

2. /cgn2 6/ptodata71/pna/US06 New COMB.seq:*

3. /cgn2 6/ptodata11/pna/US06 New COMB.seq:*

4. /cgn2 6/ptodata71/pna/US09 New COMB.seq:*

5. /cgn2 6/ptodata71/pna/US09 New COMB.seq:*

6. /cgn2 6/ptodata71/pna/US09 New COMB.seq:*

7. /cgn2 6/ptodata71/pna/US30 New COMB.seq2:*

8. /cgn2 6/ptodata71/pna/US30 New COMB.seq2:*

9. /cgn2 6/ptodata71/pna/US30 New COMB.seq3:*

9. /cgn2 6/ptodata71/pna/US30 New COMB.seq2:*

10: /cgn2 6/ptodata71/pna/US60 New COMB.seq2:*

11: /cgn2 6/ptodata71/pna/US60 New COMB.seq2:*
GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-270-437D-9
US-09-724-676-44306
US-09-724-676-44306
US-10-170-235-488
US-10-131-986-347
US-10-313-986-447
US-10-313-986-447
US-10-313-986-447
US-10-313-986-447
US-10-313-986-443
US-10-313-986-44307
US-09-724-676A-44307
US-09-724-676A-44305
US-10-313-986-175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-60-453-135-15387
US-60-453-050-15387
US-60-453-135-1
                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                          5897297 segs, 2233080881 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                 OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                        1 gaaagtatcttcaaggacgcc 21
                                                                                                                                                                                                 IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                         US-09-270-437D-9
21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1000.0
                                                                                                                                                        Perfect score:
                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                            Searched:
                                                                                 Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Regult
```

```
Sequence 9, Application US/09270437D

Sequence 9, Application US/09270437D

GENERAL INFORMATION:

APPLICANT: Chen, Yao-Tseng

APPLICANT: Gure, Ali

APPLICANT: Gure, Ali

APPLICANT: Stockert, Elisabeth

APPLICANT: Muth, Alexander

APPLICANT: Muth, Alexander

APPLICANT: Muth, Alexander

APPLICANT: Gare, Elke

TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Antiger

TITLE OF INVENTION: Antigens Per Se, And Uses Thereof

TITLE OF INVENTION: 1801ated Nucleic Acid Molecules

FILE REFERENCE: LUD 5538.1

CURRENT PELICATION NUMBER: 09/061,709

PRIOR APPLICATION NUMBER: 09/061,709

PRIOR APPLICATION NUMBER: 09/061,709

SEQ ID NO 9

LENGTH: 21

CHARLY ELLING DATE: 1998-04-17

SEQ ID NO 9

LENGTH: 21

CHARLY ELLING DATE: 1998-04-17

SEQ ID NO 9

LENGTH: 21

CHARLY ELLING DATE: 1998-04-17

CHARLY ELLING DATE: 1998-04-17
                             Sequence 21077, Sequence 45574, Sequence 45574, Sequence 4706, Ap Sequence 11275, Ap Sequence 9557, Ap Sequence 9557, Ap Sequence 55791, A Sequence 19919, A Sequence 19919, A Sequence 9553, Ap Sequence 9555, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 21; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 21; Conservative 0; Mismatches 0; Indels
1 US-60-453-050-1

US-10-144-771-21075

1 US-60-427-808-455974

US-00-532-3158-13848

US-09-575-784-4706

US-10-144-771-11275

US-09-532-3158-9557

US-09-532-3158-9557

US-60-452-680-84031

US-60-453-135-5791

US-60-453-135-5791

US-60-453-135-5791

US-10-453-135-9553

US-10-323-3158-9553

US-10-20-33-3158-9554

US-10-203-3158-9556

US-10-203-3158-9556

US-09-532-3158-9556

US-09-532-3158-9556

US-09-532-3158-9556

US-09-532-3158-9556

US-09-532-3158-9556

US-09-532-3158-9556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-270-437D-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE
```

RESULT 2
US-09-724-676-44306
Selected 44306, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TILE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Foy, Teresa M.
APPLICANT: McNabb, Andria
APPLICANT: McNabb, Andria
APPLICANT: Watenabe, Yoshihiro
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND LUNG CANCER
FILE REFERENCE: 210121.455C19
CURRENT APPLICATION NUMBER: US/10/313,986
CURRENT APPLICATION NUMBER: 10202-12-04
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: FOY, Teresa M.
APPLICANT: FOY, Teresa M.
APPLICANT: MCABAD, Andria
APPLICANT: MCABAD, Andria
APPLICANT: MCABAD, Andria
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Watanabe, Tongrong
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FRASESQ for Windows Version 4.0
SEQ ID NO 478
LENGTH: 1740
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Reed, Steven G.
APPLICANT: Read, Steven G.
APPLICANT: Wang, Tongfong
TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C19
CURRENT APPLICATION NUMBER: US/10/313,986
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 347
LENGTH: 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 21; DB 9; Length 1740; Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 21; DB 9; Length 1740; 1100.0%; Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 483, Application US/10313986
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Sco
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 GAAGTATCTTCAAGGACGCC 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 GAAAGTATCTTCAAGGACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , ORGANISM: Homo sapiens
US-10-313-986-478
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
CORGANISM: Homo sapiens
US-10-313-986-347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
US-10-313-986-478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4888, Application US/10170235
Sequence 4888, Application US/10170235
Sequence 4888, Application US/10170235
Sequence 4888, Application:
The Sequence 4888, Sequence 4888, Sequence 4888, Sequence 4888, Sequence 4888, Sequence 5888, Sequence 58888, Sequence 5888, Sequence 58888, Sequence 5888, Sequence 58888, Sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 21; DB 8; Length 1558; Pred. No. 0.99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 21; DB 6; Length 861; 100.0%; Pred. No. 0.92;
                                                                                                                                                                                                                                                 100.0%; Score 21; DB 6; Length 861; 100.0%; Pred. No. 0.92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
US-09-724-676A-44306
US-09-724-676A-44306
Sequence 44306, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TILE OF INVENTION: Variants of alternative splicing
TILE REFERENCE: 129181.4 Compugen
CURRENT PILIG DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SOFTWARE: PatentIn version 3.2
LENGTH: 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 347, Application US/10313986
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              321 daaagrarcrrcaaggacgcc 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 21; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                         321 gaaagrarcricaaggacgcc 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                           1 GAAAGTATCTTCAAGGACGCC 21
                        SOFTWARE: Patentin version 3.2
SEQ ID NO 44306
LENGTH: 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GAAAGTATCTTCAAGGACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 21, Conservative
                                                                                                                                                                                                                                                                                                                             21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Foy, Teresa M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
CORGANISM: Homo sapiens
US-09-724-676A-44306
                                                                                                                                   TYPE: DNA
CORGANISM: Homo sapiens
US-09-724-676-44306
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: HUMAN
US-10-170-235-4888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 4888
LENGTH: 1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-313-986-347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

ö

55 GAAAGTATCTTCAAGGACGCC 75

; SEQ ID NO 483 ; LENGTH: 1740

ò g

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 GAAAGTATCTTCAAGGACGCC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 GAAGTATCTTCAAGGACGCC 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-313-986-428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-313-986-485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-313-986-485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Watenabo, Yoshiniro
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND INGGNOSIS OF LUNG CANCER
TITLE OF INVENTION: WHERE: 120121.455C19
CURRENT APPLICATION NUMBER: 120121.455C19
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FASTSEQ for Windows Version 4.0
LENGTH: 1743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Roy, Teresa M.
APPLICANT: Machab, Andria
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Wang, Tongtong
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
ITILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
ITILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
CURRENT APPLICATION NUMBER: US/10/313,986
CURRENT FILLING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 560
SOFTWARE: PRAESEQ FOR WINDOWS Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                           Score 21; DB 9; Length 1740;
Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 21; DB 9; Length 1743; 100.0%; Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 21; DB 9; Length 1743;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 21; Conservative 0; Mismatches 0; Indels (
                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               red. No. 1;
Mismatches
                                                                                                                                                                                                                                                                                                                           Sequence 447, Application US/10313986 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 450, Application US/10313986
                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                    Query Match
Best Local Similarity 100.0%;
Matches 21; Conservative 0
                                                                                                                                                                                                  55 GAAAGTATCTTCAAGGACGCC 75
                                                                                                                                                                      1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 GAAAGTATCTTCAAGGACGCC 75
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Foy, Teresa M. APPLICANT: McNabb, Andria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 21, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
US-10-313-986-447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
TYPE: DNA
ORGANISM: primate
US-10-313-986-483
                                                                                                                                                                                                                                                                               RESULT 8
US-10-313-986-447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
US-10-313-986-450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS-10-313-986-450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
```

g ઠે

```
Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                    ## PEPLICANT: McNabb, Andria
| APPLICANT: Meaded, Yoshihiro
| APPLICANT: Reed, Steven G.
| APPLICANT: Reed, Steven G.
| APPLICANT: Wang, Tongtong
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
| TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
| FILE REFERENCE: 210.121.455C19
| CURRENT APPLICATION NUMBER: US/10/313,986
| CURRENT PILLING DATE: 2002-12-04
| NUMBER OF SEQ ID NOS: 560
| SOFTWARE: FASESEQ for Windows Version 4.0
| SEQ ID NO 428
| LENGTH: 1764
| TUBENGTH: 1764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 485. Application US/10313986
GENERAL INFORMATION:
APPLICANT: FOy, Teresa M.
APPLICANT: McNabb, Andria
APPLICANT: Wetwarb, Andria
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOSITIONS AND WETHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
FILE REFERENCE: 210121.455C19
CURRENT FPLING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FaelSEQ for Windows Version 4.0
SEQ ID NO 485
LENGTH: 1799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 21; DB 9; Length 1799; 11 Similarity 100.0%; Pred. No. 1; 21; Conservative 0; Min...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 21; DB 9; 100.0%; Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 44307, Application US/09724676
GENERAL INFORMATION:
Sequence 428, Application US/10313986 GENERAL INFORMATION:
```

ö

ö

1 GAAAGTATCTTCAAGGACGCC 21

```
à
                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Score 21; DB 6; Length 4060;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 1;
Matches 21; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                             Query Match 100.0%; Score 21; DB 6; Length 2137; Best Local Similarity 100.0%; Pred. No. 1; Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 44305, Application US/09724676
; Sequence 44305, Application US/09724676
; GENERAL INFORMATION:
TITLE OF INVENTION: Variants of alternative splicing
TITLE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; SOFTWARE: Patentin version 3.2
; SOFTWARE: Patentin version 3.2
; LENGTH: 4060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 44307, Application US/09724676A
; GENERAL INFORMATION:
; GENERAL INFORMATION: LTD
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; TITLE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-111-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 44307
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 9722
SOFTWARE: PatentIn version 3.2
SEQ ID NO 44307
LENGTH: 2137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321 GAAAGTATCTTCAAGGACGCC 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321 GAAAGTATCTTCAAGGACGCC 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                          321 GAAAGTATCTTCAAGGACGCC 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                               1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
CORGANISM: Homo sapiens
US-09-724-676-44305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
CORGANISM: Homo sapiens
US-09-724-676A-44307
                                                                                                                                           TYPE: DNA
CRGANISM: Homo sapiens
US-09-724-676-44307
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-09-724-676A-44307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
US-09-724-676-44305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                  a
```

RESULT 15 US-09-724-676A-44305

```
GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Variants of alternative splicing

TITLE OF INVENTION: Variants of alternative splicing

TITLE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 129181.4 Compugen

CURRENT APPLICATION NUMBER: US/09/724,676A

CURRENT PILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patentin version 3.2

SEQ ID NOS: 97222

SEQ ID NOS 4305

LENGTH: 4060

TYPE: DAA

ORGANISM: Homo sapiens

US-09-724-676A-44305

QUESTY MATCH

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps

ALCAS SEATH OF CONSERVATIVE OF MISMATCHES OF CAPPER OF MISMATCHES OF CAPPER OF
```

100.0 477 9 AIG82259 100.0 776 10 BE513300 100.0 910 12 BE881835	100.0 318 14 BQ437571 100.0 3100 11 BC019258	18.4 87.6 347 9 AA6836048 AA836048 od43c04.8 18.4 87.6 347 9 AA683695 Ma6831959 Ma681968 Ma681968 Ma64108.8 18.4 87.6 347 9 AA003676 AA003676 mg59c10.r 18.4 87.6 356 14 W71682 W71682 me34c05.r1	0e 446 10 AW318369 87.6 489 9 AA547497 87.6 573 10 BB633276 87.6 600 12 BG803155 87.6 600 12 BG803155	97.6 601 9 AA522010 97.6 601 10 BB611741 97.6 601 10 BB611741	97.0 632 10 BB612512 87.6 648 10 BB65710 87.6 712 11 AK011797	87.6 749 14 BQ180708 87.6 895 14 BQ930512	87.6 930 14 BQ895257 87.6 2202 11 AK011689	91.0 155 17 AQ34/018 84.8 325 13 B1477406 84.8 441 12 BF776116 82.9 195 9 AT000448	82.9 499 10 BB757949 81.0 332 17 AZ743062	01:0 534 13 BJL58403 81:0 418 10 AW497094 81:0 612 17 AZ667042	81.0 631 13 BJ165180 81.0 718 17 BH377427	81.0 781 17 BH327295 81.0 781 17 BH432699 80.0 108 12 BF377514	80.0 322 12 BG373492	ALIGNMENTS	BE560346 360 bp mRNA linear EST 15-AUG-2000 WFNA sections.	BE560346 BE560346.1 GI:9804066 BST.	M Homo sapiens Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleogtomi, Mammala, Butheria, Primates, Catarrhini, Hominidae, Homo.	J. (Joses I. Fo. 360) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)	Email: cgapbe-r@mail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arraved by: The I M. G. R. Consortium (IIMI)	DNA Sequencing by: Incyte Genomics, Inc.  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  Plate: LLCM379 row: m column: 03  High quality sequence start: 4  High quality sequence stop: 360.  Location/Qualifiers  1. 360
r 80 6	110	0 113 115 7	c 17	25 27 27 27 27	2 2 2 2 4 5 2 5	26 27	7 7 8 7 7 8 7 7 8		ດ ດ ມີເປັນ 4. ເປັນ			0000 444 4264			RESULT 1 BE560346 LOCUS DEFINITION	ACCESSION VERSION KEYWORDS SOURCE	ORGANIS	AUTHOR TITLE JOURNA		FEATURES SOURCE
GenCore version 5.1.4 p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.	OM nucleic - nucleic search, using sw model	Run on: April 18, 2003, 04:47:40 ; Search time 731.182 Seconds (without alignments) 465.145 Million cell updates/sec		Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0	Searched: 16154066 segs, 8097743376 residues	Total number of hits satisfying chosen parameters: 32308132	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	F: *	1: em_eBtDa:* 2: em_eBthum:* 3: em_eBtin:*	4: em_estmu:* 5: em_estoy:* 6: em_estoy:*	7: em_estro.* 8: em_htc.*	10: 95 est2:* 11: 95-htc:*	12: 9D_est4:* 14: 9D_est5:*	15: em_estrun:* 16: em_estrun:* 17: gb_gss:* 18: em_gss_hum:* 19: em_gss_lnv:* 20: em_gss_lnv:*		em gss oth em gss pro em gss rod	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES	1000000

ö

Gaps

; 0

Indels

Query Match Best Local S

Matches

BASE COUNT ORIGIN

```
/ Organism="num.compose" / Organism="num.compo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE396918 360 BST 21-JUL-2000 GRNA linear EST 21-JUL-2000 601289477F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620058 5',
                                                                                                                                                                                                                                                                                                                                                  BES60268 361 bp mRNA linear EST 15-AUG-2000 601346086F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3678885 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 361)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM356 row: I column: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Length 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 21; DB 1 ilarity 100.0%; Pred. No. 3.4; Conservative 0; Mismatches
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence start: 4
High quality sequence stop: 361.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           286 GAAAGTATCTTCAAGGACGCC 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE396918.1 GI:9342283
        ö
                                                                                                                                               286 GAAAGTATCTTCAAGGACGCC 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
BE560268
BE560268.1 GI:9803988
                                                                                      21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAAAGTATCTTCAAGGACGCC
                                                                                  GAAAGTATCTTCAAGGACGCC
        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
                 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
BE396918
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                           RESULT 3
BE560268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /do.zre=="Law.nispage" | /do.zre=="Law.nispage" | /do.zre=="Law.nispage" | /do.zre=="Law.nizpage" | /do.zre==| 
                                  /organism="Homo sapiens"

/db xref="taxon:8606"

/db xref="taxon:8606"

/clone=InkaGB:368702"

/clone lib="NIH MGC 8"

/tissue_type="Burkitt lymphoma"

/tissue_type="Burkitt lymphoma"

/lab.host="DH10B (phage-resistant)"

/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:

/note="Organ: lymph; Vector: pOTB7; Directionally

ECORI; CDNA made by oligo-dT priming. Directionally

cloned into ECORI/KhoI sites using the following 5'

cloned into ECORI/KhoI sites using the following 5'

adaptor: GGCACGGG(G). Size-selected SoObp for average

adaptor: GGCACGGG(G). Size-selected by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-CDNA synthesis kit

(Stratagne) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE269531 361 bp mRNA linear EST 13-JUL-2000 601184745F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3542483 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotz, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Butaryotz, Metazoa; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 361)

NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Dipublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM234 row: i column: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 21; DB 10; Length 361;
Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 21; DB 10; 100.0%; Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 361.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286 GAAAGTATCTTCAAGGACGCC 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE269531
BE269531.1 GI:9143153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uman.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21,
```

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

LOCUS

RESULT 2 BE269531

g

ACCESSION

ô

Gaps

ö

BASE COUNT ORIGIN

m

```
100.0%; Score 21; DB 10; Length 384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE39691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
BE396917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db xref="taxon:9606"
/dlone="IMAGE:362005"
/clone="Lib="NIH MGC 8"
/clone="Lib="NIH MGC 8"
/tlasue_type="Burkitt lymphoma"
/lab_host="DH108 (phage-resisterant)"
/note="Organ: lymph; Vector: pOTB7; Site 1: Xho1; Site 2: EcoR1; cDNA made by oligo-dT priming. Directionally cloned into EcoR1/Xho1 sites using the following 5' adaptor: GGCACGGG(0). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using Zab-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM291 row: i column: 19
High quality sequence stop: 366
High quality sequence stop: 366
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE560799 371 bp mRNA linear EST 15-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryoča, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 371)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-romail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
High quality sequence start: 6
High quality sequence stop: 371.
Location/Qualifiers
1. 371
                  1 (bases 1 to 366)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 21; DB 10; Length 366; 100.0%; Pred. No. 3.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291 GAAAGTATCTTCAAGGACGCC 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE560799.1 GI:9804519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
BES60799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ното варіеля
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uman.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
BE560799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                    PEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
```

g

```
Content Strandberg, Ph.D.

Email: cgapbs-remail.nih.go.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: Tre I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through he I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

High quality sequence start: 49

High quality sequence start: 40

Clorality sequence start: 40

High quality sequence st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE396917
601289473F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619866 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 384)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 21; DB 10; Length 371;
Pred. No. 3.5;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%; Sc
Best Local Similarity 100.0%; Pr
Matches 21; Conservative. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              296 GAAAGTATCTTCAAGGACGCC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE396917.1 GI:9342282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAAAGTATCTTCAAGGACGCC
```

```
| 1. .776 | Arganisms | Argani
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 776)

8 NIH-MG http://mgc.nci.nih.gov/.

10 Mational Institutes of Health, Mammalian Gene Collection (MGC)

11 Unpublished (1999)

12 Contact: Robert Strausberg, Ph.D.

13 Email: cgapbs-r@mall.nih.gov

14 Fung HongYkubin Laboratory

15 CDNA Library Preparation: Ling HongYkubin Laboratory

17 CDNA Library Arrayed by: The I M.A.G.E. Consortium (LLNL)

18 CONDA Library Arrayed Secondics, Inc.

19 DNA Sequencing by: Incyte Genomics, Inc.

10 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

19 Plate: LLCM327 row: f column: 19

19 High quality sequence stop: 615.

10 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE881835
601504962F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906590 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 910)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.lln.gov
High quality sequence start: 56
High quality sequence start: 56
High quality sequence stop: 746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapba-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 GAAAGTATCTTCAAGGACGCC 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE881835.1 GI:10330611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
BE881835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
JOURNAL
COMMENT
   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                  TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
BE881835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / dry xref="taxon:960"
/db xref="taxon:960"
/db xref="taxon:9667"
/clone="lib="goares NFL_T_GBC_S1"
/clone lib="goares NFL_T_GBC_S1"
/lab host="bli08"
/note="organ: pooled, Vector: pr773D-Pac (Pharmacia) with note="organ: pooled, Vector: pr773D-Pac (Pharmacia) with note="organ: pooled, Vector: pr773D-Pac (Pharmacia) with note="organ: pooled, Vector: site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized in note of plasmid DNA from three normalized in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I: M.A.G.E. clones 297480-37239, 682632-687239, 726408-728711, and 72996-731399; Subtraction by Bento Soares and M. Ratima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE513300 776 bp mRNA linear EST 07-AUG-2000 601315375F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3633810 5', mRNA sequence.
BE513300.1 GI:9720512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                        EST 07-MAR-2000
                                                   ö
                                                                                                                                                                                                                                                                                                                                                                            AI682259
wa71h05.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone
IMAGE:2301657 3' Similar to TR:000425 000425 PUTATIVE RNA BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 477)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index

Unpublished (1997)

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LLNL; contact the This Consortium (info@mage.llnl.gov) for further information. IMAGE Consortium (info@mage.llnl.gov) for further information. Insert Length: 608 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 427.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                       0, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 others
                                                   Indels
                                                       ö
                   Pred. No. 3.5;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      355 GAAGTATCTTCAAGGACGCC 375
                   Best Local Similarity 100.0%; P
Matches 21; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
                                                                                                                                                                                  309 GAAAGTATCTTCAAGGACGCC 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A1682259.1 GI:4892441
                                                                                                                                      1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GAAAGTATCTTCAAGGACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uman.
```

. source

FEATURES

ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

ACCESSION VERSION KEYWORDS

DEFINITION

RESULT 7 AI682259 LOCUS

g

BASE COUNT ORIGIN

DEFINITION

RESULT 8 BE513300

ઠે

ACCESSION VERSION KEYWORDS SOURCE

ö

Location/Qualifiers

Bource

FEATURES

BASE COUNT

Matches

ò 셤

```
3100 bp mRNA linear HTC 19-DEC-2001
Homo sapiens, Similar to IGF-II mRNA-binding protein 3, clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 8 Row: c Column: 6 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5729900 This clone has the following problem: incomplete processing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Info@boggc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Busanna Chan, Readman Chiu, Chris Piell, Erin Garland, Ran Guin,
Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Ollver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Lilas Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne; Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA836048 121 bp mRNA linear BST 31-MAR-1998 od43c04.81 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:1370694 similar to TR:000425 000425 PUTATIVE RNA BINDING PROTEIN KOC ;
                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3100) Strausberg,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission.
Submitted (13-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Iissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Genome Sequence Centre,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 21; DB 11; Length 3100; 100.0%; Pred. No. 9.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db xref="taxon:9606"
/db xref="IMAGE:3542483"
/tissue type="Lymph, Burkitt lymphoma"
/clone_Tib="NIH MGC_8"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         805 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       r: porb7"
873 g
                                                                                                                                                                                                                        BC019258:1 GI:17939534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        305 GAAAGTATCTTCAAGGACGCC 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
AA836048
AA836048.1 GI:2910367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   674 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21; Conservative
                                                                                                                                                                                                                                                                                  Homo sapiens.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                    LOCUS
                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCUS
DEFINITION
                    RESULT 11
BC019258
                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA836048
1. .910
/organism="Homo sapiens"
/db_xref="Haxon:9606"
/db_xref="Haxon:9606"
/clone="IMAGB:3906590"
/clone="IMAGB:3906590"
/clone="IMAGB:3906590"
/clone=lib="NIH MGC_71"
/tissue_type="leiomyosarcoma"
/lab_host="Bh108 (phage=resistant)"
/note="Mores" (phage=resistant)"
/note="gray unitaring the continuation of the continuatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PG45/571
AGENCOURT 7898330 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:6154021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dT.
Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIN-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Longublished (1999)

Contact: Robert Strausberg, Ph.D.
Enail: cgapba-r@mail.nim.gov
Tissue Procurement: ATC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bloscience Corporation

Clone distribution: MGC clone distribution information can be

http://image.lih.gov

Plate: LiAM13494 row: g column: 14

High quality sequence stop: 555.

Locality sequence stop: 555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 918)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 21; DB 12; Length 910; 100.0%; Pred. No. 5.3; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 21; DB 14; Length 918; 100.0%; Pred. No. 5.3; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311 GAAAGTATCTTCAAGGACGCC 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BQ437571.1 GI:21176647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      322 GAAAGTATCTTCAAGGACGCC 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Technologies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAAAGTATCTTCAAGGACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BQ437571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human.
```

VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE JOURNAL COMMENT

REFERENCE

DEFINITION RESULT 10 BQ437571

ACCESSION

Bource

BASE COUNT ORIGIN

ሯ

ö

Gapa

ö

SOURCE

COMMENT

```
AA003676 347 bp mRNA linear EST 22-JUL-1996 mg59010.rl Soares mouse embryo NbMB13.5 14.5 Mus musculus CDNA clone_IMAGE:437298 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 347)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: embryo; Vector: pBluescribe (modified);
Site 1: Mlul; Site 2: Sall; Cloned unidirectionally from
mRNA prepared from 13,500 2-cell stage embryos. Primer:
Sall(dT): 5'-CGGTCGACCGTTTTTTTTTTTTTTTTTTTT.
were cloned into the Mlul,Sall sites of a modified
pBluescribe vector using commercial linkers (NEB).
Average insert size: 1.2 kb."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:567287
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                               The WashU-HIMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
Contact: Marra M/Mouse EST Project
WashIU-HHMI Mouse EST Project
WashIngton University School of MedicineP
WashIngton University School of MedicineP
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 87.6%; Score 18.4; DB 9; Length 178; Local Similarity 95.0%; Pred. No. 55; 19. Conservative 0; Mismatches 1; Indels 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"

/strain="C57BL/6J x DBA/2J F1"

/db xref="taxon:10090"

/clone="IMAGB:1003071"

/clone=lib="Knowles Solter mouse 2 cell"

/tlssue_type="embryo"

/dev stage="2-cell"

/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 163.
Location/Qualifiers
1. .178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA003676.1 GI:1447248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAAAGTATCTTCAAGGACGC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 gaaagrgrcrrcaaggacgc 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA003676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
AA003676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
                                                                                                                    TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / AGD. MUSCLE MILLOW TO THE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bummalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

( bases 1 to 178)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COURT Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCT-CSAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 730 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST 09-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA683695 178 bp mRNA linear EST 09-DEC-1995 vm64h08.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone IMAGE:1003071 5' similar to TR:000425 000425 PUTATIVE RNA BINDING AA68740-6
                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 121)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo." 34 c 20 g 30 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ph.D., Gerald Marti, M.D. CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.2%; Score 20; DB 9; Length 121; 100.0%; Pred. No. 6.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="InAAGE:1370694"
/clone_lib="NCI_GAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Pred. No. 6.8 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA683695
AA683695.1 GI:2671086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 AAAGTATCTTCAAGGACGCC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 AAAGTATCTTCAAGGACGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 house mouse.
                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
AA683695/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
SOURCE
                                                                                                                    ORGANISM
                                                                                                                                                                                                                   REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                 KEYWORDS
```

셤 à

; 0

Gaps

ó

```
T 3'), on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2 1; double-erranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified normalization. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W71682 356 bp mRNA linear EST 17-JUN-1996 me34c05.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:389384 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 356)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Martin, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterston, R.
The WashU-HHMI Mouse EST Project
The WashU-HHMI Mouse EST Project
Contact: Marxa M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 28
IMAGE Consortium (info@image.llnl.gov) for further information. MGI:262634
Seq primer: ETPrimer
High quality sequence stop: 333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                       clone_lib="Soares mouse embryo NbME13.5 14.5"
sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

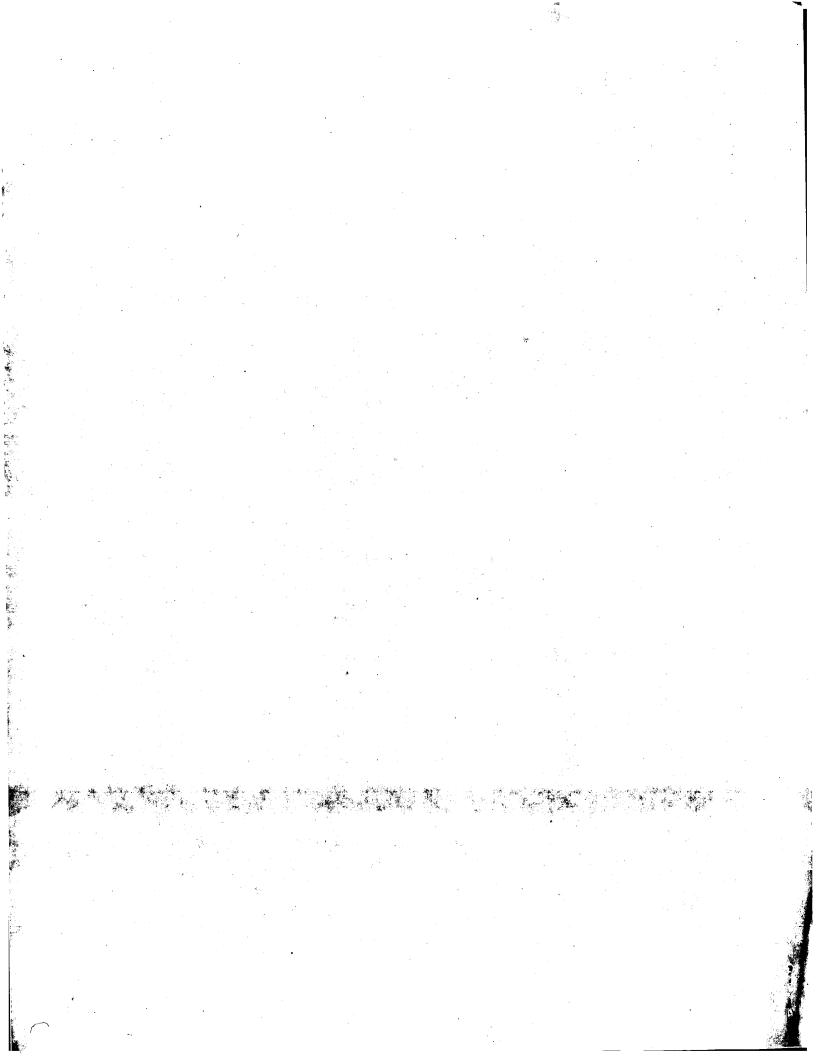
87.6%; Score 18.4; DB 9; Length 347;
Best Local Similarity 95.0%; Pred. No. 75;
Matches 19; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'dev_stage="13.5-14.5dpc total fetus"
|lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 t
                                                                                                                                                                                                            1. .347
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                   strain="C57BL/6J"
db xref="taxon:10090"
clone="IMAGE:437298"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue_type="embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 daadstercricaaddacec 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAAAGTATCTTCAAGGACGC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W71682.1 GI:1380423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81
                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
W71682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

Bource

FEATURES

```
/ Getrains merchings musecutus musecutus merchings musecutus musecutus musecutus musecutus musecutus merchings merch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 14; Length 356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.6%; Score 18.4; D
95.0%; Pred. No. 76;
tive 0; Mismatches
organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      322 GAAAGTGTCTTCAAGGACGC 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAAAGTATCTTCAAGGACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        엄
```

Search completed: April 18, 2003, 07:31:44 Job time : 737.348 secs



```
GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM nucleic - nucleic	ic search, using sw model
Run on: April	ril 18, 2003, 04:46:26 ; Search time 292 Seconds (without alignments) 2192.677 Million cell updates/sec
Title: US- Perfect score: 22 Sequence: 1 c	US-09-270-437D-10 22 1 ctgcaaggggttttgctgggcg 22
Scoring table: IDENT: Gapop	IDENTITY NUC Gapop 10.0 , Gapext 1.0
Searched: 205	2054640 seqs, 14551402878 residues
Total number of hits	s satisfying chosen parameters: 4109280
Minimum DB seq length: Maximum DB seq length:	ith: 0 rth: 200000000
Post-processing: Min Max Lis	Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database : Gerabase : 11. 22: 22: 22: 22: 22: 22: 22: 22: 22: 22:	GenEmbl:*  gb_ba:*  gb_htg:*  gb_ntg:*  gb_ov:*  gb_pov:*  gb_pi:*  gb_pi:*
,	1

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		65954	66054 Sequenc	56057	366035 S	35 H	1863	1 108	2 6 5 5	•	romo sapi	n ded n	175 HOMO	OMOH 690	9	07 Homo	79 Human	09 Rattu	47 Homo	08 Homo	95 HOMO	AL669991 Neurospor	DI HOMO	S Karri	14 Homo	50 Rattu	07 Homo	12 Homo	.56 Homo	OHOH	M AB	1651 Homo	932	3700 Human	682 Rattus	942 Rattue	0491 Rattu	663 Homo	1441 Rattus	27687 Homo	cus n	93028 Homo 8	4408 Mus musc	
SUMMARIES	ID																						AC113360																						ALIGNMENTS
d	Query Match Length DB		00.00	00.00 1743	0.00 L/43	.0 1/64	4150	1714 0 00	00.00	00.0 4181	00.0 4181	00.00	00.0 104668	00.00	5 98951	5 200956	5 208197	6 111764	6 156422	6 159082	6 153404	A 7955A	80.9 32145 2	9 58511	9 91200	9 140666	9 141085	9 147556	9 157481	9 183666	9 189947	9 191076	9 203770	9 235669	1 56509	1 83596	1 94180	1 150722	1 154218	1 165777	1 168085	1 181347	214042	1 258120	
	Score		7 (	7 6	4 (	2 6	200	2 2 2	22	22	22	22	22		8	Φ,	σ,	∞ ∘	<b>x</b> 0 0	pα	τ α τ	; -	7	۲.	۲.	7.	۲.	٠,	٠.		17.8	۲.	7	ς.	٠.	٠,	٠,	٠.	٠.	7.7	٠.	٠.	t		
	Result No.	1				ייני טיט							12	13	14		9 i	17	•	•	2 6		23	•	c 25		C 27	٠,	7 6	9 m	c 32	33	34	m (	o c	י רי	າຕ	י ר	* <	* <	7 <	) * *			

9		
4		
5		
ą		
ĕ.		
7		
ñ		
á		
3		
4		

PAT 16-FEB-2002	leostomi; o.	erson, R.A ger, G.R.,
PAT	; Eute e; Hom	, Hende
linear	human. Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.	MangyT., Wang,A., Skeiky,Y.A., Li,S.X., Kalos,M.D., Henderson,R.A., Mcneill,P.D., Fanger,N., Retter,W., Marnerakis,M., Fanger,G.R., Vedvick,T.S., Carter,D., Watanabe,Y. and Peckham.D.W.
DNA .	aniata; :arrhin	1, S.X.,
AX365954 1740 bp Sequence 347 from Patent WO0200174 AX365954 1 GI:18697455	rdata; Cre mates; Cat	y,Y.A., Li , Retter,N , Watanabe
AX365954 Seguence 347 from Patent AX365954 AX365954.1 GI:18697455	azoa, Cho eria; Pri	A., Skeik Panger,N. Parter,D.
54 56 54.1 GI	apiens ota, Meta la, Euthe	, Wang, P [,P.D., E t, T.S., C
AX365954 Sequence AX365954 AX365954	human. Homo sapiens Eukaryota, Me Mammalia, Eut	Wang, T. Mcneill Vedvick
RESULT 1 AX365954/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS	SOURCE ORGANISM REFERENCE	AUTHORS

ઠે

```
CORIXA CORPORATION (US)
                                                                                                                                               22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                  Query Match
Best Local Similarity
Matches 22; Conserv
                                                                           527 a
                                                                                                                                                                                                                                                                                                                                                  human,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
HSU76705/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                 RESULT 4
AX366035/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
                                                                                                                                                                             н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                       FEATURES
                                                                                                                                                                                                                                                                             LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                        음
                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang, T., Wang, A., Skeiky, Y.A., Li,S.X., Kalos, M.D., Henderson, R.A., Mcneill, P.D., Fanger, N., Retter, M.W., Marnerakis, M., Fanger, G.R., Vedvick, T.S., Carter, D., Watenabe, Y. and Peckham, D.W.
Compositions and methods for the therapy and diagnosis of lung cancer
Cancer. WO 0200174-A 450 03-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang, T., Wang, A., Skeiky, Y.A., Li,S.X., Kalos, M.D., Henderson, R.A., Mcneill, P.D., Fanger, N., Retter, M.W., Marnerakis, M., Fanger, G.R., Vedvick, T.S., Carter, D., Watanabe, Y. and Peckham, D.W. Compositions and methods for the therapy and diagnosis of lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAT 15-FEB-2002
                                                                                                                                                                                                                                                                                                                        PAT 15-FEB-2002
                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Compositions and methods for the therapy and diagnosis of lung cancer
                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 22; DB 6; Length 1743; llarity 100.0%; Pred. No. 5.6; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                   Length 1740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                  0; Indels
                                                                                                                                                                         .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA
                                                                                                                                                                                                                                                                                                                              DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1743 bp D
Sequence 450 from Patent WO0200174.
AX366057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent: WO 0200174-A 447 03-JAN-2002.
CORIXA CORPORATION (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           392 t
                                           Patent: WO 0200174-A 347 03-JAN-2002;
CORIXA CORPORATION (US)
                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                       1743 bp I
Sequence 447 from Patent W00200174.
AX366054
                                                                                                                                                                                                   Mismatches
                                                                                                                                 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
_406 c 418 g 395
                                                                                                 Score 22;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGCAAGGGGTTTTGCTGGGCG 477
                                                                                                                                                                         Query Match 100.0%; Sc
Best Local Similarity 100.0%; Pr
Matches 22; Conservative 0;
                                                                                                                                                                                                                                                          498 crecakeeerrrrecreece 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AX366057.1 GI:18697500
                                                                                                                                                                                                                               1 CTGCAAGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                        AX366054.1 GI:18697498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 22; Conserv
                                                                                                                                   526 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer
                                                                                                                                                                                                                                                                                                                                                                                                       human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AX36057/c
LOCUS
DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                  AX366054/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                              FEATURES
                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                               g
```

```
HSU76705
Human putative RNA binding protein Kocl mRNA, complete cds.
U76705
                                                                                                                                                                                                                                                                                                                                                                        PAT 15-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo. Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 4155)
Mueller-Pillasch, F., Lacher, U. and Wallrapp, C.
Direct Submission.
Submitted (30-607-1996) Innere Medizin I, University of Ulm, Robert-Koch-Str.8, Ulm 89081, Germany
Location/Qualifiers
                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang,T., Wang,A., Skeiky,Y.A., Li,S.X., Kalos,M.D., Henderson,R.A Mcneill,P.D., Fanger,N., Retter,M.W., Marnerakis,M., Fanger,G.R., Vedvick,T.S., Carter,D., Watanabe,Y. and Peckham,D.W. Compositions and methods for the therapy and diagnosis of lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Length 1764;
                                                                                                                                                 Length 1743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                        0; Indels
                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 22; DB 6
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 22; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent: WO 0200174-A 428 03-JAN-2002;
CORIXA CORPORATION (US)
Location/Qualifiers
                                                                                                                                                   DB 6
5.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  394 t
                                                                                                                                                                                                                                                                                                                                                                                 AX366035 1764 bp I Sequence 428 from Patent W00200174. AX366035.1 GI:18697484
                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
                                                                                         392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
-406 c 418 g 39:
                                                                                                                                                     100.0%; Score 22;
100.0%; Pred. No.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    519 crecaaccaririrecrecec 498
                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                498 CTGCAAGGGGTTTTGCTGGGCG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                      CIGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U76705.1 GI:4098296
```

CDS

```
/note="binds multiple sites in IGF-II mRNA 5'UTR; identical to KH-domain containing protein overexpressed in cancer (koc)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TETAIN TO THE TOTAL STATES THE STROCK I PUSCEPTURITY OF THE STROCK OF TH
                                                                                                                                                                                                                                                                                                                                                            C (bases 1 to 4171)
Nielsen, J., Christiansen, J., Lykke-Andersen, J., Johnsen, A.H.,
Wewer, U.M. and Nielsen, F.C.
Bubret Submission
Submitted (30-DEC-1998) Institute of Molecular Biology, University
of Copenhagen, Soelvgade 83H, Copenhagen DK-1307, Denmark
L. 4171 |
/organism="Homo sapiens"
/db_xref="taxon:9606"
/location/location"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeutic screening using signature gene sets
Patent: WO 0194629-A 3742 13-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear PAT 09-JAN-2002
                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                       (bases 1 to 417)
Nielsen, U. Christiansen, J., Lykke-Andersen, J., Johnsen, A.H., Wewer, U.M. and Nielsen, From Eactor II mRNA-binding proteins represses translation in late development Mol. Cell. Biol. 19 (2), 1262-1270 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 4171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/product="IGF-II mRNA-binding protein 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 22; DB 9
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 22; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AX333233
Sequence 3742 from Patent WO0194629.
AX333233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   853 g 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAD09828.1"
/db_xref="GI:4191612"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  764 Cracaadadaririracradace 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CTGCAAGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .4171
/gene="IMP-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267. .2006
/gene="IMP-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KALQSGPPQSRRK"
1 822 c 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AX333233.1 GI:18123867
                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human.
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
AX333233/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                     PUBMED
REFERENCE
                                                                                                                    REFERENCE
                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                           MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     硆
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠ
                                                                                                                                                                                                                                           /protein id=#AAD09223.1"
/brotein id=#AAD09223.1"
/db_xref="G1:4098297"
/translation="MMKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDC
PDESWALKAIEALSGKIELHGKPIEVBHSVPRRKORIRKLJRNIPPHLQWEVLDSILV
QYGVVBSCEQNWTDSETAVVNVTYSSKDQARQALDKLNGFQLENFTLKVAYIPDEMAA
QONPLQQPRGRRGLGQRGSSRQGSPGSVSKQRCDLPHLLLVPTQPYGAIIGKEGATI
RNITKQTQSKLIVHRKENAGAAEKSITILSTPEGTSAACKSILEIMHKEAQDIKFTEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAKAEEEIUKKITSESYENDIASANIACHE LUI ISPUGELITINPERTITYKKUND
MTPPYPQFEGSETETVHQFIPALSVGAIJGKQGQHIKQLSRFAGASIKTARAEAEDA
WRMYIJTQPPEAQFKAQGRIYGKIKEENFVSFKESVKLEAHTRVPSFAAGRYJGKGGK
TVNELQNISSAEVVVPRDQTPDENDQVVVKITGHFYACQVAQRKIQEILTQVKQHQQK
KALQSGPPQSRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAT 17-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF117108
Homo sapiens IGF-II mRNA-binding protein 3 (IMP-3) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unclassified.

1 (bases 1 to 4159)

1 (bases 1, 0 4159)

2 (ban,Y.-.T., Gure,A., Tsang,S., Stockert,B., Jager,E., Alexander,K. and Old,L.J.

1 Isolated nucleic acid molecule encoding cancer associated anticon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acid molecule encoding cancer associated antigen, the antigen itself, and uses thereof
Patent: US 6297364-A 4 02-OCT-2001,
Location/Qualifiers
                                                                                             function="putative RNA binding protein"
note="Kh-domain containing protein; overexpressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 22; DB 9; Length 4155;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 22; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 4159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 22; DB 6;
100.0%; Pred. No. 5.3;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1181 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1181 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AR171863 4159 bp
Sequence 4 from patent US 6297364.
AR171863
AR171863.1 GI:17910813
                                      tissue type="pancreas"
            _line="Patu8988s"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              851 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism≃"unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           851 g
                                                                                                                                                                                           /codon_start=1
/product="Koc1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             748 CTGCAAGGGTTTTGCTGGGCG 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    748 crechhededrirriderededed 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF117108
AF117108.1 GI:4191611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           830 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     830 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1281 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unknown
```

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS REFERENCE

RESULT 6 AR171863/c

ò

BASE COUNT ORIGIN

source

JOURNAL FEATURES

TITLE

BASE COUNT ORIGIN

RESULT 7 AF117108/c

õ 윱 LOCUS

ACCESSION VERSION KEYWORDS

ö

Gapa

Query Match

BASE COUNT ORIGIN

FEATURES

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

RESULT 9 AX365782/c

ద ઠે

DEFINITION

ACCESSION

```
/ LEGENAL KALEL OT LEAVORY OF THE WARLY TONLES I PRODKI PVSGPPLVKTGYAFVDC / trail al ton = "MNKLY ICULSENAAPSDLES I FKDAKI PVSGPPLVKTGYAFVDC PDESWALKA I EALGSKI ENGKLY I EVEHSVPKRQR I RKLOTRNI PPHLOWEVLDSLLV PDESWALKA I EALGSKI ELGENAT ENGYVESCEGVNTUSETA VVNVTYSSKDQARQALDKLAGFOLENT-KKVAZI PEDBMAA QYGVVESCEGVNTUSETA VARGASSRKOGSPGSVGASCBACH ELLLAVFTGYGYL I GKEGATI GONPLOOPREREGGORGSSRAGSPGSVASKI TILSTPEGTSAACKSI LEIMHKEAQDI KFTEB RNITKOTGSKI LOGRERAL GERGRALL KKTEB TONLETA FROM TONLOOPRENT TYKGNVE I PLATIAHNNFVGRLI GERGRALL KKTEGOTDTKI TISTPEGTSAAPSTGAPPPTSGPPPTSGOPPS ATCAKAEBINKKI RESYENDI ASMNLOAHLI PGLINLAALGEPPTSGAPPTSGOPPSAK WTPPPTPGPPGSPETTYHOFI PALLS VGALI GRACOOPIKOLS RPAGASI KI APABAAPDAK VRMVI I TGPPBEAQFRAQCRI TGRIKEBENFUSPKESTKLAANI TRVPSRAARAT GKGGK TVNBLOALS SARVVPRDQTPDBNDQVVVKI TGHFYACQVAQRKI QBILLTQVKQHQOQ KALQSGPPGSPRRK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
2 (bases 1 to 4181)
wueller-Pillasch,F., Lacher,U., Wallrapp,C., Micha,A.,
imerhackl,F., Hameister,H., Varga,G., Friess,H., Buchler,M.,
Beger,H.G., Villa,M.R., Adler,G. and Gress,T.M.
Direct Submission
Submitted (11-APR-1997) Medizinische Klinik, Internal Medicine I, Robert-Koch-Str.8, Ulm 89081, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mueller, F., Gress, T. and Adler, G.
Medicament comprising a dna sequence, which codes for the
rna-binding koc protein, and comprising a koc protein or a dna
sequence of the koc promoter
Patent: WO 0220036-A 114-MAR-2002;
Mueller, Friederike (DB)
                                                                                                                                                                                                                                                                                                                                                                                                                            /function="possible proliferation of cancer tissues" /note="KH-domain containing protein overexpressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 22; DB 9; Length 4181; 100.0%; Pred. No. 5.3; tive 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="putative RNA binding protein KOC"
/protein.id="AAC35208.1"
/db_xref="GI:2105469"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  672. .2411
/note="unnamed protein product"
                                                                                                                                                                                                                                                                    /map="7p11.5"
/cell line="Paru8988t"
/cell_type="pancreatic cancer"
1. .4181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1181 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .4602
/organism="Homo sapiens"
/db_xref="taxon:9606"
672_ .2411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AX397963 4602 bp
Sequence 1 from Patent WO0220036.
AX397963
                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     851 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   748 CrĠCAAGGGTTTTGCTGGGCG 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AX397963.1 GI:21260818
                                                                                                                                                                                                                                                                                                                                                                  gene="koc"
                                                                                                                                                                                                                                                                                                                                                                                                             /gene="koc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
AX397963/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                             TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                            AUTHORS
         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mueller-Pillasch, Lacher, U., Wallrapp, C., Micha, A., Zimmerhackl, F., Lacher, H., Varga, G., Friess, H., Buchler, M., Zimmerhackl, F., Hameister, H., Varga, G., Friess, H., Buchler, M., Cloning of a gene highly overexpressed in cancer coding for a novel KH-domain containing protein oncogene 14 (22), 2729-2733 (1997) 97322117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSU97188
Homo sapiens putative RNA binding protein KOC (koc) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang,T., Wang,A., Skeiky,Y.A., Li,S.X., Kalos,M.D., Henderson,R.A., Mcneill,P.D., Fanger,N., Retter,M.W., Marnerakis,M., Fanger,G.R., Vedvick,T.S., Carter,D., Watanabe,Y. and Peckham,D.W.
                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAT 15-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (Dases 1 to 4181)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 4181;
                                                                                                                                                                                              Length 4181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 22; Conservative 0; Mismatches 0
                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA
                                                                                                                                                                                                     100.0%; Score 22; DB 6
100.0%; Pred. No. 5.3;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent: WO 0200174-A 175 03-JAN-2002;
CORIXA CORPORATION (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1181 t
                                                                                                                                    ų
                                                                                                                                                                                                                                                                                                                                                                                                                                            AX365782 4181 bp 1
Sequence 175 from Patent WO0200174.
AX365782
                                                                                                                                    1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
830 c 851 g 118:
                                                                                      organism="Homo sapiens"
                                                                                                              /db_xref="taxon:9606"
_830 c 851 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                           Location/Qualifiers
1. .4181
                     Avalon Pharmaceuticals (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               748 crecaaeeerrrrecreeece 727
                                                                                                                                                                                                                                                                                                                         748 CIGCAAGGGGTTTTGCTGGGCG 727
                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AX365782.1 GI:18697320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CTGCAAGGGGTTTTGCTGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U97188
U97188.1 GI:2105468
                                                                                                                                                                                                                                                                                                 1 CTGCAAGGGGTTTTGCTGGGCG
                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                             Best Local Similarity
Matches 22; Conserv
                                                                                                                                         1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human.
```

source

FEATURES

JOURNAL

TITLE

BASE COUNT ORIGIN

PAT 27-MAY-2002

HSU97188/c LOCUS

RESULT 10

ð

DEFINITION

ACCESSION

VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

JOURNAL MEDLINE PUBMED

TITLE

ö

Gaps

; 0

```
Direct Submission
Submitted (01-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
(Dases 1 to 104668)
Waterston,R.
                                                                                                                                                                                                                                                                               Submitted (04-JUN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Mar 25, 2001 this sequence version replaced gi:9665195.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University, and the Washington University Genome Sequencing Center. For additional information thips://www.nhgri.nh.gov/DIR/GTB/CHR7, send mailto:egreen@hhgri.nih.gov, or see http://genome.wustl.edu/gsc
Submitted (25-MAR-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The clone sequenced to the left is CTA-271G13, 200 bp overlap; the clone sequenced to the right is AC023375. Actual start of this clone is at base position 102112 of CTA-271G13; actual end is at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is from the first BAC library from Genome Systems, Inc. (http://www.genomesystems.com).
Cell line: lymphoblastoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence from 80185 to 80225 was derived from PCR product of
                                                                                                                                                                                                                                                                                                                                                           Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
----- Summary Statistics
Center project name: H_GS117B04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone is at base position luzing unbase position 104668 of GSI-117B4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .104668
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="GS1-117B4"
/clone_lib="GSBAC1"
1042. 1339
/rpt_family="Alu"
1733. 2070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GS1-117B4 BAC DNA.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VECTOR: pBeloBAC
Selection: chloramphenicol
                                             MO 63108, USA
8 (bases 1 to 104668)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAPPING INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE INFORMATION:
                                                                                                                                                                                                                                                          Direct Submission
                                                                                                      Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haplotypes:
VECTOR: pRe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                AUTHORS
TITLE
JOURNAL
JOURNAL
                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                           REFERENCE
                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                       TITLE
  /procein ide="CAD32603.1"
/db xref="GI:21260819"
/db xref="GI:21260819"
/tranlation="MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDC PDESWALKAIFEALSGKIELHGKPIBVEHSVPRRQRIRKLQIRNIPPHLQWEVLDSLLV QYGVVBSCEGOVNTDSETAVVNVTYSSKDQARQALDKLANGFQLENFTLKYAYIPDEMAA QONPLOQPRGREGGORGSSRQGSPGSPKOKFCDLEALLAVPTOFVGAILGKEGATIRNITKQTGSKIDVHRKENAGAAEKSITILSTPEGTSAACKILLVYPTOFVGAILGKEGATIRNITKQTGSKIDVHRKENGAAEKSITILSTPEGTSAACKILLVYPTOFVGAILGKEGATIRNITKQTGSKIDVHRKENGAAEKSITILGTOFFTILTSPLQETLLVYTOFVGAILGKEGATIRNITKQTGSKIDVHRKENSANULQAHLIPGLNITATSPLQETLLYYNGRVETTTTVKGNVETCARAEBENKKTRESYENDIAASMULQAHLIPGLNIKALGFPPTSGAPPPTSGPPSAMTPPYPQGSETETVVQTPALIGKGGAIIGKGGGKTIYGKGAGKIYGKGGKTYVRITGHFYACQVAQRKIQBILTQVKQUQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (21-JAN-2000) Genome Sequencing Center, Washington
Noiversity School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 104668)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (10-SEP-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (30-SEP-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
7 (bases 1 to 104668)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 104668)
Sulston, J.E. and Waterston, R. Toward a complete human genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (03-AUG-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104668 bp DNA linear PRI 04. HOMO SADJENS BAC clone GS1-117B4 from 7, complete sequence. AC021876. SG1:13446341 HTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 22; DB 6; Length 4602; Best Local Similarity 100.0%; Pred. No. 5.2; Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                  16 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 104668)
Du,F., Stoneking,T. and Moeller,D.
The sequence of Homo sapiens BAC clone GS1-117B4
Unpublished (2001)
3 (bases 1 to 104668)
Waterston,R.H.
                                                                                                                                                                                                                                                                                                                                             918 g 1298 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1169 CTGCAAGGGTTTTGCTGGGGCG 1148
                                                                                                                                                                                                                                                                                                                     KALQSGPPQSRRK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MO 63108, USA
5 (bases 1 to 104668)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                             907 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9847074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
PUBMED
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
AC021876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
```

```
12928.
                                                                                                                                                                                                                                                                                          AC023375
                                                       repeat_region
                                                                                 repeat_region
                                                                                                              misc_feature
  misc_feature
                             misc_feature
                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                            AC023375
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST AA474176 (NID:g2202403) ve52g08.rl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST AA163596 (NID:g1739542) mn38g02.rl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST A1536708 (NID:94450843) tm87g10.x1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST AA163596 (NID:g1739542) mn38g02.rl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST AA474176 (NID:92202403) ve52g08.rl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST A1606545 (NID:94615712) vb29b12.y1"
                                                                                                                                                                     EST A1536708 (NID:94450843) tm87g10.x1"
                                                                                    EST R99288 (NID:9985889) yq71b08.81"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST BF217988 (NID:g11111574)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rpt family="MIR"
0706. 10841
note="similar to EST AU127673 (NID:g10988027)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST AU127673 (NID:910988027)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST BF241103 (NID:g11155028)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST AX070710 (NID:g12580495)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST AU127673 (NID:910988027)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST BF241103 (NID:911155028)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l673. .8760

rpt_family="L1"

1769. .8789

rpt_family="AT_rich"

10047. .9305

rnote="similar to EST BE308143 (NID:99164347)"
     EST BF469008 (NID:g11538191)"
                                                                                                                                                                                                                                           476. 4694
/rpt_family="Malk"
4955. 4821
/rpt_family="Ralu"
/rpt_family="Malk"
5363. 5487
/rpt_family="Malk"
560. 5728
/rpt_family="Malk"
6641. 6750
/rpt_family="Malk"
6641. 7750
                                                                                                     168. .3193
rpt_family="AT_rich"
432. .3453
                                                                                                                                              rpt_family="AT_rich"
447. .3677
                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="MIR"
7826. .8136
/rpt_family="Alu"
8384. .8663
/rpt_family="Alu"
8596. .8944
/note="Similar to I
                                              2277. .2563
/rpt_family="Alu"
2461. .2908
/note="similar to E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0723. .10841
note="similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="similar to
                                                                                                                                                                                                        3654. .3956
/rpt_family="Alu"
4476. .4694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2253. .12638
rpt_family="MaLR"
2928. .13050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         052. .9177
note="similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12928. .13050
/note="similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               052. .9177
note="similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0706. .10841
note="similar to
                                                                                                                                                              447. .3677
note="similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1047. .9280
note="similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     052. .9177
note="similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rpt_family="MIR"
0437. .10549
          'note="similar to
                  .062. .2084
rpt_family="(A)n"
                                                                                                                                                                                        487. .3593
rpt_family="Alu"
654. .3956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .10372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                        repeat_region
                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                           repeat_region
                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                               misc_feature
                                                                                                                                                                 misc_feature
```

```
Biren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavkiy, L., Anderson, S., Baldwin, J., Burkett, G., Campopiano, A., Costle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Dodge, S., Domino, M., Doyle, M., Garlano, Y., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grant, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grant, J., Largocque, K., Denose, C., Kann, L., Karatas, A., Howland, J., Landers, T., Largocque, K., Lehoczky, J., Levine, R., Klein, J., Landers, T., Macdonald, P., Marquis, N., McCarthy, M., Lieu, C., Liu, G., Lock, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Manga, V., Morrow, J., Naymon, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., and Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission

Direct Submission

Submitted (14 PEB-2000) Whitehead Institute/MIT Center for Genome Submitted (14 PEB-2000)

Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Birren, B., Lintcon, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Gardyna, Gardyna, S., Gardes, S., Goyette, M., Grand, J., Cardyna, S., Ginde, S., Goyette, M., Grand, M., Gage, D., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Karatas, A., Klein, J., Lascoque, K., Lamazaretes, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158105 bp DNA linear HTG 24-AUG-2002
me 7 clone RP11-571M6 map 7, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 158105)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
(NID:g11155028)
                                                                     EST AV612377 (NID:99748047)"
                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                             Score 22; DB 9; Length 104668; Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 7, clone RP11-571M6 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
        EST BF241103
                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens chromosome 7 clon
SEQUENCE, 37 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC023375.2 GI:7209933
HTG; HTGS_PHASE1; HTGS_DRAFT.
            /note="similar to
12945. .13050
/note="similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 18478 Cracaacacarriracracaca 18499
                                                                                                                                                                                                                                              /rpt_family="Alu"
14561. .14722
                                                                                                                           13115. .13172
/rpt_family="L2"
13571. .13877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%;
Matches 22; Conservative 0.
```

TITLE JOURNAL COMMENT

```
6644 66543: gap of 100 bp 66544 72068: contig of 5525 bp in length 72069 72168: gap of 100 bp 72169 7427: contig of 6259 bp in length 78428 7827: gap of 100 bp 78528 83366: contig of 6259 bp in length 83367 83466: gap of 100 bp 83467 89726: contig of 6260 bp in length 83467 89799: contig of 8153 bp in length 89827 99799: contig of 8153 bp in length 89827 89799: contig of 8153 bp in length 89827 89799: gap of 100 bp 67500 pp 67500 p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106169 106268: gap of 100 bp 106269 114387: contig of 8119 bp in length 11438 114487: gap of 100 bp 121729 121719: contig of 6125 bp in length 121720 121819: gap of 100 bp 121820 130088: contig of 8269 bp in length 130089 130188: gap of 100 bp 130189 139207: contig of 9019 bp in length 130189 139207: contig of 9019 bp in length
                                         p of 100 bp
contig of 3039 bp in length
p of 100 bp
contig of 3054 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139208 139307; gap of 100 bp
139308 158105; contig of 18798 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                       oof 100 bp contig of 3662 bp in length
                                                                                                                                                                                                                                                                                                                              contig of 2899 bp in length
                                                                                                                                                                                                                                                                                                                                                                                          30: gap of 100 bp 46601: contig of 4471 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01: gap of 100 bp 51387: contig of 4686 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51487: gap of 100 bp 55227: contig of 3740 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55327: gap of 100 bp 59146: contig of 3819 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               p of 100 bp contig of 3293 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39: gap of 100 bp 66443: contig of 3804 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       p of 100 bp contig of 8089 bp in length ap of 100 bp contig of 8119 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone lib="RPCI-11 Human Male BAC" 1036
                                                                                                                                                                                96: gap of 100 bp 35269: contig of 2973 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   905. .6404
note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          505. .8366
note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .137. .2213
note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2314. .3566
/note="аввеmbly_fragment<sup>:</sup>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3667. .4804
'note="assembly_fragment'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3467. 10126
'note="assembly_fragment'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
|db_xref="taxon:9606"
|chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="RP11-571M6"
                                                                                                                                                                                                                                                           gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                          46701: gap of
                                                                                                        9043 29142: gap of 9143 32196: con
                                                                                                                                                                                                                                                                                                                       39131: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59246: gap of
62539: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0227. .11460
                                                                                                                                                                                                                                                                                            39031
                                                                                                                                                                                                                                                                                                                                                                42030
                                                                                                                                                                                                                                                   5270 35369:
                                                                                                                                                                                                                                                                                                                                                                                          42130:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62639:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55328
59147
59247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62540
62640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
Murphy, T., Naylor, J., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Muslph, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Plaani, C., Pollvar, T.H., Oliver, J., Peterson, K., Pierre, N., Plaani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stange-Thomann, N., Schauber, S., Severy, P., Spencer, B., Tesfange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Vassiliev, H., Viell, R., Vo, A., Milson, B., Wu, X., Wyman, D., Ye, W. J., Direct Submission.
                                                                                                                                                                                                                                                                                                                                             Submitted (34-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Max 8, 2000 this sequence version replaced gi:6970513.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 37 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the dans are impresented.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert size: 174000; agarose-fp
Insert size: 154505; sum-of-contigs
Quality coverage: 3.2 in Q20 bases; agarose-fp
Quality coverage: 3.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: 14227
Center clone name: 571 M.6
Center clone name: 571 M.6
Sequencing vector: M13; M77915; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 133946 bases at least Q40
Consensus quality: 149818 bases at least Q30
Consensus quality: 149412 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www-seg.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 bp
of 1077 bp in length
100 bp
of 1253 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4805 4904: gap of 100 bp 4905 6404: contig of 1500 bp in length 6505 8366: contig of 1862 bp in length 8367 8466: gap of 100 bp 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1036: contig of 1036 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 bp
of 1138 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 bp
2137 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10226: gap of 100 bp 11460: contig of 1234 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig of 1537 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34: gap of 100 bp 16434: contig of 1000 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig of 2366 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            p of 100 bp contig of 1918 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   p of 100 bp contig of 2092 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10: gap of 100 bp
25903: contig of 2693 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig of 2137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            con.
13697:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13698 13797; gap of 15398; cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34: gap of 18900: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21018: gap of 23110: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18901 19000: gap of 19001 20918: con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1037 1136; gap of
1137 2213; cor
2214 2313; gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1567 3666; gap of
1667 4804; cc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3566:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16435 16534: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15434:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23210:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10227 114,
11461 11560:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21019
```

PRI 27-JUN-2002

ö

Gaps

ö

misc\_feature

Query Match

ð

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL REFERENCE

AUTHORS TITLE JOURNAL

COMMENT

LOCUS DEFINITION

RESULT 14 AC090069

```
Unpublished
Unpublished
E (bases I to 200956)
Direct Submission
E (bisect I to 200956)
E (bise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaul, R. K., Olson, M. V., Zhou, Y., James, R. A., Rouse, G., Wu, Z., Saenphimmachak, C., Phelps, K. A., Buckley, D., Kibukawa, M., Raymond, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 200956)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Overlapping Sequences:
5': RP11-348P10 (UWGC:bc0377) AC124045
3': RP11-578F5 (UWGC:bc0477) AC105902, 95352-bp overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200956 bp DNA linear PRI 27-JUJ Homo appiens chromosome 3 clone RP11-68104, complete sequence. AC104165 AC104165.2 GI:21617715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: unknown; 42% of reads Sequencing vector: unknown; 42% of reads Sequencing vector: plasmid; 58% of reads Chemistry: Dye-terminator Er; 80% of reads Chemistry: Dye-terminator Big Dye; 20% of reads Chemistry: Dye-terminator Big Dye; 20% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 200732 bases at least Q40 Consensus quality: 200990 bases at least Q20 Consensus quality: 200947 bases at least Q20 Insert size: 200956; sum-of-contigs Quality coverage: 10.4x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                        Length 98951;
                                                           /clone="CTD-2162G15"
/clone="CTD-2162G1Fch human BAC library D"
22060 c 20767 g 26935 t 605 others
                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.genome.washington.edu
Contact: uwgchtgs@u.washington.edu
Drafting Center: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project Information
Center project name: chr-3
Center clone name: RP11-68104 (bc0528)
                                                                                                                                                                                                                  Score 18.8; DB 2;
Pred. No. 1.6e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Summary Statistics
   /db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence Quality Assessment:
                                                                                                                                                                                                                                                                                                                                                                                                           Db 10782 Crácaladadatrrracrardad 10803
                                                                                                                                                                                                                                                                                                                                                      22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center Code: UWGC
                                                                                                                                                                                                                                85.5%;
                                                                                                                                                                                                                                                                                                                                                         1 CTGCAAGGGGTTTTGCTGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Unpublished
                                                                                                                                                                                                                                                                                              20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and Haugen, E.D.
                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                             28584 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS
DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
AC104165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERÊNCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Consensus quality: 91863 bases at least Q40
Consensus quality: 97429 bases at least Q20
Consensus quality: 97429 bases at least Q20
Consensus quality: 97439 bases at least Q20
Consensus quality: 97483 bases at least Q20
Consensus quality: 97483 bases at least Q20
Betimated insert size: 103000; agarose-fp estimation
Estimated insert size: 98351; sum-of-contigs estimation
Quality coverage: 5.7 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* NOTE: This is a 'working draft' sequence record is
* is not known and their order in this sequence record is
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                 AC090069

Homo sapiens chromosome 5 clone CTD-2162G15, WORKING DRAFT
SOUGNOE, 7 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (Date 1 to 98951)
2 (Date 2 to 98951)
Direct Submission
Submitted (14-FEB-2001) Production Sequencing Facility, DOE Joint
Submitted (14-FEB-2001) Production Sequencing Facility, DOE Joint
Submitted (14-FEB-2001) Production Sequencing Facility, DOE Joint
Cenne (14-FEB-2001) Production Sequencing Facility, DOE Joint
Center: Joint Genome Institute
                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 98951)
DDE Joint Genome Institute.
Sequencing of Human Chromosome 5
                                                                                                                                                          Gaps
                                                                                                                                                          ö
                                                                                        100.0%; Score 22; DB 2; Length 158105; 100.0%; Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27136: contig of 9851 bp in length
27236: gap of unknown length
53346: contig of 26110 bp in length
53446: gap of unknown length
98951: contig of 45505 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1640: contig of 1640 bp in length
1740: gap of unknown length
4817: contig of 3077 bp in length
4917: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gap of unknown length
contig of 5562 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig of 6606 bp in length
gap of unknown length
                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACO90069.1 GI:12830173
HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
Homo sapiens
Homo sapiens
                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Project Information
Center Project Name: 689916
Center clone name: CITB-H1_2162G15
/note="assembly_fragment"
16535. .18900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            veb site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cocation/Qualifiers
                                                                                                                                                                                                                                                                       Db 148579 CTGCAAGGGTTTTGCTGGGCG 148600
                                                                                                                                                                                                                                1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center Code:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1641
1741
4818
4918
10480
10580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27137
27237
53347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53447
                                                                                                                                       Best Local Similarity
Matches 22; Conserv
```

source

FEATURES

1074   799   5028   3183   3186   7174   7174   7174   7174   7174   7174   7174   7174   7174   7174   7174   7175   7175   7171   7174   7171   7175   7171   7174   7171   7175   7171   7175   7171   7175   7177   7	4991 2631 2446	1662 4991 2446	1243	9869 14339 3560	3031	3311	1662	2446	1073	3909	2110	0 8 0 0 ×	×800	6318	1243	4784	1073 1073	2631	2446	1243
1074   799   5028   3183     1074		-	1 1 1				1694	2370	1139	3946	2109	- 1		6129	1250	4768	1083	2602	2449	- ; ;
4899 5028  774 799  10749 10616  1150 1602  8868 8810  5884 5889  5884 5889  771 799  11706 11675  369 4800  3177 5288  5	3186 16678 1629	7427 7939 4106 760	2496 5399	21498 4106 7939	3366	7427	3186	5849	<800	3186 2097	8571	760	3005							
10749 10749 1107	3183	7261	2395	21139	7411	7272	8214	5836	419	3260	85568	741	2905							
	5028 799 10616	1602 8810 5889 1529	11675	<800 5288 2950	<800	3725	5288	6934	<800	<800 3725	6934	3725	<800	5028	1133	1069	1133	6934	3264	1697 3529
Manual   M	4899	1 1 1	11706	369 5177 2916	137	3857	5343	6819	569	135	6741	3707	703	5047	1134	1070	- ; ;	: :	- ;	- ; ;
This entry estimates All manual Quality le leartry le leartry le leartry le leartry le control leartry le control leartry le control leartry le leartry lea	entry has been annotated with sequence quality nates computed by the Phrap assembly program. nanually edited bases have been reduced to quality zero. Ity levels above 40 are expected to have less than for in 10,000 bp.  by base quality values are not generally visible from the mix flat falle format but are available as part	This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one with	Subclone; and the assembly was confirmed by restriction digest. Sequence Validation: This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest	ents with sequence-predicted fragments is given below. lectronically-digested sequence consists of both insert and r, in order to accurately represent the entire circular BAC. fragments below a variable cutoff (approximately 400-800 bp) of resolved in the findernrint and honce of more	e table. There are no significant remaining discrepancies en the experimental and predicted values. Uniquely ordered ents are separated by dashed lines.	Map FngrPrnt SeqDerMap FngrPrnt SeqDerMap FngrPrnt	5288 8696 8571 3534	6934 6068 6154	< 800 11400 11207 449	9 1439 96 <800 5736 0 <800 4100 4106 2978	3725 779 760 8146	<pre>&lt;800 1221 1170 4465 &lt;800 278 &lt;800 2239</pre>	1919 8458 8571 45	5028 12014 11879 4368 	6934 1177 1170 4633	5889 153 <800 1462	1816 1993 1932 2058 	<800 132 <800 1321	<800 4939 4965 528	1919 466 <800 1640 3529 1311 1279 8779

Ouery Match
Best Local Similarity 90.9%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Qy 1 CTGCAAGGGTTTTGCTGGGG 22 Db 27941 CTGCCAGGGTTTTGCTGGGTG 27962

ô

0; Gaps

Search completed: April 18, 2003, 06:17:22 Job time : 385 secs

Lung cancer relate Human KOC DNA. Ho

Rat differential t Permease fccI nucl DNA encoding novel

DNA encoding cance Human lung cancer Human KOC DNA. H Drosophila melanog Bacterium 2412.1 Gesophagus cancer Human cancer relat Human genomic DNA Corn tassel-derive Human colon cancer

Human prostate exp Human immune/haema DNA encoding novel Human gene express Human colon cancer Corn acid triacylg

Streptococcus poly Drosophila melanog Drosophila melanog Drosophila melanog E. coli strain DSM

Human Kruppel-like Human Kruppel-like Human nervous syst Human nervous syst

fuman acetyl-Coenz

3

019

Knuth A,

щ Jager Nucleotides representing cancer-associated genes, used to develop products for the diagnosis, monitoring and treatment of cancers

lung cancer-lung tumour lung tumour lung tumour

W4510 F B O

000000

Result

Sequence:

ü ü

Searched:

Database

```
Cancer associated antigen; KOC-1; cancer; vaccine; CT7; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCR primer for DNA encoding cancer associated antigen KOC-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stockert E,
                                                                                                                                                                                                            ABN64702
ABK85261
ABL72849
                                                                                                                                                                                                                                                                                                                      AAST0767
AAZ17200
AAA02465
AAZ34953
ABN67088
ABL02757
ABL22680
                                                                                                                                                                                                                                                                                        ABV54482
AAK77132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAL42134
AAL42135
ABA15166
ABA15164
ABA15164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US05766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0061709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ36156 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gure A, Tsang S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-FEB-2000 (first entry)
                                                     4181
4601
861
1206
1985
1985
18776
302250
75899
                                                                                                                                                                                                                                                                                                                                    782
784
859
11563
22286
47339
4750
55547
6232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-013284/01.
                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9954738-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-OCT-1999
                                                                                                                                                             117.2
117.2
116.2
116.2
116.2
116.2
116.2
116.2
116.2
116.2
116.2
116.2
116.2
116.2
116.2
116.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ3615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR primer for DNA
Human bone marrow
Probe #25064 used
Human bone marrow
Probe #12084 used
                                                                                                           (without alignments)
505.551 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                          N. Geneseq 101002:*

| SIDS2/gcgdata/geneseqrgeneseqn-embl/NA1980.DAT;*
| SIDS2/gcgdata/geneseqrgeneseqn-embl/NA1981.DAT;*
| SIDS2/gcgdata/geneseqrgeneseqn-embl/NA1981.DAT;*
| SIDS2/gcgdata/geneseqrgeneseqn-embl/NA1981.DAT;*
| SIDS2/gcgdata/geneseqrgeneseqn-embl/NA1984.DAT;*
| SIDS2/gcgdata/geneseqrgeneseqn-embl/NA1984.DAT;*
| SIDS2/gcgdata/geneseqrgeneseqn-embl/NA1986.DAT;*
| SIDS2/gcgdata/geneseqrgeneseqn-embl/NA1980.DAT;*
| SIDS2/gcgdata/geneseqrgeneseqn-embl/NA1980.DAT;*
| SIDS2/gcgdata/geneseqrgeneseqn-embl/NA1980.DAT;*
| SIDS2/gcgdata/geneseqrgeneseqn-embl/NA1980.DAT;*
| SIDS2/gcgdata/geneseqrgeneseqn-embl/NA1990.DAT;*
| SIDS2/gcgdata/geneseqrgeneseqneembl/NA1990.DAT;*
| SIDS2/gcgdata/geneseqrgenembl/NA1990.DAT;*
| SIDS2/gcgdata/geneseqrgenembl/NA1990.DAT;*
| SIDS2/gcgdata/geneseqrgenembl/NA20018.DAT;*
| SIDS2/gcgdata/geneseqrgenembl/NA20022.DAT;*
| SIDS2/gcgdata/geneseqrgenembl/NA20022.DAT;*
| SIDS2/gcgdata/geneseqrgenembl/NA20022.DAT;*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                      April 18, 2003, 04:12:35 ; Search time 98 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human
Probe
Human
Probe
Human
Human
GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                           2185239 seqs, 1125999159 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                               . nucleic search, using sw model
                                                                                                                                                                                1 ctgcaaggggttttgctgggcg 22
                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ36156
AAK50392
AA156378
AAK37520
AAI43398
AAL49254
ABL49254
ABL49299
                                                                                                                                                                                                              IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                  US-09-270-437D-10
22
                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1000.00
                                                                                                                                                                  Perfect score:
                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22222222222
                                                        OM nucleic
```

the probes of the invention.

&\$99999999999888

```
per perimers AAZ36155-56 were used to amplify a cancer associated antigen gene designated KOC-1. The specification also describes a cancer associated antigen designated CT7. The CT7 polymucleotide was isolated associated antigen designated CT7. The CT7 polymucleotide was isolated from SK-MEL-37 melanoma cells. The polymucleotide has some homology with MGGE-10, limited to about 210 carboxy terminal amino acids. The amino cerminal of the protein has a repetitive pattern, with repeats rich in terminal of the protein has a repetitive pattern, with repeats rich in termine, proline, glutamine and leucine, and an almost invariable core of serine, proline, glutamine and leucine, and an almost invariable core of peptides which provoke lysis by cytolytic T cells. The polymucleotides and polypeptides can be used for treating a cancerous condition and an application with an antigens can be used as an immunogenic or vaccine composition with an adjuvant, e.g. a cytokine, a saponin, or granulocyte macrophage-colony continuating factor (GM-CSF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; SEQ ID NO: 24949; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human bone marrow expressed single exon probe SEQ ID NO: 24949.
                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                            21; Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 22; DB 21
100.0%; Pred. No. 0.52;
                                                                                                                                                                                                                                                                                                                                                     Sequence 22 BP; 2 A; 4 C; 10 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen W, Rank DR;
Claim 108; Page 13; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0608408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 Crgcaagggriffgcrgggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAK50392 standard; DNA; 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-488900/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200157276-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAK50392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
AAK50392/c
```

셤

ઠ

```
ö
                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                            Probe #25064 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 22; DB 22; Length 282; 100.0%; Pred. No. 0.72; 1.1ve 0; Mismatches 0; Indels (
                                         Query Match
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                     Probe; microarray; human; placenta; antenatal diagnosis;
genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 282 BP; 77 A; 79 C; 70 G; 56 T; 0 other;
                 Sequence 282 BP; 77 A; 79 C; 70 G; 56 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 25; SEQ ID No 25064; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAK37520/c
ID AAK37520 standard; DNA; 588 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97 CIGCAAGGGTTTTGCTGGGCG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                AAI56378 standard; DNA; 282 BP.
                                                                                                                            97 crecaaedetrirecredece 76
                                                                                                     CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2001; 2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
nes 22; Conservative
                                                                                                                                                                                                                                                       17-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-488897/53.
                                                                                                                                                                                                                                                                                                                        genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                WO200157272-A2.
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                               AA156378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                            RESULT 3
AAI56378/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 요
                                                                                                                                                                                                                  ð
8 X G
                                                                                                                                 셤
                                                                                                           à
```

```
The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y Match 100.0%; Score 22; DB 22; Length 588; Local Similarity 100.0%; Pred. No. 0.78; hes 22; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 588 BP; 156 A; 139 C; 143 G; 150 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human lung cancer-associated cDNA antigen L523S.
                                                                                                                                                                                                                                                                                                             Claim 25;. SEQ ID No 12084; 654pp; English.
                                                                                                                                                                                                        Chen W, Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96
                                        04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-023657.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CTGCAAGGGGTTTTGCTGGGCG 22
             30-JAN-2001; 2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 CTGCAAGGGGTTTTGCTGGGCG
                                                                                                                                                                                                     Hanzel DK,
                                                                                                                                                                                                                                   WPI; 2001-488897/53.
                                                                                                                                                                                                      Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe #12084 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; SEQ ID NO: 12077; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 22; DB 22; Length 588; larity 100.0%; Pred. No. 0.78; Conservative 0; Mismatches 0; Indels
                                                            Human bone marrow expressed single exon probe SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe, microarray, human, placenta, antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 588 BP; 156 A; 139 C; 143 G; 150 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen W, Rank DR;
                                                                                              expressed exon;
                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 crecaAccerriricriccece 96
                                                                                                                                                                                                                                                                                    2000US-0207456

2000US-0608408

2000US-0632366

2000US-0234687
                                                                                                                                                                                                                                                                                                                                21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1398/c
AAI43398 Btandard; DNA; 588
                                                                                                                                                                                                                                                                                                                                                                                                                                     Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genetic disorder; ss.
                                                                                            Human; bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-488900/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                        WO200157276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200157272-A2
                                                                                                                                                                                                                                                                                    26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                           Homo sapiens
                              06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2001
 AAK37520;
                                                                                                                                                                                                                                                                                                                                                                                                                                  SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA143398;
```

REGULT 5
AA143398/C
ID AA143398/C
AAC AA14:
AX AA14:
AX AA14:
AX AA14:
AX BE Probe
XX Probe
XX Genel
XX Genel
XX Homo

셤 ò

Penn

ô

Gaps

ö

ö

which

```
comprising an immunogenic portron of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polynuclectides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polynucleotides encoding P2 or antigen presenting calls expressing P2 and then administered to the patient to inhibit
Isolated polypeptide comprising an immunogenic portion of a lung tumor protein is used for detecting and monitoring progression of lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polynucleotides encoding lung tumor polypeptides, useful for treating
lung cancer or stimulating an immune response -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson R.
PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;
IS, Carter D, Watanabe Y, Peckham DW;
                                                                                                                                                                                                                                                                                                        100.0%; Score 22; DB 21; Length 1740; llarity 100.0%; Pred. No. 0.9; Conservative 0; Mismatches 0; Indels 0;
                                                                                          This invention describes a novel isolated polypeptide (I)
                                                                                                                                                                                                                                                                             Sequence 1740 BP; 526 A; 406 C; 417 G; 391 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human lung tumour L523S cDNA sequence SEQ ID NO:347.
                                                                  Claim 1a; Page 258-259; 261pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Page 330; 374pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL49254 standard; cDNA; 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0630940.
2000US-0643597.
2000US-0662786.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-OCT-2000; 2000US-0685696.
12-DEC-2000; 2000US-0735705.
07-MAY-2001; 2001US-0850716.
                                                                                                                                                                                                                                                                                                                                                                                                       498 CTGCAAGGGGTTTTGCTGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUN-2001; 2001WO-US21065
                                                                                                                                                                                                                                                                                                                                                                              1 CTGCAAGGGGTTTTGCTGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McNeill PD, Fanger N,
Vedvick TS, Carter D,
                                                                                                                                                                                                                                                        development of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-090513/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immune response; ss
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; ABB74997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200200174-A2.
                                      in a patient -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang T,
McNeill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL49254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL49254/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                   ò
```

(first entry)

The present invention describes human lung tumour proteins. Human lung

Henderson RA;

2000US-0606421.

```
The present invention describes human lung tumour proteins. Human lung actions and polynucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies, tusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
tumour proteins and polymucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polymucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polynucleotides encoding lung tumor polypeptides, useful for treating lung cancer or stimulating an immune response -
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                Human lung tumour L523S recombinant polynucleotide SEQ ID NO:447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Henderson RA;
                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fanger GR;
                                                                                                                                                                   100.0%; Score 22; DB 24; Length 1740; 100.0%; Pred. No. 0.9; ive 0; Mismatches 0; Indels 0;
                                                                                                                                         Sequence 1740 BP; 526 A; 406 C; 417 G; 391 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g A, Skeiky YAW, Li SX, Kalos MD,
Fanger N, Retter MW, Marnerakis M,
Carter D, Watanabe Y, Peckham DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 367; 374pp; English.
                                                                                                                                                                                                                                                                                                                                                뗦.
                                                                                                                                                                                                                                                             498 CTGCAAGGGTTTTGCTGGGCG 477
                                                                                                                                                                                                                                        CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                ABL49297 standard; cDNA; 1743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0606421.

2000US-0630940.

2000US-0643597.

2000US-062786.

2000US-078596.

2000US-078596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUN-2001; 2001WO-US21065
                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002-090513/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immune response; ss
                                                                                                                                                                                Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-090513/
P-PSDB; ABB75053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200200174-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-OCT-2000; 12-DEC-2000; 07-MAY-2001; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang T, Wang
McNeill PD,
Vedvick TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-AUG-2000;
21-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention.
                                                                                                                         invention.
                                                                                                                                                                                                                                                                                                                                                                               ABL49297;
                                                                                                                                                                                                                                                                                                                     RESULT 8
ABL49297/c
                                                                                                                                                                                                                                             Н
                                                                                                                                                                                                                                                                                                                                                    В
                 8$88888888
                                                                                                                                                                                                                                              ઠ
                                                                                                                                                                                                                                                                                                                                                          ö
```

Gaps

ö

477

22

(first entry)

g

셤

ò

```
Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
                                                                                                                                                                                Human lung tumour L523S recombinant polynucleotide SEQ ID NO:428.
                                                                          ABL49283 standard; cDNA; 1764 BP
                                                                                                                                                                                                                                                                                                                                                                                                                      02-AUG-2000; 2000US-0630940.
21-AUG-2000; 2000US-0643597.
15-SER-2000; 2000US-0662786.
09-OCT-2000; 2000US-0659696.
12-DEC-2000; 2000US-0735705.
07-MAY-2001; 2001US-0850716.
                                                                                                                                                                                                                                                                                                                                                                       28-JUN-2001; 2001WO-US21065
                                                                                                                                                                                                                                   immune response; ss
                                                                                                                                                                                                                                                                                                   WO200200174-A2.
                                                                                                                                              01-MAY-2002
                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                         28-JUN-2000;
                                                                                                                                                                                                                                                                                                                                        03-JAN-2002
                                                                                                             ABL49283;
                                                          ABL49283/
                                                                          ð
                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes human lung tumour proteins. Human lung activaties, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or estimalating an immune response. ABL48959 to ABL49300 and ABB74946 to ABLA9570 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                             Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polynucleotides encoding lung tumor polypeptides, useful for treating lung cancer or stimulating an immune response -
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                               Human lung tumour L523S recombinant polynucleotide SEQ ID NO:450
                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Henderson RA;
                                  100.0%; Score 22; DB 24; Length 1743; llarity 100.0%; Pred. No. 0.9; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 22; DB 24; Length 1743; 100.0%; Pred. No. 0.9; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fanger GR;
Sequence 1743 BP; 527 A; 406 C; 418 G; 392 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1743 BP; 527 A; 406 C; 418 G; 392 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, I
McNeill PD, Fanger N, Retter MW, Marnerakis M,
Vedvick TS, Carter D, Watanabe Y, Peckham DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 370; 374pp; English.
                                                                                                                                      498 criccaadecerriricerecece 477
                                                                                                      22
                                                                                                                                                                       RESULT 9
ABL49299/c
ID ABL49299 Btandard; CDNA; 1743
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUN-2000, 2000US-0606421.
02-AUG-2000, 2000US-0630940.
21-AUG-2000, 2000US-0643597.
15-SEP-2000, 2000US-0662786.
09-OCT-2000; 2000US-068596.
12-DEC-2000, 2000US-0735705.
07-MAY-2001, 2001US-0850716.
                                                                                                    1 CTGCAAGGGGTTTTTGCTGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JUN-2001; 2001WO-US21065
                                                                                                                                                                                                                                                                                            01-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-090513/12.
P-PSDB; ABB75054.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORI-) CORIXA CORP
                         Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                     response; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200200174-A2
                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention.
                                                                                                                                                                                                                                                             ABL49299;
                                                                                                                                                                                                                                                                                                                                                                                   1mmune
```

```
ö
                                                                                                                                                                                                                                                                                                                                                               The present invention describes human lung tumour proteins. Human lung tumour proteins and polynucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABL49559 to ABL49300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                     Polynucleotides encoding lung tumor polypeptides, useful for treating lung cancer or stimulating an immune response -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                       Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                Fanger GR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 22; DB 24; Length 1764; 100.0%; Pred. No. 0.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1764 BP; 534 A; 417 C; 419 G; 394 T; 0 other;
                                               Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD,
McNeill PD, Fanger N, Retter MW, Marnerakis M,
Vedvick TS, Carter D, Watanabe Y, Peckham DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                   Claim 1; Page 355-356; 374pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ36150 standard; DNA; 4159 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   519 creckAcccirrrrccreccc 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CTGCAAGGGGTTTTGCTGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                           2002-090513/12.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 22; Conserv
                                                                                                                                                        WPI; 2002-090513/
P-PSDB; ABB75048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ36150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ36150/c
ID AAZ3615
XX
AC AAZ3615
XX
DT 11-FEB-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
```

ö

Gaps

ö

crechaederrrrecreece 477

498

CTGCAAGGGGTTTTGCTGGGCG 22

ઠે

Chen Y,

```
99US-0285479
                                                                                                                                               WPI; 2000-628399/60.
P-PSDB; AAB11328.
                                                                                       (CORI-) CORIXA CORP.
                                                                                                                      Fan L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200194629-A2.
                                                                                                                                                                                                            protein is used
in a patient -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-SEP-2000;
20-SEP-2000;
20-SEP-2000;
22-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUN-2000;
                            30-DEC-1999;
10-JAN-2000;
                                                           22-FEB-2000;
              17-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-DEC-2001
   02-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABL65405;
                                                                                                                   Wang T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL65405/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
   The present sequence represents a cancer associated antigen gene designated KOC-1. The specification also describes a cancer associated antigen designated CT7. The CT7 polymucleotide was isolated from antigen designated CT7. The CT7 polymucleotide was isolated from CSC SK-MEL-37 methanoma cells. The polypeptide has some homology with MAGE-10, limited to about 210 carboxy terminal amino acids. The amino terminal of the protein has a repetitive pattern, with repeats rich in serine, proline, glutamine and leucine, and an almost invariable core of the peptide given in AAVAS877. The CT7 polypeptide can be processed to peptides which provoke lysis by cytolytic T cells. The polymucleotides and polypeptides can be used for treating a cancerous condition and screening for or diagnosing cancerous conditions. The cancer associated antigens can be used as an immunogenic or vaccine composition with an adjuvant, e.g. a cytokine, a saponin, or granulocyte macrophage-colony stimulating factor (GM-CSF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                           old LJ;
                                                                                                                                                                                                                                                                                                                     Nucleotides representing cancer-associated genes, used to develop products for the diagnosis, monitoring and treatment of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 22; DB 21; Length 4159;
Pred. No. 1;
                                                                                                                                                                                                                                                           Knuth A,
                                              Cancer associated antigen; KOC-1; cancer; vaccine; CT7; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4159 BP; 1281 A; 830 C; 851 G; 1181 T; 16 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                           Jager E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                     DNA encoding cancer associated antigen KOC-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human lung cancer-associated cDNA L523S.
                                                                                                                                                                                                                                                             Stockert E,
                                                                                                                                                                                                                                                                                                                                                                  Claim 88; Page 39-40; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC65900 standard; cDNA; 4181 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           748 criccaaccirririccredece 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22
                                                                                                                                                                                                                                (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%;
Matches 22; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CTGCAAGGGGTTTTGCTGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-APR-2000; 2000WO-US08896
                                                                                                                                                                        99WO-US05766
                                                                                                                                                                                                      98US-0061709
                                                                                                                                                                                                                                                              Tsang S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine; detection; ss.
                                                                                                                                                                                                                                                                                          WPI; 2000-013284/01.
                                                                                                                                                                                                                                                                Gure A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-FEB-2001
                                                                                  Homo sapiens
                                                                                                                W09954738-A1
                                                                                                                                                                        16-MAR-1999;
                                                                                                                                                                                                      17-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-OCT-2000
                                                                                                                                            28-OCT-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC65900;
```

RESULT 12 AAC65900,

g

ò

```
This invention describes a novel isolated polypeptide (I) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polymuclectides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T.Cells isolated from a patient are treated with P2, polynuclectides encoding P2 or antigen presenting development of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, cancer, colon, breast, ovary, oesophagus, kidney, thyroid, stomach, lung, prostate, pancreas, carcinoma, antitumour, cancerous, cytostatic, gene therapy, antineoplastic, Wilm's tumour, adenocarcinoma,
                                                                                                                                                                                                                                                                                                                                       Isolated polypeptide comprising an immunogenic portion of a lung tumor protein is used for detecting and monitoring progression of lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21; Length 4181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4181 BP; 1303 A; 830 C; 851 G; 1181 T; 16 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lung cancer related gene sequence SEQ ID NO:3742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 22; DB
Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ed. No. 1;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1a; Page 184-186; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       748 CTGCAAGGGGTTTTGCTGGGCG 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL65405 standard; DNA; 4181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-234034P.
2000US-234052P.
2000US-234509P.
99US-0466396.
99US-0476496.
2000US-0480884.
2000US-0510376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2001; 2001WO-US10838.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-209473P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-209531P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-233133P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-233617P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-234009P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 22; Conservative
```

ABL49119 standard; cDNA; 4181 BP.

RESULT 14 ABL49119/c

셤

د د د

```
Sequence 4181 BP; 1303 A; 830 C; 851 G; 1181 T; 16 other;
                                                                                                                                                                                                Carter KC,
                     2000US-235082P.
2000US-235134P.
2000US-235280P.
                                                                  2000US-236028P.
2000US-236032P.
2000US-236033P.
                                                                                  2000US-236034P.
2000US-236109P.
2000US-236111P.
                                                                                                 2000US-236842P.
2000US-236891P.
2000US-237172P.
                                                         2000US-235840P
2000US-235863P
                                                                                                                 2000US-237173P
                                                                                                                                                                           2000US-245084P
                                                                                                                                                                                               Augustus M,
Weaver Z;
                                                                                                                                                                                    (AVAL-) AVALON PHARM.
                                                                                                                                                                                                              WPI; 2002-188264/24.
               25-SEP-2000;
25-SEP-2000;
25-SEP-2000;
                              25-SEP-2000;
26-SEP-2000;
26-SEP-2000;
                                             27-SEP-2000;
27-SEP-2000;
27-SEP-2000;
                                                              27-SEP-2000;
                                                                                                                                                                                              Young PE, 1
Soppet DR,
```

```
The present invention describes a method (MI) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) a signature gene set, where (I) comprises a sequence (S) selected from 847 sequences (given in ABLG1664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used for producing a product which anti-neoplastic agent, and can be used for producing a product which is set to the anti-neoplastic agent as a neti-neoplastic agent as a structure and/or properties of the agent. MI can be used in the set to essure the cancer such as colon, breast, stomach, lung, thyroid, cancer such as colon, breast, stomach, lung, thyroid, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating ductal cancer, arcinoma, papillary carcinoma and Wilm's tumour.
Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
                                                                                                                                                                                                                 Claim 1, SEQ ID 3742; 44pp; English.
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes human lung tumour proteins. Human lung tumour proteins and polynuclectides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynuclectides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating cancer or stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to ABB7500 represent sequences used in the exemplification of the present
                                                                                                   Human; lung tumour; lung cancer; cytostatic; immunostímulant; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotides encoding lung tumor polypeptides, useful for treating lung cancer or stimulating an immune response -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        Henderson RA;
Fanger GR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 22; DB 24; Length 4181; 100.0%; Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4181 BP; 1303 A; 830 C; 851 G; 1181 T; 16 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                       Human lung tumour L523S cDNA sequence SEQ ID NO:175.
                                                                                                                                                                                                                                                                                                                                                                                                                     / YAW, Li SX, Kalos MD,
Retter MW, Marnerakis M,
Watanabe Y, Peckham DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 266-267; 374pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABA99958 standard; DNA; 4601 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              748 CricchAddddriririccridddd 727
                                                                                                                                                                                                                                                               28-JUN-2000; 2000US-066421.
02-AUG-2000; 2000US-0630940.
21-AUG-2000; 2000US-0643597.
15-SEP-2000; 2000US-0662786.
09-OCT-2000; 2000US-0685696.
12-DEC-2000; 2000US-0735705.
07-MAY-2001; 2001US-0850716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                   Wang A, Skeiky YAW
                                                                                                                                                                                                                                      28-JUN-2001; 2001WO-US21065.
                                          01-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  Wang T, Wang A, Skeik
McNeill PD, Fanger N,
Vedvick TS, Carter D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-090513/12.
                                                                                                                      immune response; ss
                                                                                                                                                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; ABB74960
                                                                                                                                                                           WO200200174-A2.
                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                         03-JAN-2002
               ABL49119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nvention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
ABA99958/C
ID ABA99
XX
AC ABA99
ઠે
```

Horrigan S;

Ebner R, Endress G,

Query Match Best Local Similarity 100. Matches 22; Conservative

ABA99958;

ö

Gaps

ö

100.0%; Score 22; DB 24; Length 4181; 100.0%; Pred. No. 1; tive 0; Mismatches 0; Indelg 0

05-JUL-2002 (first entry)

Human KOC DNA

KOC; promoter; human; cytostatic; dermatological; vulnerary; tumour; chemotherapy; allogenic bone marrow transplant; pancreatic carcinoma; domain-containing protein overexpressed in cancer; immunostimulant; gene therapy; chronic pancreatitis; pluripotency; aging; wound healing; radiation therapy; skin regeneration; cell differentiation; cancer; ds.

Homo sapiens.

WO200220036-A1

14-MAR-2002.

01-AUG-2001; 2001WO-DE02948.

06-SEP-2000; 2000DE-1043964. 14-FEB-2001; 2001DE-1006829.

(MUEL/) MUELLER F.

Adler G; Mueller F, Gress T,

WPI; 2002-292230/33

New promoter of the KOC gene, useful for diagnosis and treatment of cancer, for inducing cellular dedifferentiation and for identifying modulators

Claim 2; Fig 1a-b; 74pp; German.

Unit invention describes a mover now course course.

Overexpressed in cancer) promoter. The products of the invention have overexpressed in cancer) promoter. The products of the KOC protein and can be cytostatic, dermatological, vulnerary and immunostimulant activity, are cytostatic, dermatological, vulnerary and immunostimulant activity, are cytostatic, dermatological, vulnerary and the KOC protein and can be ceeded for gene therapy. The KOC promoter is also useful (1) for diagnosis of tumours that express KOC, particularly for differentiating between of tumours that express KOC, particularly for differentiating between chronic pancreatitis and pancreatic carcinoma; (ii) to detect to cells; and (iii) to evaluate treatments; (iv) to impart pluripotency to cells; and (iii) to evaluate treatments; (iv) to impart pluripotency to cells; and (iii) to evaluate treatments; (iv) to improve engraftment of expansion of hematopoietic stem cells; (vii) to improve engraftment of expansion of hematopoietic stem cells; (viii) to improve engraftment of the processes; (x) as prophylactic agents during chemotherapy/radiation the health of the promoter can also be used (i) for including for cosmetic purposes; and (xii) to immunise against malignant including for cosmetic purposes; and (xii) to immunise against malignant concluding for cosmetic purposes; and (xii) to immunise against malignant including for cosmetic purposes; and (xii) to immunise against malignant concluding the cancer (for controlling protein expression); and (iv) in gene therapy of cancer (for controlling protein expression of kot to the promoter and modulate its activity. The promoter makes possible to the promoter and modulate its activity. The promoter makes possible to the promoter and modulate its activity. The promoter makes possible to the promoter and modulate its activity. The promoter makes possible of the promoter and modulate its activity when it inflammation it its activity. The promoter in the promoter its activity of an inflammatory in the promot is not sensitive to other physiological states, e.g. inflammation, it represents a tumour marker with 100% sensitivity and specificity. This sequence represents the human KOC gene described in the disclosure of This invention describes a novel KOC (KH domain-containing protein the invention.

Sequence 4601 BP; 1462 A; 906 C; 918 G; 1298 T; 17 other;

Gaps ö 100.0%; Score 22; DB 24; Length 4601; 100.0%; Pred. No. 1; .ive 0; Mismatches 0; Indels 0; Query Match Best Local Similarity 100.0 Matches 22; Conservative

1168 cráchadádáriríráciádáda 1147 1 CTGCAAGGGGTTTTGCTGGGCG 22 ð

Search completed: April 18, 2003, 05:45:18 Job time : 100 secs

```
137, App
2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 347, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Appli
Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Appli
Appli
                                                              April 18, 2003, 04:53:41; Search time 21.5 Seconds (without alignments) 313.809 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1
Sequence 1
Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence Sequence Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                        Issued Patents NA:*

(cgn2_6/ptodata/1/ina/5A_COMB.seq:*

(cgn2_6/ptodata/1/ina/5B_COMB.seq:*

(cgn2_6/ptodata/1/ina/6A_COMB.seq:*

(cgn2_6/ptodata/1/ina/6B_COMB.seq:*

(cgn2_6/ptodata/1/ina/Regi:*

(cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-643-597-347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-605-785-350
                                                                                                                                                                                              441362 segs, 153338381 residues
                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                            nucleic search, using sw model
                                                                                                                                       ctgcaaggggttttgctgggcg 22
                                                                                                                                                           IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                            US-09-270-437D-10
22
                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1863
1863
1863
3095
3487
111827
48908
5436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                            OM nucleic
                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                       Sequence:
                                                                 Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Result
No.
```

```
ô
                                                                                                                37, App
Appli
3, Appli
7, Appli
7, Appli
7, Appl
7, Appl
7, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                      Sequence Sequence Sequence 1
                                                                                                                                  Sequence
Sequence
Sequence
                                                                                                                                                                                   Sequence
Sequence
Sequence
                                                                                                                  Sequence
                                                                                                                                                                                                                                      Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Railos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Nancy
APPLICANT: Li, Samuel X.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Mang, Aljun
APPLICANT: Moneill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS POR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS POR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND STATISTIC OF INVENTION: COMPOSITIONS AND CURRENT PELLING DATE: 2000-08-21
CURRENT EPLING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE FRANCES FASTESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 22; DB 4; Length 1740; 100.0%; Pred. No. 0.077; ve 0; Mismatches 0; Indels C
          US-09-352-616A-350
US-08-820-170A-26
US-09-203-659-26
US-09-565-28-26
US-09-665-78-58-26
US-09-134-607A-8
US-09-134-607A-13
US-09-134-607A-13
US-09-173-559-27
US-09-565-518-27
US-09-565-518-27
US-09-565-518-27
US-09-665-518-27
US-09-665-518-27
US-09-665-518-27
US-09-661-468-27
US-09-661-468-27
US-09-61-468-27
US-09-61-468-27
US-09-61-468-27
US-09-61-468-27
US-09-61-468-27
US-09-61-468-27
US-09-61-468-27
                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09061709B; Patent No. 6297364; GENERAL INFORMATION: APPLICANT: Chen, Yao-Tseng; APPLICANT: Tsang, Solam; APPLICANT: Tsang, Solam; APPLICANT: Stockert, Elisabeth; APPLICANT: Jager, Elke; APPLICANT: Old, Lloyd J.
                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 347, Application US/09643597; Patent No. 6426072; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGCAAGGGGTTTTGCTGGGCG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGCAAGGGGTTTTGCTGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
CORGANISM: Homo sapiens
US-09-643-597-347
                                                                                                                                                                                                                                                                                                                                                                                                          JS-09-643-597-347/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-061-709-4/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         498
셤
```

```
RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated TITLE OF INVENTION: Artigen, The Antigens Per Se, And Uses Thereof FILE REFERENCE: LUD 5338 CURRENT APPLICATION NUMBER: US/09/061,709B CURRENT FILING DATE: 1998-04-17 NUMBER OF SEQ ID NOS: 8 SEQ ID NO 4 LENGTH: 4159
                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                        Score 22; DB 4; Length 4159;
Pred. No. 0.091;
                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: PastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McNeill, Patricia D.
VENTION: COMPOSITIONS AND
VENTION: AND DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
US-09-643-597-175/c
; Sequent 175, Application US/09643597
; Patent No. 6426072
                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pi
Matches 22; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                       748 CIGCAAGGGGTTTTGCTGGGCG 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bangur, Chaitanya S.
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (3506)
OTHER INFORMATION: n=A,T,C or G
                                                                                                                                                                                                                                                                                                                   1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (3347)
OTHER INFORMATION: n=A,T,C or
NAME/KEY: unsure
CCCATION: (3502)
OTHER INFORMATION: n=A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Henderson, Robert A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (3538)
OTHER INFORMATION: n=A,T,C or NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n=A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 n=A, I, C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    n=A, T, C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kalos, Michael D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang, Tongtong
Fan, Liqun
                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MCNeill,
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 2101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (3646)
OTHER INFORMATION: r
NAME/KEY: unsure
LOCATION: (3940)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (3520)
OTHER INFORMATION:
NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 4181
                                                                                                                                                                                       ; FEATURE:
US-09-061-709-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQ ID NO 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                     셤
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 22; DB 4; Length 4181; 100.0%; Pred. No. 0.091; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SCHULE, JUNGEN
APPLICANT: BLUN-OEHHER, GARRIELE
APPLICANT: BLUN-OEHHER, GARRIELE
APPLICANT: BLUN-OEHHER, GARRIELE
APPLICANT: BALINKA, JUNGEN
TITLE OF INVENTION: BACTERIAL PLASMIDS
FILE REFERENCE: 11347/268416/BET
CURRENT APPLICATION NUMBER: US/09/676,974
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: OFT/EP98/01720
PRIOR APPLICATION NUMBER: DE 197 13543.9
PRIOR FILING DATE: 1998-04-01
PRIOR PRILING DATE: 1997-04-02
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09676974
Patent No. 6391631
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: unsure
LOCATION: (4088)
OTHER INFORMATION: n=A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 748 crecaaeserrrrecreece 727
                                                                                                                                                   NAME/KEY: unsure
LOCATION: (4036)
OTHER INFORMATION: n=A, T, C or G
NAME/KEX: unsure
LOCATION: (4056)
OTHER INFORMATION: n=A, T, C or G
                                                                                                                                                                                                                                                                                           NAME/KEY: unsure
LOCATION: (4062)
OTHER INFORMATION: n=A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (4115)
; OTHER INFORMATION: n=A,T,C or G
US-09-643-597-175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CorG
INFORMATION: n=A, T, C or G
                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: unsure
LOCATION: (4080)
OTHER INFORMATION: n=A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%;
Matches 22, Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: A, T, C or NAME/KEY: modified_base
                                                               INFORMATION: n=A, T, C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1290)
OTHER INFORMATION: A, T,
NAME/KEY: modified base
LOCATION: (5341)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: A, T, NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: modified base
                                                                                      NAME/KEY: unsure
LOCATION: (3974)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 5552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COCATION:
```

```
US-09-325-932A-128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps.
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09443087

Patent No. 6146864

GRENEALL INFORMATION:
APPLICANT: Debbie Yaver
APPLICANT: Michael W. Berka
TITLE OF INVENTION: POLYDEPTIGES Having Choline Oxidase
TITLE OF INVENTION: POLYDEPTIGES HAVING CARRIER APPLICATION NUMBER: US/09/443,087

CURRENT FILING DATE: 1999-11-18

EARLIER FILING DATE: 1999-11-24

NUMBER OF SEQ ID NOS: 2

SOFTMARE: PASSEEQ for Windows Version 3.0

SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Yaver, Debbie S.
APPLICANT: Berva, Randy M.
APPLICANT: Berva, Randy M.
APPLICANT: Berva, Midnel M.
TITLE OF INVENTION: Polypeptides Having Choline Oxidase
TITLE OF INVENTION: Activity and Nucleic Acids Encoding Same
TITLE OF INVENTION: Activity and Nucleic Acids Encoding Same
FILE REFERENCE: 5735.000-08;
CURRENT APPLICATION UNBER: US/09/199,229
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FASELSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.9%; Score 15.6; DB 3; Length 1863; 81.8%; Pred. No. 99; 4; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3; Length 1863;
                                                                                                                                    DB 4; Length 5552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                  Query Match 73.6%; Score 16.2; D
Best Local Similarity 85.7%; Pred. No. 63;
Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70.9%; Score 15.6; 81.8%; Pred. No. 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1359 CTTGAAGGGGCTCTGCTGGGCG 1338
                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 1, Application US/09199229
; Patent No. 6063607
                                                                                                                                                                                                                                                      1798 TGCAAGGGTTTCGGGGGGG 1818
) OTHER INFORMATION: A, T, C or G
) NAME/KEY: modified_base
); LOCATION: (5400)
US-09-676-974-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Fusarium venenatum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 81.8 Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 81.8
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Fusarium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
US-09-443-087-1/c
                                                                                                                                                                                                                                                                                                                                                            US-09-199-229-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-199-229-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-443-087-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                    요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
US-09-325-932A-128/c
US-09-325-932A-128/c
US-09-325-932A-128/c
Sequence 128, Application US/09325932A
Sequence 128, Application US/09325932A
Sequence 128, Application US/09325932A
GENERAL INFORMATION:
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of forestry plant develo
TITLE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FeatSEQ for Windows Version 3.0
SSEQ ID: NO 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gape
                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Debbie Yaver
APPLICANT: Randy M. Berka
APPLICANT: Michael W. Rey
APPLICANT: Michael W. Rey
TITLE OF INVENTION: POlypeptides Having Choline Oxidase
TITLE OF INVENTION: Activity And Nucleic Acids Encoding Same
FILE REFERENCE: 5735.200-US
CURRENT FILING DATE: 2000-10-12
PRIOR FILING DATE: 1999-11-18
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FREESEQ for Windows Version 3.0
ISSUED IN NOS: 2
INVENTION: ACTIVITY OF THE SECOND NOS: 2
INVENTION OF SEQ ID NOS: 2
INVENTION OF SEQ ID NOS: 2
INVENTION OF SECOND SECOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70.9%; Score 15.6; DB 4; Length 3095; 81.8%; Pred. No. 1.1e+02; ive 0; Mismatches 4; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 1863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 15.6; DB
Pred. No. 99;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
US-09-453-702B-164/c
; Sequence 164, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
Harlicand, Valerie
Nicole T.
                                                                                                                                                                             US-09-687-298-1/c
; Sequence 1, Application US/09687298
; Patent No. 6320103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1359 circakkádádcirciáciádáda 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2984 crcccaccerrrrrcacccc 2963
1359 crrchadececrerecreece 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CTGCAAGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 70.9%;
Best Local Similarity 81.8%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CRGANISM: Fusarium venenatum
US-09-687-298-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 81.8
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Pinus radiata
```

```
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                            RESULT 11
US-09-453-702B-137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-948-277A-2
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09739455
Patent No. 6413756
GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TILLE REFERENCE: CLO.00653
CURRENT APPLICATION NUMBER: US/09/739,455
CURRENT FILING DATE: 2000-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                    Welch, Rod
NWENTION: No. 6365723el Sequences of E. coli 0157
OF SEQUENCES: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                   COUNTER: W1

ZIP: 53701-2113

ZIP: 53701-2113

COMPUTER: Diskete, 3.50 inch. 1.44Mb storage COMPUTER: Diskete, 3.50 inch. 1.44Mb storage COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 8.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REGISTRATION NUMBER: 27386
REGISTRATION NUMBER: 27386
TELECOMPUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 15.6; DB 4;
Pred. No. 1.1e+02;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear MOLECULE TYPE: DNA (genomic); SEQUENCE DESCRIPTION: SEQ ID NO: 164;: US-09-453-7028-164
                                                                                             ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (1)...(11827)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (608) 251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1644 crádakáradrirrracracraci 1623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (608) 251-9:
INFORMATION FOR SEQ ID NO: 164.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
Plunkett, Guy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 81.8%;
Matches 18; Conservative
                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-739-455-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 3
LENGTH: 11827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-739-455-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                        Gaps
                                                                                                                                                                                                                                                                                         Burland, Valerie
Perna, Nicole T.
Plunkett, Guy
Welch, Rod
TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
CORRESPONDENCE ADDRESS:
                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
Score 15.6; DB 4; Length 11827; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 48908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTEY: W1

COUNTEY: W3

ZIP: 53701-2113

COMPUTER: FREADABLE FORM:

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: WORD FEFFOR 8.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/453,702B

FILING DATE: 03-Dec-1999

CLASSIFICATION CONTRACT

APPLICATION NUMBER: 60/110,955

FILING DATE: 04-DEC-1998

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 15.6; DB 4;
Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Seay, Nicholas J.
REGIETRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 137:
US-09-453-702B-137
                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                       APPLICANT: Blattner, Frederick R.
                                                                                                                                                                                                             Sequence 137, Application US/09453702B Patent No. 6365723 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (608) 251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08948277A; Patent No. 5849581; GENERAL INFORMATION: APPLICANT: APPLICANT: Zhang, Ning
                                                                                                              Db 10677 creccresesrerrecreases 10656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 18224 Cresardescrircrecresce 18245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (608) 251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
                                                                            recece 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 137
SEQUENCE CHARACTERISTICS:
LENGTH: 48908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
70.9%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.9%;
ilarity 81.8%;
Conservative
                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1 Sout
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: WI
```

õ

```
US-09-280-116-151/c
Sequence 151, Application US/09280116A
Sequence 151, Application US/09280116A
Sequence 151, Application US/09280116A
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
TITLE OF INVENTION: NUMBER: US/09/280,116A
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
SOFTWARE: PATENTIN Ver. 2.0
SSOFTWARE: PATENTIN Ver. 2.0
SSOFTWARE: 100 No 151
LENGTH: 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 5436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69.1%; Score 15.2; DB 4; Length 726; 85.0%; Pred. No. 1.3e+02; tive 0; Mismatches 3; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: HUMAN NATURAL KILLER CELL ACTIVATION TITLE OF INVENTION: FACTOR II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15.4; DB 2;
Pred. No. 1.5e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: trypsin-like serine proteases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature

| LOCATION: (1) ... (726)

| OTHER INFORMATION: n = a, t, c or g

US-09-280-116-151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08832488
Patent No. 6448044
                            REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 197-0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (650) 343-4342
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 5436 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: DIREAT
US-09-169-203-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       615 regaaccerrrrccaccec 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 TGCAAGGGGTTTTGCTGGGC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: LI, HADDONG
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 94.1%;
Matches 16; Conservative
ITTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4007 CTGCAAGGGATTTTGCT 4023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 85...
The 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CTGCAAGGGGTTTTGCT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-08-832-488-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 70.0%; Score 15.4; DB 2; Length 5436; Best Local Similarity 94.1%; Pred. No. 1.5e+02; Matches 16; Conservative 0; Mismatches 1; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PATENT NO. 35.08009

GREERAL INFORMATION:
APPLICANT: Amaral, M. Catherine
APPLICANT: Zhang, Ming
APPLICANT: Chen, Jin-Long
TITLE OF INVENTION: Regulators of UCP3 Gene Expression
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CTTY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
COUNTRY: USA
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BEN P
APPLICANT: Chen, Jin-Long
TITLE OF INVENTION: Regulators of UCF3 Gene Expression
NUMBER OF SEQUENCES: 2
CORRESPONDENCES: 2
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30
CONFRATE: PatentIn Release #1.0, Version #1.30
CONFRATE PAPLICATION DATA:
APPLICATION NUMBER: US/08/948,277A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 197-009
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION ON 343-4341
TELEFRAX: (650) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/948,277
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-169-203-2
; Sequence 2, Application US/09169203
; Patent No. 5976808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4007 CTGCAAGGGATTTTGCT 4023
                                                                                                                                                                                                                                                                                                                                                    ZIP: 94010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-948-277A-2
```

RESULT 13

g ò

```
0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 69.1%; Score 15.2; DB 4; Length 857; Best Local Similarity 85.0%; Pred. No. 1.38+02; Matches 17; Conservative 0; Mismatches 3; Indels C
                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER IN FO COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/832,488

FLING DATE:

CLASSIPICATION: 435

ATTORNEY AGENT INFORMATION:

NAME: BROOKES, ANDERS A.

REGISTRATION NUMBER: PF266

TELEPAN: (301) 309-8504

TELEPAN: (301) 309-8512

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 857 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DAM (GENOMIC)

FRATURE:

MANDAMETRY AND AND COMPANIES

TYPE: NAME TYPE: DAM (GENOMIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sig_peptide
82..130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mat_peptide 133..756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OLECULE ...
PEATURE:
RAME/KEY: CDS
LOCATION: 82..756
FEATURE:
NAME/KEY: sig_pept'
LOCATION: 82..130
FEATURE:
NAME/KEY: mat_pe
LOCATION: 133...
US-08-832-488-1
ROCKVILLE
CITY: ROCKVI
STATE: MD
COUNTRY: US
```

Search completed: April 18, 2003, 07:34:23 Job time : 32.5 secs

à

```
(without alignments)
241.975 Million cell updates/sec
                                                                                                                                                                                                      April 18, 2003, 06:35:31 ; Search time 91.3333 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1: /cgn2 6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      639749 segs, 502280978 residues
                                                                                                                                                                                                                                                                                                                                               US-09-270-437D-10
22
1 ctgcaaggggttttgctgggcg 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                             OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published
                                                                                                                                                                                                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database :
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                          Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	% Query Match Length DB	DB	In	Description
				:		
0	22	100.0	282	10	US-09-864-761-32671	Sequence 32671, A
o U	22	100.0	588	10	US-09-864-761-16177	Seguence 16177. A
m U	22	100.0	1740	10	US-09-735-705-347	
Ω	22	100.0	1740	10	US-09-850-716A-347	
υ Ω	22	100.0	1740	10	US-09-897-778-347	Seguence 347, App
ω υ	22	100.0	1743	10	US-09-897-778-447	447
0	. 22	100.0	1743	10	US-09-897-778-450	Sequence 450. App
ω υ	22	100.0	1764	10	US-09-850-716A-428	Segmence 428, App
ი <sub>U</sub>	22	100.0	1764	10	US-09-897-778-428	
0 10	22	100.0	4159	10	US-09-899-651-4	
c 11	22	100.0	4181	10	US-09-735-705-175	175
c 12	22	100.0	4181	10	US-09-954-456-715	Sequence 715. App
c 13	22	100.0	4181	10	US-09-850-716A-175	175.
c 14	22	100.0	4181	10	US-09-897-778-175	Sequence 175. App
c 15	17.2	78.2	302250	10	US-09-962-832-154	Sequence 154. App
16	16.8	76.4	549	10	US-09-560-863-190	Sequence 190. App
C 17	16.4	74.5	75899	10	US-09-854-883-243	243.
c 18	16.2	73.6	296	10	US-09-294-093B-2223	2223
19	16.2	73.6	368004	10	US-09-949-654-3	

Sequence 1, Appli	Sequence 15056, A	Sequence 4150, Ap	Sequence 14293, A	Sequence 692, App	Sequence 5, Appli	Sequence 139, App	Sequence 2520, Ap	Sequence 1470, Ap	Sequence 1627, Ap	Sequence 1485, Ap	Sequence 5517, Ap	Sequence 1265, Ap	Sequence 93, Appl	Sequence 2783, Ap	Sequence 1626, Ap	Sequence 164, App	Sequence 7731, Ap	Sequence 3, Appli	137	Sequence 79, Appl	Sequence 2116, Ap	Sequence 1, Appli	m	Sequence 687, App	Sequence 7109, Ap
US-09-738-626-1	US-09-878-574-15056	US-09-923-876-4150	US-09-878-574-14293	US-09-998-598-692	US-10-084-994-5	US-09-796-753-139	US-09-867-701-2520	US-09-867-701-1470	US-09-738-626-1627	US-09-867-701-1485	US-09-867-701-5517	US-09-880-107-1265	US-09-967-768A-93	US-09-738-626-2783	US-09-738-626-1626	US-10-114-170-164	US-09-815-242-7731	US-09-817-181-3	US-10-114-170-137	US-09-969-108-79	US-09-954-456-2116	US-09-939-964-1	US-09-925-301-301	US-09-833-381-687	US-09-960-352-7109
σ	2	2	10	2	σ	σ	10	2	σ	10	2	10	10	σ	σ	σ	10	10	Φ	10	10	σ	10	10	10
3309400	261	269	272	518	2700	3649	377	422	426	439	454	454	454	747	1455	3487	3489	8522	48908	145831	145831	536165	830	163	289
3.6	. 8	1.8	8.1	8.1	71.8	1.8	6.0	6.0	70.9	6.0	6.	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.	6.	6.0	6.	0.	۲.	69.1
7	7	7	7	7	7	_	7	7	~	~	~	~	7	7	7	7	7	7	7	7	7	~	~	9	9
?	œ	∞.	∞.	۰.	۳.	Φ.	ų.	٩	ø.	9	७.	9.	٠.	9	9.	9	9.	9	9.	9.	9.	9.	4.	7	7
16	12	15	15	15	15	15	15	15	15.6	15	15	15	15	15	15	15	15	15	15	12	15	15	15	15	15
50		22	23	. 24	25	56	c 27	28	c 59	30	c 31	.c 35	c 33	c 34	35	c 36	37	c 38	39	40	41	c 42	c 43	C 44	c 45

## ALIGNMENTS

```
General Information (1970)

Sequence 3261, Application US/09864761

Retent No. US2002004763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharton G.

APPLICANT: Penn, Sharton G.

APPLICANT: Penn, Sharton G.

APPLICANT: Hanzel, David R.

APPLICANT: Chen Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID FORDER TO THE OF INVENTION: HUMBER: US/09/864,761

CURRENT APPLICATION NUMBER: US/09/864,761

PRIOR APPLICATION NUMBER: US/09/864,761

PRIOR APPLICATION NUMBER: US/09/863,66

PRIOR APPLICATION NUMBER: US/09/813,66

PRIOR APPLICATION NUMBER: US/09/813,66

PRIOR APPLICATION NUMBER: US/00/00-09-27

PRIOR APPLICATION NUMBER: US/00/00-09-29

PRIOR PLINIO DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/0066

PRIOR PLINIO DATE: 2001-01-30

PRIOR PLINIO DATE: 2001-01-30
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TOTRENT APPLIACATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FASESEQ for Windows Variable of STATE OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 22; DB 10; Length 588;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 22; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: MAP TO AC021876.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8
                                                                                                                                                 PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
LENGTH: 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 22; DB
Best Local Similarity 100.0%; Pred. No. 0.3
Matches 22; Conservative 0; Mismatches
                                  APPLICATION NUMBER: PCT/US01/00670
                                                                                                                   APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 347, Application US/09850716A Patent No. US20020115139A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 347, Application US/09735705
Patent No. US20020052329A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   498 crechadederririderedece 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bangur, Chaitanya
Hosken, Nancy
2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang, Tongtong
Fan, Liqun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kalos, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fanger, Gary
Li, Samuel X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
COGANISM: Homo sapiens
US-09-735-705-347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
US-09-850-716A-347/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATI
OTHER INFORMATI
US-09-864-761-16177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16177, Application US/09864761

Patent No. US20020048763A1

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEPUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: MAP TO AC021876.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8
; OTHER INFORMATION: SWISSPROT HIT: 029125, EVALUE 3.20e-01
; OTHER INFORMATION: NT HIT: U76705.1, EVALUE 0.00e+00
US-09-864-761-32671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 22; DB 10; Length 282; 100.0%; Pred. No. 0.28; 1. Pred. o. Mismatches 0; Indels
                                                                                                                            PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION UNDRER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE KHEKEKNCE: AGOMACA-A-I.
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PELING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-06-30
PRIOR PELLING DATE: 2000-06-30
PRIOR PELLING DATE: 2000-06-30
PRIOR PLILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 69/532,366
PRIOR PELLING DATE: 2000-10-04
PRIOR PELLING DATE: 2000-10-04
PRIOR PELLING DATE: 2000-10-30
PRIOR PELLING DATE: 2001-01-30
        APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00661
                                                                                 APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -09-864-761-16177/c
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 32671
LENGTH: 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR
PRIOR
PRIOR
```

g 8

Gaps

ö

```
Query Match 100.0%; Score 22; DB 10; Length 1743; Best Local Similarity 100.0%; Pred. No. 0.3; Matches 22; Conservative 0; Mismatches 0; Indels 0.
               APPLICANT: Peckham, David W.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DAYE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FASTER FASTER FOR WINDOWS VETSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

100.0%; Score 22;
Best Local Similarity 100.0%; Pred. No.
Matches 22; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 450, Application US/09897778
Patent No. US2020147143A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Marnerakis, Margarita
APPLICANT: Fanger, Gary R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   498 CTGCAAGGGGTTTTGCTGGGCG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           498 crecaAccerrirecrecece 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-897-778-447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
US-09-850-716A-428/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-897-778-450/c
                                                                                                                                                                                                                                            SEQ ID NO 447
LENGTH: 1743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-897-778-450
                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Panger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Peckham, David W.
APPLICANT: Peckham, David W.
APPLICANT: Peckham, David W.
APPLICANT: Penger, Neil
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEG ID NOS: 467
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 347
LENGTH: 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
100.0%; Score 22; DB 10; Length 1740;
Best Local Similarity 100.0%; Prad. No. 0.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10; Length 1740;
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: McNeill, Parricia D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REPERSURS: 210121.455C15
CURRENT APPLICATION UNDER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FaucSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 22; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 347, Application US/09897778
Patent No. US20020147143A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 447, Application US/09897778
Patent No. US20020147143A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           498 CTGCAAGGGTTTTTGCTGGGCG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, Tongtong
APPLICANT: Marnerakis, Margarita
APPLICANT: Panger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Watanabe, Yoshihiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 498 criscaakseserririscrisseses 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CTGCAAGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 22, Conservative
                                                                                                                                                                                                                                                                                                       TYPE: DNA
CORGANISM: Homo.sapiens
US-09-850-716A-347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-897-778-347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
US-09-897-778-347/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-897-778-447/C
                                                                                                                                                                                                                                                       SEQ ID NO 347
LENGTH: 1740
```

g ò

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10; Length 1743; 0.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 428, Application US/09850716A

Patent No. US20020115139A1

GENERAL INFORMATION:

APPLICANT: Ralos, Michael D.

APPLICANT: Retter, Marc W.

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C15

CURRENT APPLICATION NUMBER: US/09/850,716A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indele
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Watanabe, Yoshilhiro
APPLICANT: Handerson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Neil
TITLE OF INVENTION: OMBOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARR: FastsEQ for Windows Version 4.0
SEQ ID NO 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
```

a ઠ

Gaps

.. 0

g ò

```
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert B.
APPLICANT: Fanger, Neil Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARER: FastSEQ for Windows Version 3.0
SSEQ ID NO 175
LENGTH: 4181
                                                                                                                                                                                                                    DB 10; Length 4159;
                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                         Score 22;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-735-705-175/c
; Sequence 175, Application US/09735705
partent no. US20020052329A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COCATION: (3347)
OCTHER INFORMATION: D=A,T,C or G
NAME/KEY: unsure
LOCATION: (3502)
OCTHER INFORMATION: D=A,T,C or G
NAME/KEY: unsure
LOCATION: (3506)
OCTHER INFORMATION: D=A,T,C or G
NAME/KEY: unsure
LOCATION: (3520)
OCTHER INFORMATION: D=A,T,C or G
NAME/KEY: unsure
LOCATION: (3520)
OCTHER INFORMATION: D=A,T,C or G
NAME/KEY: unsure
LOCATION: (3530)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AME/KEY: unsure
OCATION: (3940)
THER INFORMATION: n=A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3549)
OTHER INFORMATION: n=A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 n=A, T, C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kalos, Michael D.
Bangur, Chaitanya S.
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
Wang, Aijun
                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                      748 checkAddddrrrrrdcridddc 727
                                                                                                                                                                                                                                                                                                                     1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                    100.0%;
nilarity 100.0%;
Conservative 0;
; PRIOR FILLNG DATE: 1998-04-17; NUMBER OF SEQ ID NOS: 8; SEQ ID NO 4; LENGTH: 4159; TYPE: DNA; PRATURE: US-09-899-651-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang, Tongtong
Fan, Liqun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: unsure
LOCATION: (3646)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tsang, Solam
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Jager, Elke
APPLICANT: Jager, Elke
APPLICANT: John J. John J.
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer
TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
FILE REPERBUCE: LUD 5538
CURRENT APPLICATION NUMBER: US/09/899,651
PRIOR APPLICATION NUMBER: US/09/061,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 428, Application US/09897778

Sequence 428, Application US/09897778

Sequence 428, Application US/09897778

Sequence 428, Application US/09897778

Sequence 428, Application

APPLICANT: Warnerakis, Margarita

APPLICANT: Fanger, Gary R.

APPLICANT: Carter, Darick

APPLICANT: Henderson, Robert A.

APPLICANT: Feckham, David W.

APPLICANT: Feckham, David W.

APPLICANT: Feckham, David W.

APPLICANT: Fanger, Neil

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 428

LENGTH 1764
                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10; Length 1764;
                                                                                                                                                                                                                                      DB 10; Length 1764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 22; DB 1
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 22; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                           100.0%; Score 22;
100.0%; Pred. No. C
ive 0; Mismatche
                         CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 428
LENGTH: 1764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09899651
Patent No. US20020111470A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       519 crecaaddaririrecredece 498
                                                                                                                                                                                                                                                                                                                                                                                        519 crechhededririrecredece 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                          1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Chen, Yao-Tseng
APPLICANT: Gure, Ali
                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
CORGANISM: Homo sapiens
US-09-897-778-428
                                                                                                                                                 TYPE: DNA
CORGANISM: Homo sapiens
US-09-850-716A-428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
US-09-897-778-428/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-899-651-4/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
```

셤 δ

```
ö
                                                                                                                                           Gарв
                                                                                                                                           ö
                                                                     Query Match 100.0%; Score 22, DB 10; Length 4181; Best Local Similarity 100.0%; Pred. No. 0.32; Matches 22; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                        Sequence 175, Application US/09850716A
GENERAL NO. US20020115139A1
GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
CURRENT APPLICANTION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOSTWARE: FESTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: unsure
LOCATION: (3502)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3506)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
                                                                                                                                                                                                                                     748 crecaAddedririacredece 727
                                                                                                                                                                                    1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: ungure
LOCATION: (3538)
OTHER INFORMATION: n=A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: unsure
LOCATION: (3549)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3646)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3340)
OTHER INFORMATION: n=A,T,C or G
OTHER INFORMATION: n=A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: unsure
LOCATION: (3968)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3974)
OTHER INFORMATION: n=A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (4080)
OTHER INFORMATION: n=A, T, C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: unsure
LOCATION: (3347)
OTHER INFORMATION: n=A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  n=A, T, C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: unsure
LOCATION: (4036)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (3520)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: unbure
LOCATION: (4062)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: unsure
LOCATION: (4056)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                    RESULT 13
US-09-850-716A-175/C
                       US-09-954-456-715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 175
LENGTH: 4181
                                                                                                                                                                                                                                     g
                                                                                                                                                                                       ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ## APPLICATE: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
TITLE OF INVENTION: Sets
FILE SPERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/69/954,456
CURRENT APPLICATION NUMBER: US/60/233,617
FRIOR PELICATION NUMBER: US/60/234,052
PRIOR PELING DATE: 2000-09-26
PRIOR PELING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR PELING DATE: 2000-09-26
PRIOR PELING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 22; DB 10; Length 4181; Best Local Similarity 100.0%; Pred. No. 0.32; Matches 22; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: Patentin version 3.0
LENGTH: 4181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 715, Application US/09954456 Patent No. US20020115057A1 GENERAL INFORMATION:
                                                                                               NAME/KEY: unaure

LOCATION: (4036)

OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unaure

LOCATION: (4066)

OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unaure

LOCATION: (4062)

OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unaure

LOCATION: (4080)

OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unaure

LOCATION: (4080)

OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unaure

LOCATION: (4080)

OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unaure

LOCATION: (4080)

OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unaure

LOCATION: (4018)

OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unaure

LOCATION: (4018)
                          KEY: unsure
:ION: (3974)
? INFORMATION: n=A,T,C or G
INFORMATION: n=A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  748 cráckádádáririrácrádáda 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
OTHER INFORMATION: n=a,t,g or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
US-09-954-456-715/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
```

ö

0; Gaps

Indels

Length 302250;

DB 10;

```
0; Mismatches
                                                                                                                                                                                       Score 17.2; I
Pred. No. 65;
                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: April 18, 2003, 10:14:02 Job time : 149.5 secs
                                                                                                                                                                                                                                                                                                                                 Db 91459 Criccaaddddracadcridddcd 91438
                         PatentIn version 3.0
                                                                                                                                                                                         Query Match 78.2%;
Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                         1 CTGCAAGGGGTTTTGCTGGGCG
NUMBER OF SEQ ID NOS: 259
SOFTWARE: Patentin version
SEQ ID NO 154
LENGTH: 302250
                                                                                               TYPE: DNA
COGANISM: Homo sapiens
US-09-962-832-154
                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ebner, Reinhard
APPLICANT: Ebner, Reinhard
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
TITLE OF INVENTION: Sets
FILE REPERENCE: 689290-74
CURRENT APPLICATION NUMBER: US/69/235,077
PRIOR APPLICATION NUMBER: US/60/235,280
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,280
PRIOR FILING DATE: 2000-09-25
                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) NAME/KEY: misc feature

) LOCATION: 3347, 3502, 3506, 3520, 3538, 3549, 3646, 3940, 3968, 3974,

LOCATION: 4036, 4056, 4062, 4080, 4088, 4115

) OTHER INFORMATION: n = A,T,C or G

US-09-897-778-175
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 22; DB 10; Length 4181;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 22; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                        DB 10; Length 4181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
FILE REPERBENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 175
LENGTH: 4181
                                                                                                                                                                                                      Query Match 100.0%; Score 22; DB 10; Length 4 Best Local Similarity 100.0%; Pred. No. 0.32; Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 175, Application US/09897778
Patent No. US20020147143A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Marnerakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Carter, Darrick
APPLICANT: Wedvick, Thomas S.
APPLICANT: Wedvick, Thomas S.
APPLICANT: Henderson, Yoshiniro
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 154, Application US/09962832 Patent No. US20020110821A1 GENERAL INFORMATION:
                      ; NAME/KEY: unsure
; LOCATION: (4088)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (4115)
; OTHER INFORMATION: n=A,T,C or G
US-09-850-716A-175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          748 CrecaAeeerrrrccreece 727
                                                                                                                                                                                                                                                                                                                                                        748 crechhededririrecredece 727
                                                                                                                                                                                                                                                                                                        1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-09-962-832-154/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-897-778-175/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                    ò
```

Sequence:

Run on: ŏ

Searched:

```
22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      υ
                                                 April 18, 2003, 05:48:17 ; Search time 1211 Seconds (without alignments) 456.759 Million cell updates/sec
                                                                                                                                                                                                                                       GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                   24791104 segs, 12571243825 residues
                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cgn2_6/ptodata/1/pna/US102B
                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                - nucleic search, using sw model
                                                                                                         1 ctgcaaggggttttgctgggcg 22
                                                                                                                         IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ptodata/
                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                      US-09-270-437D-10
22
                                                                                      Title:
Perfect score: .
                                                                                                                          Scoring table:
                                nucleic
                                                                                                                                                                                                                                                    Database :
```

```
/ Ggn2_6/prodata/1/pna/US6003_COMB.seq:*

/ Ggn2_6/prodata/1/pna/US6005_COMB.seq:*

/ Ggn2_6/prodata/1/pna/US6005_COMB.seq:*

/ Ggn2_6/prodata/1/pna/US6005_COMB.seq:*

/ Ggn2_6/prodata/1/pna/US6009_COMB.seq:*

/ Ggn2_6/prodata/1/pna/US6010_COMB.seq:*

/ Ggn2_6/prodata/1/pna/US6011_COMB.seq:*

/ Ggn2_6/prodata/1/pna/US6011_COMB.seq:*

/ Ggn2_6/prodata/1/pna/US6011_COMB.seq:*

/ Ggn2_6/prodata/1/pna/US6011_COMB.seq:*

/ Ggn2_6/prodata/1/pna/US6011_COMB.seq:*

/ Ggn2_6/prodata/1/pna/US6012_COMB.seq:*

/ Ggn2_6/prodata/1/pna/US6013_COMB.seq:*

/ Ggn2_6/prodata/1/pna/US6013_
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 25064, A		Sequence 25064, A Sequence 323, App	Sequence 323, App	Sequence 395, App	Sequence 395, App	11611	Sequence 703, App	3437	Sequence 1393, Ap	1393,	Sequence 1393, Ap	Sequence 1393, Ap	Sequence 12084, A	Sequence 16177, A	Sequence 12077, A	Sequence 12084, A	Sequence 4493, Ap	347, Ag
SUMMARIES ID	PCT-US01-00663-25064 US-09-864-761-32671	US-10-203-134-24949	US-10-203-13/-25064 US-09-758-442-323	US-10-217-623-323	US-09-076-898-395	US-09-076-898A-395	US-09-912-292-11611	US-08-668-236-703	· US-09-534-846B-34372	US-09-076-897-1393	US-09-076-897A-1393	US-09-076-897B-1393	US-09-076-897C-1393	PCT-US01-00663-12084	US-09-864-761-16177	US-10-203-134-12077	US-10-203-137-12084	US-09-399-932-4493	PCT-US01-47576-347
DB	128	42	4 6	42	14	14	34	ដ	50	14	14	14	14	ч	33	42	42	17	н
Length DB	282	282	282	285	301	301	301	369	369	404	404	404	404	588	588	588	588	843	1740
* Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	22	55	7 77	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22
Result No.	00	т С	ט ט	<b>9</b> U	ο,	ω υ	σ 0	010	c 11	c 12	c 13	c 14	c 15	c 16	c 17	c 18	c 19	c 50	c 21

ö

```
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Grey WINTERTON: GREW EXPRESSION ANALYSIS BY MICROARRAY
ITLE OF INVERTYON: GREW EXPRESSION ANALYSIS BY MICROARRAY
FILE REPRESENCE: Accord a. X. I.
CURRENT APPLICATION WINDER: US 60/180,312
RRIOR PLILIAG DATE: 2000 -05-23
RRIOR PLILIAG DATE: 2000 -05-23
RRIOR PLILIAG DATE: 2000 -05-23
RRIOR PLILIAG DATE: 2000 -06-23
RRIOR PLILIAG DATE: 2001 -01-20/1801/00665
RRIOR PLILIAG DATE: 2001 -01-20/1801/00661
RRIOR PLILIAG DATE: 2001 -01-20/1801/00661
RRIOR PLILIAG DATE: 2000 -05-21
RRIOR PRILIAGA DATE: 2000 -05-21
RRIOR PLILIAGA DATE: 2000 -05-21
RAUGH
Gaps
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTHER INFORMATION: MAP TO AC021876.2

OTHER INFORMATION: EXPRESSED IN BONE MARKOW, SIGNAL = 6.5

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8

OTHER INFORMATION: SWISSPROT HIT: Q29125, EVALUE 3.20e-01

OTHER INFORMATION: NT HIT: U76705.1, EVALUE 0.00e+00

CTHER INFORMATION: EST_HUMAN HIT: BE545535.1, EVALUE 0.00e+00

US-09-864-761-32671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 282;
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22; DB 33;
No. 5.4;
  ö
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
Pred.
                                                                                                                                                                               Sequence 32671, Application US/09864761
GENERAL INFORMATION:
  ;
                                       22
                                                                      76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                           1 CTGCAAGGGGTTTTGCTGGGCG
                                                                                CTGCAAGGGGTTTTGCTGGGCG
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
      22;
                                                                                97
      Matches
                                                                            셤
                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INCOMMATION:
APPLICANT: Molecular Dynamics, Inc.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
TITLB OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXPRESSION IN HUMAN PLACENTA
TITLE OF INVENTION: HUMBER: PCT/USO1/00663
CURRENT FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PELING DATE: 26 May 2000 (26.05.00)
PRIOR PELING DATE: 26 May 2000 (26.05.00)
PRIOR FILING DATE: 03 August 2000 (20.08.0)
PRIOR FILING DATE: 03 August 2000 (30.08.0)
PRIOR PILING DATE: 27 September 2000 (21.09.00)
PRIOR PILING DATE: 27 September 2000 (27.09.00)
PRIOR PILING DATE: 27 September 2000 (21.09.00)
PRIOR PILING DATE: 21 September 2000 (21.09.00)
PRIOR PILING DATE: 30 June 2000 (30.06.00)
NUMBER OF SEQ ID NOS: 38837
SECTIANES NOISCULAR Dynamics Sequence Listing Engine
                                                                                      Sequence 483,
Sequence 447,
Sequence 440,
Sequence 450,
Sequence 447,
Sequence 487,
Sequence 487,
Sequence 487,
Sequence 487,
Sequence 487,
Sequence 487,
                                                                                  Sequence 347,
                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTHER INFORMATION: MAP TO AC021876.2
CTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8
CTHER INFORMATION: SWISSPROT HIT: 029125, EVALUE 3.20e-01
CTHER INFORMATION: NT HIT: U76705.1, EVALUE 0.00e+00
CTHER INFORMATION: EST HUMAN HIT: BE545535.1, EVALUE 0.00e+00
PCT-US01-00663-25064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 22; DB 1; Length 282;
Pred. No. 5.4;
    US-09-542-615A-347

US-09-606-421A-347

US-09-606-421B-347

US-09-630-940B-347

US-09-630-940B-347

US-09-630-940B-347

US-09-630-735-705-347

US-09-735-705-347

US-09-897-778-347

US-09-897-778-347

US-10-007-700-347

US-10-117-982-478

US-10-117-982-483

US-10-117-982-483

US-10-117-982-483

US-10-117-982-483

US-10-117-982-483

US-09-897-778-447

US-09-897-778-450

US-09-897-778-447

US-10-007-778-447
                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-117-982-447
US-10-117-982-450
PCT-US01-47576-428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25064, Application PC/TUS0100663 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
100.0%;
                                                                                      117440
117440
117440
117440
117440
117440
117443
1174433
1174433
1174433
1174433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
          1000.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 25064
LENGTH: 282
```

```
Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: BST_HUMAN HIT: BES45535.1, EVALUE 0.000+00 US-10-203-137-25064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 22; DB 42; Length 282;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 29; Length 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PR031
CURRENT APPLICATION NUMBER: US/09/758,442
CURRENT FILING DATE: 2001-01-11
PRIOR FILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR APPLICATION NUMBER: 60/180,628
NUMBER PILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: SWISSPROT HIT: Q29125, EVALUE 3.20e-01
                                                                         CURRENT FILING DATE: 2002-08-02

PRIOR FILING DATE: 3002-08-02

PRIOR FILING DATE: 04 February 2000 (04.02.00)

PRIOR FILING DATE: 04 February 2000 (04.02.00)

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,366

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 03 August 2000 (03.08.00)

PRIOR FILING DATE: 03 October 2000 (03.10.00)

PRIOR FILING DATE: 27 September 2000 (27.09.00)

PRIOR FILING DATE: 27 September 2000 (27.09.00)

PRIOR FILING DATE: 21 September 2000 (21.09.00)

PRIOR FILING DATE: 21 September 2000 (21.09.00)

PRIOR FILING DATE: 31 September 2000 (31.09.00)

PRIOR FILING DATE: 30 June 2000 (30.06.00)

NUMBER OF SEQ ID NOS: 38837

SOSTWARE: MOLECULAR DYNAMICS SEQUENCE LIGHTING ENGINE SECIT NO.02 CENT. NO.02 CENT. NO.02 CENT. NO.03 CE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: NT HIT: U76705.1, EVALUE 0.00e+00
                                                       ON NUMBER: US/10/203,137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (109)
OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (112)
; OTHER INFORMATION: n equals a,t,g, or
US-09-758-442-323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: MAP TO AC021876.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 323, Application US/09758442 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    crecaacecririscreece 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 323
LENGTH: 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
US-09-758-442-323/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 25064
LENGTH: 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ч
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACID PROBES USEFUL FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Molecular Dynamics, Inc.
APPLICANT: Molecular Dynamics, Inc.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hansel, David R.
APPLICANT: Hansel, David K.
APPLICANT: Chen, Wensheng
ITILE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
ITILE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
ITILE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN BONE MARROW
FILE REFERENCE: PB 0004 WO 6 CURRENT APPLICATION NUMBER: US/10/203,134
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2002-08-02
PRIOR PILING DATE: 26 May 2000 (04.2.00)
PRIOR FILING DATE: 26 May 2000 (25.05.00)
PRIOR PELING DATE: 03 August 2000 (32.366
PRIOR PILING DATE: 03 August 2000 (33.08.00)
              Gaps
              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:

J OTHER INFORMATION: EST_HUMAN HIT: BE545535.1, EVALUE 0.00e+00
US-10-203-134-24949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Score 22; DB 42; Length 282;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 22; Conservative 0; Mismatches 0; Indels
              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.4;
hag 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: SWISSPROT HIT: Q29125, EVALUE 3.20e-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION: NT HIT: U76705.1, EVALUE 0.00e+00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 38628
SOFTWARE: Molecular Dynamics Sequence Listing Engine
           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 27 September 2000 (27.09.00)
   Mismatches.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             October 2000 (03.10.00)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 30 June 2000 (30.06.00)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                     -10-203-134-24949/c
Sequence 24949, Application US/10203134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/10203137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
OTHER INFORMATION: MAP TO AC021876.2
   ò
                                                                     CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                    crecaageerrrrecreece 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 crecaaedecririrecredece 76
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-203-137-25064/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 24949
LENGTH: 282
22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2506
Matches
                                                                                                                                    97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER
                                                                                                                             셤
                                                                  ઠે
```

음 ò

ö

ö

ö

g ò

```
US-09-076-898A-395/c
US-09-076-898A-395, Application US/09076898A
Sequence 395, Application US/09076898A
GENERAL INFORMATION:
PAPPLICANT: Rosen, Craig A., et. al.
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/076,898A
CURRENT PILING DATE:
PRIOR PILIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. 5.5
Matches 22; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (261)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (263)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (264)
OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 22;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: n equals a,t,g, or C US-09-076-898A-395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature LoCATION: (115) OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (118)

JTHER INFORMATION: n equals a,t,g,

NAME/KEY: misc feature
FILING DATE: May 13, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REPERENCE/POCKET NUMBER: PO31
TELECOMMUNICATION INFORMATION:
TELEFAK: (301) 309-8439
INFORMATION FOR SEQ ID NO: 395:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 crecaaeeeerrrrecreeece 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%;
Matches 22; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 2204
SOFTWARE: Patentin Ver. 2.
SEQ ID NO 395
LENGTH: 301
                                                                                                                                                                                                                                                                                                                                             LENGTH: 301 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CTGCAAGGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
US-09-076-898-395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-076-898-395/c

Sequence 395, Application US/09076898

Sequence 395, Application US/09076898

Sequence 395, Application US/09076898

APPLICANT: Craig A. Rosen, et. al.

APPLICANT: Craig A. Rosen, et. al.

TITLE OF INVENTION: Human Genes, Sequences, and Expression Products - PO31

NUMBER OF SEQUENCES: 2204

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                  Gaps
                                                                  ö
                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

Sequence 323, Application US/10217623

Sequence 323, Application US/10217623

GENERAL INFORMATION:

TILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

TILE REFERENCE: PM031C1N

CURRENT APPLICATION NUMBER: US/10/217,623

CURRENT FILING DATE: 2002-08-14

PRIOR APPLICATION NUMBER: 09/758,442

PRIOR APPLICATION NUMBER: 09/758,442

PRIOR APPLICATION NUMBER: 60/119,065

PRIOR PILING DATE: 2000-01-31

PRIOR PILING DATE: 2000-01-31

PRIOR PILING DATE: 2000-02-04

NUMBER OF SEQ ID NOS: 710

SEQ ID NO 323

LENGTH: 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IndelB
                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING STERM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
FILING DATE: May 13, 1998
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 22; Conservative 0; Mismatches 0;
                                   Pred. No. 5.4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (112)
CTHER INCRMATION: n equals a,t,g, or
US-10-217-623-323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (109)
OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047,004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155 creckAddddrrrrccreddcg 134
                               Best Local Similarity 100.0%; P
Matches 22; Conservative 0;
                                                                                                                                                                                                    155 crecaaeeerrrrecreece 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                     1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20850
```

셤 δ

ö

Gaps

; 0

ઠે 윱

```
PRIOR FILING DATE: 1997-05-13

PRIOR PELING DATE: 1998-05-14

PRIOR PILING DATE: 1998-10-15

PRIOR PILING DATE: 1998-11-12

PRIOR PILING DATE: 1998-11-12

PRIOR PILING DATE: 1998-11-12

PRIOR PILING DATE: 1999-06-04

PRIOR PILING DATE: 1999-06-04

PRIOR PILING DATE: 1999-08-04

PRIOR PILING DATE: 1999-08-04

PRIOR PILING DATE: 1999-08-04

PRIOR PILING DATE: 1999-08-04

PRIOR PILING DATE: 1999-06-04

PRIOR PILING DATE: 1999-06-12

PRIOR PILING DATE: 1999-06-13

PRIOR PILING DATE: 1999-06-13

PRIOR PILING DATE: 1999-06-14

PRIOR PILING DATE: 1999-06-15

PRIOR PILING DATE: 1999-06-16

PRIOR PILING DATE: 1999-01-11

PRIOR PILING DATE: 1999-01-14

PRIOR PILING DATE: 1999-01-21

PRIOR PILING DATE: 1999-01-26

PRIOR PILING DATE: 1999-01-26

PRIOR PILING DATE: 1999-01-26

PRIOR PILING DATE: 1999-02-05

PRIOR PILING DATE: 2000-03-01

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (6)..(b)
OTHER INFORMATION: n is equal to a,t,g,
NAME/KEY: misc feature
LOCATION: (1157..(115)
OTHER INFORMATION: n is equal to a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA GOGANISM: Homo sapiens FEATURE: NAME/KEY: misc_feature LOCATION: (6)._(6)
                                                                                                                                                      US-09-11-229-11611/c

Sequence 11611, Application US/09912292

Sequence 11611, Application US/09912292

Sequence 11611, Application US/09912292

TILE OF INVENTION: Human Genes, Sequences, and Expression Products 101

FILE REPERENCE: PO-101

CURRENT APPLICATION NUMBER: US/09/912,292

CURRENT FILING DATE: 1993-08-09

PRIOR FILING DATE: 1993-08-09

PRIOR FILING DATE: 1993-08-09

PRIOR FILING DATE: 2001-05-18

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 08/196,482

PRIOR APPLICATION NUMBER: 08/196,482

PRIOR APPLICATION NUMBER: 09/196,482

PRIOR APPLICATION NUMBER: 09/196,482

PRIOR APPLICATION NUMBER: 09/196,482

PRIOR APPLICATION NUMBER: 09/198,587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR PILING DATE: 1994-02-15
PRIOR PILING DATE: 1994-03-15
PRIOR PILING DATE: 1994-03-31
PRIOR PILING DATE: 1994-03-31
PRIOR APPLICATION NUMBER: 08/275,627
PRIOR PILING DATE: 1994-03-31
PRIOR PILING DATE: 1994-03-31
PRIOR PILING DATE: 1994-03-31
PRIOR PILING DATE: 1994-01-15
PRIOR APPLICATION NUMBER: 08/345,704
PRIOR PILING DATE: 1994-11-21
PRIOR APPLICATION NUMBER: 09/401,881
PRIOR PILING DATE: 2001-05-18
PRIOR PILING DATE: 1995-03-10
PRIOR PILING DATE: 1995-03-10
PRIOR PILING DATE: 1995-03-10
PRIOR PILING DATE: 1997-01-30
PRIOR PILING DATE: 1996-01-30
PRIOR PILING DATE: 1996-02-3
PRIOR PILING DATE: 1996-02-3
PRIOR PILING DATE: 1996-02-3
PRIOR PILING DATE: 1996-11-19
PRIOR PILING DATE: 1996-11-12
PRIOR APPLICATION NUMBER: 08/971,050
PRIOR PILING DATE: 1996-11-12
PRIOR PILING DATE: 1996-11-12
PRIOR APPLICATION NUMBER: 08/971,050
PRIOR PILING DATE: 1996-11-18
PRIOR APPLICATION NUMBER: 08/971,038
PRIOR PILING DATE: 1996-11-18
PRIOR APPLICATION NUMBER: 08/971,038
PRIOR PILING DATE: 1996-11-18
PRIOR APPLICATION NUMBER: 08/971,038
PRIOR PILING DATE: 1996-11-25
PRIOR APPLICATION NUMBER: 08/971,038
PRIOR APPLICATION NUMBER: 08/971,038
PRIOR PILING DATE: 1996-11-25
PRIOR APPLICATION NUMBER: 08/971,038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 09/783,587
FILING DATE: 2001-02-15
APPLICATION NUMBER: 08/196,481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/047,004
                                                              162 crecaadescririecreses 141
1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1996-12-06
```

```
0
                                                                                                              150 crecaaederrirecreeded 129
                                                                          1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              May 13, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
                                        22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Maryland
  Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
US-09-076-897-1393/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 34372
LENGTH: 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Struat, Susan G.
APPLICANT: Bills, Pamela Ray
APPLICANT: Bills, Pamela Ray
APPLICANT: Bills, Pamela Ray
APPLICANT: Altus, Christina T.
APPLICANT: Hilman, Jennifer L.
APPLICANT: Hilman, Jennifer L.
APPLICANT: HOWINGLEOTIDES AND POLYPEPTIDES DERIVED FROM A TITLE OF INVENTION: HOWAN NEURONAL PRECURSOR CELL LINE
                                                                                                                                                                                                                                                                                                                                    Length 301;
                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/668,236
                                                                                                                                                                                                                                                                                                                                    DB 34;
5.5;
                                    or c
                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: INCYTE PHARMACEUTICALS, INC.
3330 HILLVIEW AVENUE
                                                                                                                                                                                                                                         NAME/KEY: misc_feature

1.0CATION: (289)

. OTHER INFORMATION: n is equal to a,t,g, or

US-09-912-292-11611
                                                                                             ör
                                                                                                                                                                                                                  or
                                                                                                                                                        g
              LOCATION: (1187...(118)
OTHER INFORMATION: n is equal to a,t,g, or NAME/KEY: Mance feature
LOCATION: (2617...(261)
OTHER INFORMATION: n is equal to a,t,g, or NAME/KEY: misc_feature
LOCATION: (2637...(364)
OTHER INFORMATION: n is equal to a,t,g, or NAME/KEY: misc_feature
LOCATION: (2637...(264)
OTHER INFORMATION: n is equal to a,t,g, or OTHER INFORMATION: n is equal to a,t,g, or OTHER INFORMATION: n is equal to a,t,g, or OTHER INFORMATION: n is equal to a,t,g, or
                                                                                                                                                                                                                                                                                                                            uvery Match
Best Local Similarity 100.0%; Pred. No. : Matches 22; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 703, Application US/08668236
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: LUTHER, BARBARA J.
REGIESTRATION NUMBER: 3395-(
REFRENCE/DOCKET NUMBER: PD-(
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 crechhedederririderedece 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 02.
TELEPHONE: (415) 05.
TELEFAX: (415) 052-0195
INFORMATION FOR SEQ ID NO: 70.
SEQUENCE CHARACTERISTICS:
LENGTH: 369 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: Word Pe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                           1 CTGCAAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
US-08-668-236-703/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-668-236-703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                               à
```

```
RESULT 11
US-09-534-846B-34372/c
US-09-534-846B-34372/c
Sequence 34372, Application US/09534846B
Sequence 34372, Application US/09534846B
Sequence 34372, Application US/09534846B
Sequence 34372, Application:
APPLICANT: Setlhamer, Jeffrey J.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Naughton, Rebecca B.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING GROWTH, DEVELOPMENT, AND TITLE OF INVENTION: DIFFERENTIATION MOLECULES
TITLE OF INVENTION: DIFFERENTIATION MOLECULES
TITLE OF TABLE OF THE STATE O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1393, Application US/09076897
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products - P032
NUMBER OF SEQUENCES: 7180
CORRESPONDENCE ADDRESS:
                                                                                               ö
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 22; DB 20; Length 369; 100.0%; Pred. No. 5.7; tive 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prior application data removed - refer to file wrapper or PALM NUMBER OF SEQ ID NOS: 38710 SOFTWARE: PERL Program
DB 10; Length 369;
                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCIT Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/076,897
           100.0%; Score 22; DB 1
100.0%; Pred. No. 5.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: hu00797632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: unsure

LOCATION: 2, 78, 92, 175, 210, 271, 341

COTHER INFORMATION: a, t, c, g, or other

US-03-534-846B-34372
```

```
RESULT 14

US-09-076-897B-1393/c
; Sequence 1393, Application US/09076897B
; Sequence 1393, Application US/09076897B
; Sequence 1303, Application US/09076897B
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products - PO32
; NUMBER OF SEQUENCES; ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
; STREET: PALY ROCKVILLe
; STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-076-897C-1393/C
US-09-076-897C-1393/C
Sequence 1393, Application US/09076897C
Sequence 1393, Application US/09076897C
GENEAL INFORMATION:
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 32
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 32
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 32
CURRENT FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 1999-05-13
PRIOR PELING DATE: 60/047,005
NUMBER OF SEQ ID NOS: 7180
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 22; DB 14; Length 404; ilarity 100.0%; Pred. No. 5.8; Conservative 0; Mismatches 0; Indele C
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
CORPTRE: HP Vectra 486/33
CORPTARE: ASCIT Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/076,897B
FILING DATE: May 13, 1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING APPLICATION NUMBER:
ATIONNEY/AGENT: INFORMATION:
       159 CTGCAAGGGGTTTTGCTGGGCG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 1393:
SEQUENCE CHARACTERISTICS:
LENGTH: 404 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 creckAddedririrecredece 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: A. Anders Brookes
REGISTRATION NUMBER: 36.373
REFERENCE DOCKET NUMBER: PO-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc feature
LOCATION: (122)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
US-09-076-897B-1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 22; Conserv
          음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1393, Application US/09076897A
GENERAL INFORMATION:
APPLICANT: Rosen, et. al.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products - PO32
NUMBER OF SEQUENCES: 7180
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 22; DB 14; Length 404;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 22; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 14; Length 404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
COPENATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/076,897A
FILING DATE: MAY 13, 1998
CLASSIFICATION S36
PRIOR APPLICATION 536
PRIOR APPLICATION 536
PRIOR APPLICATION 1536
PRIOR APPLICATION NUMBER: PO-32
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A Ander8 Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PO-32
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8439
INFORMATION FOR SEQ ID NO: 1393:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

100.0%; Score 22;
Best Local Similarity 100.0%; Pred. No. 9
Matches 22; Conservative 0; Mismatch
                                                            REGISTRATION NUMBER: 36,373
REFRENCE/POCKET NUMBER: 90-32
TELECOMMUNICATION INFORMATION:
TELEPANE: (301) 309-8504
INFORMATION FOR SEQ ID NO: 1393:
SEQUENCE CHARACTERISTICS:
LENGTH: 404 base pairs
TELNGTH: 404 base pairs
TENGTH: 404 base pairs
TENGTH: 404 base pairs
TENGTH: 404 base pairs
TOPOLOGY: linear
TOPOLOGY: linear
  60/047,005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 creckkederrirrecredece 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CTGCAAGGGGTTTTGCTGGGCG 22
                       FILING DATE: May 13, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 404 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-09-076-897A-1393/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-076-897A-1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20850
```

ò 윱

```
CCATION: (123)

OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature

LOCATION: (124)

OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature

LOCATION: (129)

OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature

LOCATION: (290)

OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature

LOCATION: (331)

OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature

LOCATION: (333)

OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature

LOCATION: (341)

OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature

LOCATION: (342)

OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature

LOCATION: (365)

OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature

LOCATION: (365)

OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature

LOCATION: (365)

OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature

LOCATION: (365)

OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature

LOCATION: (365)
OTHER INFORMATION: n equals a,t,g, or c
```

159 CTGCAAGGGGTTTTGCTGGGCG 138 g

ઠ

Query Match
Best Local Similarity 100.0%; Score 22; DB 14; Length 404;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 22; Conservative 0; Mismatches 0; Indels (

Search completed: April 18, 2003, 09:35:41 Job time : 1212 secs

us-09-270-437d-10.rnpn

```
US-09-270-437D-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-270-437D-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 347, App Sequence 478, App Sequence 478, App Sequence 450, App Sequence 428, App Sequence 485, App Sequence 44307, A Sequence 44307, A Sequence 44305, A Sequence 44305, A Sequence 44305, A Sequence 55, App Sequence 55, App Sequence 479, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Appl
Sequence 34372, A
Sequence 56784, A
                                                                                                                                             April 18, 2003, 06:35:28:; Search time 245:167 Seconds (Without alignments) 400.770 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pending Patents NA New:*

1: /cgn2_6/ptodata71/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata71/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata71/pna/US06_NEW_COMB.seq:*
4: /cgn2_6/ptodata71/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata71/pna/US08_NEW_COMB.seq:*
6: /cgn2_6/ptodata71/pna/US09_NEW_COMB.seq:*
7: /cgn2_6/ptodata71/pna/US09_NEW_COMB.seq:*
8: /cgn2_6/ptodata71/pna/US10_NEW_COMB.seq:*
9: /cgn2_6/ptodata71/pna/US10_NEW_COMB.seq:*
10: /cgn2_6/ptodata71/pna/US10_NEW_COMB.seq:*
11: /cgn2_6/ptodata71/pna/US60_NEW_COMB.seq:*
GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-314-344-34372
US-10-313-986-478
US-10-313-986-478
US-10-313-986-478
US-10-313-986-447
US-10-313-986-447
US-10-313-986-428
US-10-313-986-428
US-10-313-986-428
US-10-313-986-443
US-10-313-986-443
US-10-724-676-44307
US-10-724-676-44305
US-09-724-676-44305
US-09-724-676-44305
US-10-313-986-175
US-10-313-986-175
US-10-313-986-175
US-10-313-986-175
US-10-313-986-175
US-10-313-986-175
US-10-313-986-175
US-10-313-986-175
US-10-313-986-179
US-10-313-986-179
US-10-313-986-179
US-10-313-986-179
US-10-313-986-179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                            5897297 seqs, 2233080881 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                       US-09-270-437D-10
22
1 ctgcaagggttttgctgggcg 22
                                                                                                 - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                              IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1740
1740
1743
1743
1743
1743
1743
1799
2137
2137
2137
2137
4161
4181
4181
4181
4181
17251
1663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1000.00
                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                      Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM nucleic
                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                                                                      Run on:
```

```
Sequence 1, Appliseduence 15, Appliseduence 35, Appliseduence 156, Appliseduence 1586, Appliseduence 1995, A Sequence 1995, A Sequence 1600, Appliseduence 55, Appliseduence 28495, A Sequence 12413, Sequence 1271, A Sequence 137, Appliseduence 1271, A Sequence 137, Appliseduence 18985, A Sequence 18985, A Sequence 18985, A Sequence 18395, A Sequence 18395, A
9 US-10-144-771-2615

11 US-60-453-135-1

12 US-60-453-050-1

12 CS-60-457-50-1

13 US-60-947-911-356

6 US-09-949-016-91995

7 US-09-949-016-91996

7 US-09-949-016-19196

7 US-09-949-016-18819

7 US-09-949-016-18819

7 US-09-949-016-16006

6 US-09-948-124-62

8 US-09-912-293-146413

9 US-10-314-3444-11271

6 US-09-912-293-164413

8 US-10-314-344-11271

6 US-09-912-293-90564

6 US-09-912-293-90564
                                                                                                                                                      6 7
                                         324604 1
373882 7
395 6
601 7
601 7
45755 7
254405 7
712680 7
78125 6
178256 6
15105345
```

## ALIGNMENTS

```
Sequence 10, Application US/09270437D

GENERAL INFORMATION:

APPLICANT: Chen, Yao-Tseng

APPLICANT: Gure, Ali

APPLICANT: Teang, Solam

APPLICANT: Alsander, Elsabeth

APPLICANT: Alsander, Elsabeth

APPLICANT: Alsander

APPLICANT: Alsolated Nucleic Acid Molecules Encoding Cancer Associated Antige.

TITLE OF INVENTION: Antigens Per Se, And Uses Thereof

FILE REFERENCE: LUD 5538.1

CURRENT APPLICATION NUMBER: US/09/270,437D

FRIOR APPLICATION NUMBER: 09/061,709

PRIOR FILING DATE: 1999-04-17

NUMBER OF SEQ ID NOS: 23

SEQ ID NO 10

LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 22; DB 5; Length 22; 100.0%; Pred. No. 0.73; ive 0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
US-10-314-344-34372/c
Sequence 34372, Application US/10314344
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Belegaene, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuare, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CTGCAAGGGGTTTTGCTGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGCAAGGGGTTTTGCTGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
```

ô

```
Gaps
                                                                                                                                                                                                                                                          - See File Wrapper or PALM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Watanabe, Yoshihiro
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Tongtong
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C19
CURRENT APPLICATION NUMBER: US/10/313,986
CURRENT FILING DATE: 2002-12-04
CURRENT FILING DATE: 2002-12-04
CURRENT FIRING DATE: AMIONS: 560
SOFTWARE: FREESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 22; DB 6; Length 404; 100.0%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (392)...(392)
CTHER INFORMATION: n is equal to a,t,g, or C
US-09-912-293-56784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
PRIOR APPLICATION NUMBER: 08/220,691
PRIOR FILING DATE: 1994-03-31
PRIOR APPLICATION NUMBER: 09/741,830
PRIOR APPLICATION NUMBER: 09/813,155
PRIOR PLING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
Remaining Prior Application data removed - 5
NUMBER OF SEQ ID NOS: 244538
SEQ ID NO 56784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (333)...(333)
OTHER INFORMATION: n is equal to a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (341)...(341)
OTHER INFORMATION: n is equal to a,t,g,
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (365)..(365)
OTHER INFORMATION: n is equal to a,t,9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc feature
LOCATION: (122)..(124)
OTHER INFORMATION: n is equal to a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (129)..(129)
OTHER INFORMATION: n is equal to a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DUCATION: (290)..(290)
OTHER INFORMATION: n is equal to a,t,9,
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 347, Application US/10313986
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (331)
OTHER INFORMATION: n is equal to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 CrccAAGGGGTTTTGCTGGGCG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CIGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%;
Matches 22; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Foy, Teresa M. APPLICANT: McNabb, Andria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature CATION: (331)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIMEN. --
PEATURE:
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-313-986-347/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                             TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING GROWTH, DEVELOPMENT, AND TITLE OF INVENTION: DIFFERENTIATION MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Rosen, et. al.
APPLICANT: Rosen, et. al.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 100
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 100
FILE REFERENCE: PO-100
CURRENT APPLICATION NUMBER: US/09/912,293
CURRENT FILING DATE: 2001-07-26
PRIOR FILING DATE: 1993-08-09
PRIOR FILING DATE: 1993-08-09
PRIOR PILING DATE: 1993-02-12
PRIOR PLING DATE: 1993-08-09
PRIOR PLING DATE: 1993-08-09
PRIOR PLING DATE: 1993-08-09
PRIOR PLING DATE: 1994-08-15
PRIOR PLING DATE: 2001-05-18
PRIOR PLING DATE: 2001-05-18
PRIOR PLING DATE: 2001-05-18
PRIOR PLING DATE: 1994-02-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                TITLE OF INVENTION: POLITUCLECTILES ENCOULING ON RECOLLINGS
FILE REPERENCE: POLITON: POLITUCLECTILES
FILE REPERENCE: POLITON: DIFFERENTIATION MOLECULES
FILE REPERENCE: POLITOL-2 CON
CURRENT APPLICATION NUMBER: US/10/314,344

CURRENT FILING DATE: 2002-12-05

PRIOR PILING DATE: 1992-07-19

PRIOR FILING DATE: 1992-07-17

PRIOR FILING DATE: 1992-11-19

PRIOR PILING DATE: 1992-11-19

PRIOR PILING DATE: 1992-11-19

PRIOR PELING DATE: 1992-08-03

PRIOR PELING DATE: 1994-01-19

PRIOR PELING DATE: 1994-02-14

PRIOR PELING DATE: 1994-07-28

PRIOR PELING DATE: 1995-05-10

PRIOR PELING DATE: 1995-05-10

PRIOR PELING DATE: 1995-05-10

PRIOR PELING DATE: 1995-05-10

PRIOR PELING DATE: 1995-07-20

PRIOR PELING DATE: 1994-01-10

PRIOR PELING DATE: 1994-01-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 22; DB 9; Length 369; ilarity 100.0%; Pred. No. 1.1; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: hu00797632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: 2, 78, 92, 175, 210, 271, 341
; CTHER INFORMATION: a, t, c, g, or other
US-10-314-344-34372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 56784, Application US/09912293
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 crecaAddedririderdeded 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
US-09-912-293-56784/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q ID NO 34372
LENGTH: 369
```

ò

ö

```
TYPE: DNA
ORGANISM: Homo sapiens
US-10-313-986-450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CTGCAAGGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-313-986-450/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-313-986-428/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                               RESULT 5

US-10-313-986-478/C

i Sequence 478, Application US/10313986

i Sequence 478, Application US/10313986

i SEQUENCE 478, Application US/10313986

i APPLICANT: Revy, Teresa M.

APPLICANT: Reed, Steven G.

APPLICANT: Reed, Yoshiniro

APPLICANT: Watanabe, Yoshiniro

APPLICANT: Wang, Tongtong

ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

ITILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

ITILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

ITILE OF INVENTION: WHOBER: US/10/313,986

CURRENT FILING DATE: 2002-12-04

NUMBER OF SEQ ID NOS: 560

SOFTWARE: FestSEQ for Windows Version 4.0

SEQ ID NO 478

LENGTH 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 483, Application US/10313986

GENERAL INFORMATION:

APPLICANT: FOY, Teresa M.

APPLICANT: Matanabe, Yoshihiro

APPLICANT: Watanabe, Yoshihiro

APPLICANT: Weed, Steven G.

APPLICANT: Weed, Steven G.

APPLICANT: Weed, Steven G.

APPLICANT: Wang, Tongtong

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

TITLE OF INVENTION: 2002-12-04

WINDER OF SEQ ID NOS: 560

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 483

LENGTH: 1740
                                                                                             Query Match
100.0%; Score 22; DB 9; Length 1740;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 22; DB 9; Length 1740;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

100.0%; Score 22; DB 9; Length 1740;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                      498 CTGCAAGGGTTTTGCTGGGCG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 498 CTGCAAGGGGTTTTGCTGGGCG 477
                                                                                                                                                                                             1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CTGCAAGGGGTTTTGCTGGGCG 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-313-986-347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
US-10-313-986-478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) TYPE: DNA
; ORGANISM: primate
US-10-313-986-483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-313-986-483/C
                                                                                                                                                                                                                                           g
                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      윱
```

498 Criccaaccerriricerecece 477

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
Sequence 447, Application US/10313986

Sequence 447, Application US/10313986

GENERAL INFORMATION:
APPLICANT: FOR THE THERA THE APPLICANT: MCNabb, Andria
APPLICANT: McNabb, Andria
APPLICANT: Meanabe, Yoshihiro
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND MACHORY
FILE REFRENCE: 210121.455C19
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 560
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 447

LENGTH::1743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MCNabb, Andria
APPLICANT: MCNabb, Andria
APPLICANT: MCNabb, Andria
APPLICANT: Matanabe, Yoshihiro
APPLICANT: Watenabe, Yoshihiro
APPLICANT: Wang, Tongtong
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: WIND DIAGNOSIS OF LUNG CANCER
ITILE REPERRENCE: 210121.455C19
CURRENT APPLICATION NUMBER: US/10/313,986
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 1743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

Query Match

Best Local Similarity 100.0%; Pred. No. 1.3;

Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 22; DB 9; Length 1743; 100.0%; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 450, Application US/10313986; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 428, Application US/10313986
; GENERAL INFORMATION:
APPLICANT: FOY, Teresa M.
APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        498 crecaacecirrirecrecece 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   498 CTGCAAGGGGTTTTGCTGGGCG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) ORGANISM: Homo sapiens
US-10-313-986-447
```

```
RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 485, Application US/10313986
; Sequence 485, Application US/10313986
; GENERAL INPORATION:
APPLICANT: Foy, Teresa M.
APPLICANT: McNabb, Andria
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
CURRENT APPLICATION NUMBER: US/10/313,986
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 485
LENGTH: 1799
                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 22; DB 6; Length 2137; 100.0%; Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Score 22; DB 9; Length 1799;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                           100.0%; Score 22; DB 9; Length 1764; 100.0%; Pred. No. 1.3;
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.455C19
CURRENT APPLICATION WHERE: U5/10/313,986
CURRENT PILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 428
LENGTH: 1764
                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 44307, Application US/09724676
| SEQUENCE 44307, Application US/09724676
| GENERAL INFORMATION:
| APPLICANT: Compugen LTD
| TITLE OF INVENTION: Variants of alternative splicing
| TITLE OF INVENTION: Variants of alternative splicing
| TITLE OF INVENTION: Variants of alternative splicing
| CURRENT APPLICATION NUMBER: US/09/724,676
| CURRENT FILING DATE: 2000-11-28
| SOFTWARE: PatentIn version 3.2
| SEQ ID NO 44307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                517 crechaddedririrdcridddcd 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           519 CrGCAAGGGGTTTTGCTGGGCG 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CORGANISM: Homo sapiens
US-09-724-676-44307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Homo sapiens
US-10-313-986-485
                                                                                                                                                                                                                                   TYPE: DNA
CORGANISM: Homo sapiens
US-10-313-986-428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
US-09-724-676-44307/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-313-986-485/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                               à
```

```
TITLE OF INVENTION: TRANSCRIPTS, J. Craig
TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
CURRENT APPLICATION NUMBER: US/10/170,235
CURRENT FILING DATE: 2003-03-17
SEQ ID NO 31225
LENGTH: 3897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 22; DB 8; Length 3897; liarity 100.0%; Pred. No. 1.5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6; Length 2137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                US-02-74-676A-44307/C
US-09-724-676A-44307, Application US/09724676A

| Sequence 44307, Application US/09724676A
| GENERAL INFORMATION:
| APPLICATION: Observed of alternative splicing TITLE OF INVENTION: Variants of alternative splicing FILE REFERENCE: 129181.4 Compugen
| CURRENT APPLICATION NUMBER: US/09/724,676A
| CURRENT FILING DATE: 2000-11-28
| NUMBER OF SEQ ID NOS: 97222
| SEQ ID NO 44307
| LENGTH: 2137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICAT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129101.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 4060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Pred. No. 1.4;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 22;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14

10.09-724-676-44305/c

1. Sequence 44305, Application US/09724676

1. GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-170-235-31225/c
; Sequence 31225, Application US/10170235
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334 crechhederrrrrecredece 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               764 crecasecerrirecresece 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CTGCAAGGGGTTTTGCTGGGCG 22
764 crecaagederririecresecs 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 22; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CORGANISM: Homo sapiens
US-09-724-676A-44307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: HUMAN
US-10-170-235-31225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
```

US-09-724-676-44305

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                Gaps
                                                                .
Query Match 100.0%; Score 22; DB 6; Length 4060; Best Local Similarity 100.0%; Pred. No. 1.5; Matches 22; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 22; DB 6; Length 4060; Best Local Similarity 100.0%; Pred. No. 1.5; Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                RESULT 15
US-09-724-676A-44305/c
; Sequence 44305, Application US/09724676A
; GENERAL INFORMATION:
; TILLE OF INVENTION: Variants of alternative splicing
; TILLE OF INVENTION: Variants of alternative splicing
; TILLE OF INVENTION: Variants of alternative splicing
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; SCFTWARE: Patentin version 3.2
; SCF ID NO 44305
; LENGTH: 4060
; TYPE: DNA
; ORGANISM: HOMO sapiens
US-09-724-676A-44305
                                                                                                                                764 CTGCAAGGGTTTTGCTGGGCG 743
                                                                                                    1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
```

Search completed: April 18, 2003, 10:03:47 Job time : 256.167 secs

셤

	a constant	•			•
	•				
		• .			·
i i					
€ 25 -					
					•
		•			
	P				•
	(1) (1) (1)				
				•	
		v i i i i i i i i i i i i i i i i i i i		; · · · · ·	
			•		
				· · · · · · · · · · · · · · · · · · ·	
か. む					
			e de la companya de La companya de la co		
					· ·
			•		
					3
		•			, is
	er S				
For				•	
c d.					
				•	

OM nucleic

Run on:

Seguence:

Minimum DB Maximum DB

Database

Result

Searched:

```
AL744135 Danio rer
BQ166727 WED934 D
BW728827 ULE-ECI-
BH73419 601809561
AI54505 Eb66d03.x
BI338062 367520 MA
BE330968 252846 BA
BE899763 202763 MA
BE899763 202763 MA
BE899763 202763 MA
BE899763 20226004
BE8997203 60151550
BO715397 AGENCOURT
BG106781 602290632
BM563299 AGENCOURT
BG106781 602290632
BM563299 AGENCOURT
BG106781 602290632
BM563299 AGENCOURT
BG106781 602290632
BM563299 AGENCOURT
AA200129 MU10a06.r
BP991263 BM291263
AA200129 MU10a06.r
AM2700 MC84401.rl
AM3750 MC84401.rl
AM4750 MC84401.rl
AM8750 MC84401.rl
AM8750 MC84401.rl
AM8752 MC84401.rl
AM8752 MC8451.rl
AM8752 MC8451.rl
AM8650 BM77528
BB777528
BB777528
BB777528
BB777228 BB777528
BB777228 UL M-AP0-
BB777228 UL M-AP0-
BB777228 UL M-AP0-
BB777228 UL M-BB3-
BB777244 BB7711444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo saptems and saptems are but and saptems and saptems are surfaced as the same and saptems are but arrayota; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi; Butteria; Butheria; Primates; Catarrhini; Hominidae; Homo.

El (bases I to 790)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Incyte Genomics, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LiAMAG44 row: f column: 24

High quality sequence stop: 667.

Salzoe

Incre

1. 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BES45535
601070391F1 NIH_MGC_12 Homo saplens cDNA clone IMAGE:3456407 5',
mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                     BH592483
BF183419
AI54505
BI338062
BF230968
BE899763
AI658303
BG027293
BG027293
BG115397
BG1165781
BG1165781
BG1165781
BG1165781
BG1165781
BG1165781
                                                                                                                                                                                                              W10000
BP200129
BP200129
BP200129
W47750
A0340144
A0340144
AA270892
A1745603
AW12298
BP899524
W54455
AA880520
AI886520
AI836336
BB777528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BE545535.1 GI:9774180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE545535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human.
 RESULT 1
BE545535/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE545535 601070391
BI520069 603071386
A2019431 RPCI-23-2
BG699047 602678681
AQ022143 CIT-HSP-2
AL597825 DKFZD313C
                                                                  April 18, 2003, 04:47:40 ; Search time 766 Seconds (without alignments) 465.145 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is the number of results predicted by chance to have a
ter than or equal to the score of the result being printed,
dived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
 GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                 16154066 seqs, 8097743376 residues
                                                                                                                                                                                                                       hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                 US-09-270-437D-10
22
1 ctgcaagggttttgctgggcg 22
                                             nucleic search, using sw model
                                                                                                                                                                                                                                                                                                           first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE545535
BI520069
AZ019431
BG699047
AQ022143
ALS97825
                                                                                                                                                             IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        em gas mam: *
em gas mus: *
em gas other: *
em gas pro: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of res
score greater than or equal to
and is derived by analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H
                                                                                                                                                                                                                                               seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_gss:*
em_gss_hum:*
em_gss_inv:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      em_gas_pln: *
em_gas_vrt: *
em_gas_fun: *
                                                                                                                                                                                                                                                                                                                                           em_estba:*
em_esthum:*
em_esthun:*
em_estru:*
em_estro:*
em_estro:*
em_htc:*
em_htc:*
gb_est2:*
gb_est2:*
gb_est4:*
gb_est4:*
gb_est4:*
em_est6un:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         em_gss_rod:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10
11
11
12
17
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                  EST:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0
92.7
88.2
86.4
85.5
                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of
                                                                                                                              Perfect score:
                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.4
19.4
19.4
19.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
```

```
268 cháchaddadririraridadad 247
                                                                                                                                                                                                                                                                                                                                                                                                             AZ019431.1 GI:7094815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 TGCAAGGGGTTTTGCTGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              house mouse.
                                                                                                                                                                                                                                                                                                                                                                                           AZ019431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
BG699047/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                    LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                      AZ019431
                                                                                                                                                                                                                     RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠ
                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I 1 (bases 1 to 743)

1 (bases 1 to 743)

2 NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbe-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
Contact: Robert Strausberg, Ph.D.
Email: cgapbe-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: LiAmitabution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiML at:
http://image.llnl.gov
Plate: LiAmitatos Eutherit: 9
High quality sequence stop: 704.
High quality sequence stop: 704.
High quality sequence stop: 704.
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="INAGE:3456407"
/clone=lib="NIH MGC 12"
/clone=lib="NIH MGC 12"
/tissue_vppe="cervical carcinoma cell line"
/lab host="DH108"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life
Rechnologies."
I a 193 c 209 g 167 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anote—World Minds of the Market of the Marke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BIS20069 743 bp mRNA linear BST 29-AUG-2001
63071386PL NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5163429 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.7%; Score 20.4; DB 13; Length 743; 95.5%; Pred. No. 72; ive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Score 22; DB 10; Length 790;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 22; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.743

^organis="Homo sapiens"

/db xref="texon:9666"

/clone="IMAGE:5163429"

/clone="IMAGE:5163429"

/tissue_type="medulla"

/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              416 crecaaededririrecredede 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BI520069.1 GI:15344861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
BI520069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 21, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BI520069/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
```

```
DESCRIPT:

ACOLOGICAL TOTAL ACOLOGICAL STATEMENT OF THE S
```

```
119 t
                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                        62 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 CTGCAAGGGGTTTTGCTGTGAG 279
                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA-collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                    22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALS97825.1 GI:15160516
                                                                                                                                                                                                                                                                                                                                                                                     85.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGCAAGGGGTTTTGCTGGGCG
                                                                                                                                                                                                                                                                                                                                       109 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Ansorge W
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 a
                                                                                                                                                                                                                                                                                                                                        81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human.
                                                                                                                                                                                                                                                                                                                                                                                                                   20;
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALS97825/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEYWORDS
                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 372)
Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K.,
Goldan, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
Simon, M. and Venter, J.C.
Building (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ022143 372 bp DNA linear GSS 09-JUN-1998
CIT-HSP-2308A16.TF CIT-HSP Homo sapiens genomic clone 2308A16, DNA
                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLMANLO702 row: a column: 21
                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 813)
MIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.4%; Score 19; DB 12; Length 81
100.0%; Pred. No. 3.2e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 t
                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4811420"
                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 770. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1998)
Other GSSs: CIT-HSP-2308A16.TR
Contact: Mark Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 g
              BG699047.1 GI:13966953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ022143
AQ022143.1 GI:3200879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 706 crecaassestrirecres 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CTGCAAGGGGTTTTGCTGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence.
 BG699047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190
                                                 uman.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
AQ022143/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                         REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
```

ઠે 셤

```
A66 bp mRNA linear BST 14-AUG-2001
DKFZp313C1017_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
AL597825
Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
7212 Medical Center Dr., Rockville, MD 20850, USA
7213 301 838 0200
Fax: 301 838 0208
Faxills madams@tigr.org
6 mills madams@tigr.org
6 mills madams@tigr.org
7 mills mill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 466)
Ansorge, W., Wirkner, U., Mewes, H.W., Weil, B. and Wiemann, S.
EST (Ansorge, W., Wirkner, U., Mewes, H.W., Weil, B. and Wiemann, S.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Berlin.
6, 14059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pTriplEx2; Site_1: SfilA; Site_2: SfilB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="raxon:9606"
/clone="2308A46"
/clone lib="CTT-HSP"
/sex="Male"
/sex="Male"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2: HindIII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No si sequence available.
This clone (DKFZp313C1017) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Am Klopferspitz 18a D-82152 Martinsried, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 18.8; DB 17;
Pred. No. 3.1e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db xref="taxon.9606"
/dlone="bkPzp313C1017"
/clone_llb="313 (synonym: hlcc2)"
/dev stage="adult"
/lab_host="bH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118
```

Query Match Best Local (

ORIGIN

Matches

DEFINITION ACCESSION VERSION KEYWORDS

RESULT 7

g

8

DR6F10S

ORGANISM

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE.

FEATURES

```
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
7e1: 319 335 8250
Fax: 319 335 9555
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
                                                                                                                                                                                                                                           US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                      Tel: 5105595773
Tel: 5105595773
Email: canderan@pw.usda.gov
This EST was generated by sequencing from the 3' end of the clone.
Sequences have been trimmed to remove vector sequence and low quality sequence with phred score less than 20.
Seq primer: T7 primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

I (bases 1 to 714)

Bonaldo, M. P., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           714 bp mRNA linear EST 01.
UI-E-EO1-aiv-f-19-0-UI.rl UI-E-EO1 Homo sapiens CDNA clone
UI-E-EO1-aiv-f-19-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 17.8; DB 14; Length 375; Pred. No. 8.7e+02; 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  discovery
Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BM728827
BM728827.1 GI:19050160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 TGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 rechastrecririscredare 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 80.9%;
Best Local Similarity 90.5%;
Matches 19; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BM728827/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                             Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Triticum aestivum

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;

Triticaea; Triticum.

1 (bases 1 to 375)

Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J.,

The structure and function of the expressed portion of the wheat genomes - 5.15 DAP spike cDNA library

Unpublished (2000)

Contact: Olin Anderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQ166727
WHE0924 DOT_H14ZT Wheat 5-15 DAP spike cDNA library Triticum aestivum cDNA clone WHE0924_DOT_H14, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                               DR6F10S 615 bp DNA linear GSS 06-JUN-2002 Danio rerio genomic clone DKey-6F10, genomic survey sequence.
                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                               Danio rerio
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 615)
Humphray, S. J., Huckle, E. and Hunt, S. E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                     ö
                                                       Score 18.8; DB 9; Length 466;
Pred. No. 3.3e+02;
0; Mismatches 2; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.8%; Score 18; DB 17; L
100.0%; Pred. No. 8.2e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue type="Testis"
/note="vector pIndigoBAC-536"
106 c 117 g 195 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Danio rerio"
/db_xref="taxon:7955"
/clone="DKey-6F10"
                                                                                                                                                                   300 CTGCCAGGGTTTTGCTGGGTG 279
                                                                                                                                              1 CTGCAAGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                  AL744135
AL744135.1 GI:21354443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BQ166727.1 GI:20310411
                                                               85.5%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              271 rechadederririecies 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 TGCAAGGGGTTTTGCTGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                        20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bread wheat
                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                            zebrafish
```

RESULT 8 BQ166727/c LOCUS

ద

ò

BASE COUNT ORIGIN

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

ö

Gaps

ö

EST 01-MAR-2002

ö

Seg primer: M13 Reverse

```
/ 1253
/ Organism="Homo saplens"
/ Organism="Homo saplens"
/ Organism="Homo saplens"
/ Clone="IMAGE:4040174"
/ Clone="IMAGE:4040174"
/ Clone="IMAGE:4040174"
/ Clone="IMAGE:4040174"
/ Lissue_type="large_cell_carcinoma"
/ Lissue_type="large_cell_carcinoma"
/ Lissue_type="large_cell_carcinoma"
/ Lissue_type="large_cell_carcinoma"
/ Lissue_type="large_cell_carcinoma"
/ Lissue_type="large_cell_carcinoma"
/ Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Superseript_IRT (Extrategene) and
Superseript_IRT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                                                                                                        BF183419
601809561R1 NIH_MGC_18 Homo sapiens CDNA clone IMAGE:4040174 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 (bases 1 to 1253)

18 NIH-MGC http://mgc.nci.nih.gov/.

19 NIH-MGC http://mgc.nci.nih.gov/.

10 Unpublished (1999)

10 Contact: Robert Strausberg, Ph.D.

11 Contact: Robert Strausberg, Ph.D.

12 Email: cgapbs-rømail.nih.gov.

13 Contact: Robert Strausberg, Ph.D.

14 Email: cgapbs-rømail.nih.gov.

15 Contact: Robert Strausberg, Ph.D.

16 Contact: Robert Strausberg, Ph.D.

17 Strausper Preparation: Ling Hong/Rubin Laboratory

18 Contact: Double Programment: Double Ling Hong/Rubin Laboratory

18 Contact: Double Programment: Double Ling Hong/Rubin Laboratory

18 Contaction: MGC clone distribution information can be http://image.lini.gov

18 Contaction MGC clone distribution information can be http://image.lini.gov

19 Plate: LLCM857 row: j column: 15

19 High quality sequence start: 3

19 High quality sequence start: 3

10 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST 07-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Czaniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                      Gарв
  genomic DNA inserted into pHOS1 using BstXI linkers" 141 c 161 g 234 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AIS45505
LOCUS AIS45505 AIS46505 AIS46603.x1 Zebrafish WashU MPIMG EST Danio rerio cDNA clone
                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                       Length 719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.9%; Score 17.8; DB 12; Length 1253; 90.5%; Pred. No. 1.3e+03; 1ve 0; Mismatches 2; Indels 0;
                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 others
                                                                                             Score 17.8; DB 17;
Pred. No. 1.1e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      398 g
                                                                                          ch 80.9%; Scc
1 Similarity 90.5%; Pre
19; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH_MGC Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                     BF183419.1 GI:11061718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1087 İĞCAAĞĞĞİTİTİĞCCĞĞCCĞ 1067
                                                                                                                                                                                  2 TGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                  14 rechadedererrechedece 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 TGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 90.5%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
                    183 a
                                                                                        Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                 BF183419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human.
                                                                                                                                                                                                                                                                                                      RESULT 11
BF183419/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT ORIGIN
                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                        LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
                                                                                                                                                                                                                               셤
                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                  /tissue_tine=tine=teral eye"
/dev_stage="fetal eye"
/dev_stage="fetal eye"
/dev_stage="fetal eye"
/dev_stage="fetal"
/lab host="WHIOB (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacial with a modified polylinker; Site 1: EcoR 1; Site 2: Not 1;
UI-ESO1 is a normalized CDNA library containing the following tissue(s): fetal eye. The library was constructed according to Bonaldo. Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oilso-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (GTGTATAC: This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BHS92483
BOGCQ90TF BOGC Brassica oleracea genomic clone BOGCQ90, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brassica oleracea

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosida II; Brassicales; Brassicaceae; Brassica.

Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other GSSS: BOGCQ90TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TP

Class: sheared ends.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 17.8; DB 14;
Pred. No. 1.1e+03;
0; Mismatches 3;
                                               /organism="Homo sapiens"
/db_xref="texon:9606"
/clone="UT-E-EO1-aiv-f-19-0-UI"
/clone_lib="UT-E-EO1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Brassica oleracea"
/strain="TO1000DH3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:3712"
/clone="BOGC090"
/clone_llb="BOGC"
       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CTGCAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 crrchweeeirrrecreeus 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BH592483
BH592483.1 GI:17844935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 86.4%;
Matches 19; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brassica oleracea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BH592483
```

ઠે a ö

FEATURES

EST 30-JUL-2001

Casas, E.,

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

```
1 (bases 1 to 556)
Sonstegard, T.S., Capuco, A.V., Van Tassell, C.P., Ashwell, M.S. and
Welle, K.D.
Mapping of Expressed Sequence Tags from a normalized bovine mammary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus
Wataryotas Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                   Appropriate Contact: Smith TPL., Casas, E. Stone, T., T. L., Casas, E. Stone, T., Heaton, M. P., Grosse, W. M., Bennett, G. A., Laegreid, W. W. and Keele, J. W. Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)

Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sall; Library made from pooled tissue from day 11, 13, 15, 20,
                                                                                                                                                                                                                                                                                                               Sus scrofa
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (Dases 1 to 543)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          556 bp mRNA linear 55246 BARC 5BOV Bos taurus cDNA 5', mRNA sequence. BF230968.1 GI:11169364 BST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                             11338062 543 bp mRNA linear
61720 MARC 1PIG Sus scrofa CDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 17.4; DB 13;
Pred. No. 1.5e+03;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="taxon:9823"
|clone lib="MARC 1PIG"
|tissue type="pooled"
|/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTATCCCAGTACAGACA
Plate: 129 row: E column: 23
seq prime: ATTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and 30 embryos.
121 c 14
                                                                                                                                                                                                 BI338062
BI338062.1 GI:15031345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 79.1%;
Best Local Similarity 94.7%;
Matches 18; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  480 CAAGGGGTTTTGCTGGGAG 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 CAAGGGGTTTTGCTGGGCG 22
159 CAAGGGGTTTTGCTGGGGG 177
                                                                                                                                              BI338062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₩
COW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
BF230968
                                                                                                                                                                                                                                                                                       SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
COMMENT
                                                                                                                                                                                                       ACCESSION
VERSION
KEYWORDS
                                                                                         RESULT 13
BI338062
                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
        엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Stephen L. Johnson

Contact: Stephen L. Johnson

Washington University School of Medicine

Washington University School of Medicine

#444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

#518 134 286 1800

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 316 286 1810

Fax: 316 286 1810

Fax: 316 286 1810

Fax: 316 286 1810

Fax: 316 286 1810

Fax: 316 286 1810

Fax: 316 286 1810

Fax: 316 286 1810

Fax: 316 286 1810

Fax: 316 286 1810

Fax: 316 286 1810

Fax: 316 286 1810

Fax: 316 286 1810

Fax: 316 286 1810

Fax: 316 286 1810

Fax: 316 286 1810

Fax: 316 286 1810

Fax: 316 286 1810

Fax: 316 286 1810

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                       i (bases i to 271)

Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, S., Hillier, L., Kheising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., Mashu Zebrafish EST Project 1998
Unpublished (1998)
                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="26 somite embryos, adult livers, shield stage embryos" /lab_host="XLI-blue MRF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                 contains element MSR1 repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.1%; Score 17.4; DB 9; Length 27 94.7%; Pred. No. 1.2e+03; rive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Danio rerio"
/db_xref="taxon:7955"
/clone="IMAGE:3716837"
/clone lib="Zebrafish WashU MPIMG EST"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 269 POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: T7 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                    IMAGE:3716837 3' similar to element;, mRNA sequence.
                                                                                      AIS45505
AIS45505.1 GI:4462878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAGGGGTTTTGCTGGGCG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                            zebrafish
```

Bource

FEATURES

EST 14-NOV-2000

BASE COUNT ORIGIN

Matches

ð

ö

Gaps . 0

```
Search completed: April 18, 2003, 07:31:49 Job time : 771.167 secs
                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                 Email: tadeGanri.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PORWARD: AGGAAACGTATGACCAT
BACKWARD: AGGAAACAGCTATGACCAT
RACKWARD: GTTTTCCAGTCACGAC
Plate: 108 row: H column: 3
Seq primer: ATTTAGGTGACATATAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                       / Organism="Bos taurus"
/db_xref="taxon:9913"
/dlome lib="BARC SBOV"
/tissue_type="pooled"
/lab_host="Petor: pGMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST 25-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.

1 (bases 1 to 573)

Smith; T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NB 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4366
Fax: 402 762 4390
Simple pass sequencing. Bases called and alt trimmed with phred
v0.980994.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 556;
                                                                 USDA, ARS, Beltgville Agricultural Research Center Bd19. 200 Rm 2A, Beltgville, MD 20705, USA THI: 301 504 8416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE899763 573 bp mRNA linear 202763 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 79.1%; Score 17.4; DB 12; Best Local Similarity 94.7%; Pred. No. 1.5e+03; Matches 18; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR PRIMERS
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
gland cDNA library
Unpublished (2000)
Contact: Sonstegard TS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE899763.1 GI:10387237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            320 TGCAAGGGGTTTTGCTGTG 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 TGCAAGGGGTTTTGCTGGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
BE899763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
```

셤 8

```
1...573
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="wARC_2BOv"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCWV SPORT6; Site 1: Not1; Site 2: Sal1;
Library made from pooled tissue From testis, thymus,
semitendonosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
55 a 97 c 112 g 199 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
79.1%; Score 17.4; DB 12; Length 573;
Best Local Similarity 94.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0;
Plate: 42 row: G column: 17
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         311 TGCAAGGGTTTTGCTGTG 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 TGCAAGGGGTTTTGCTGGG 20
```

,																
<b>.</b>			. •													
r F															·	
						*							-			
	v.		**************************************									ž.			ń.	
								•								
	aut Talan at Talan at Talan			er in de la companya							· A				* * * * * * * * * * * * * * * * * * *	
No. of Street, or other teams.										N.						
														•		
						7										
					· .					•			v.			
***	·					·		•								
		***							. January		198 <mark>8</mark>			to surface to the		
	\$				* 10 m			· · · · · · · · · · · · · · · · · · ·		# #			*			
	,	. १९५५ १			• • • • • • • • • • • • • • • • • • •			•					•	an in the second	Arag	
. dl. 5						e personal	e e								Tage	
	# 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1									· .				Š	**	
	y g							**			·				re	

	000000	The Part of the Part of		_
	פעווייי	version	5.1.4 D5 4578	_
140	(000		1	_
1116T T KdO2	107 1993	- 2003	COPYLIGIT (C) 1993 - 2003 Compileen 1.+d	

Run on:   April 18, 2003, 04:46:26   (without alignments)   2192.677 Million cell updates/ecc   1   10   10   10   10   10   10   1	OM nucleic - nu	cleic a	nucleic search, using aw model	
US-09-270-437D-11  1 tccttgcgcgctccag 22  table: IDENTITY_NUC  Gapop 10.0, Gapext 1.0  2054640 seqs, 14551402878 r  mber of hits satisfying chosen para DB seq length: 200000000  cessing: Minimum Match 100%  Listing first 45 summaries  GenEmbl:*  1: 9D ba:* 2: 9D bres:* 3: 9D pat:* 5: 9D pat:* 6: 9D pat:* 7: 9D ph:* 8: 9D pat:* 7: 9D ph:* 8: 9D pat:* 11: 9D pat:* 12: 9D pat:* 13: 9D pat:* 14: 9D pat:* 15: 9D pat:* 16: 9D pat:* 17: 9D ph:* 18: 9D pat:* 19: 9D pat:* 19: 9D pat:* 11: 9D pat:* 12: 9D pat:* 13: 9D pat:* 14: 9D pat:* 15: 9D pat:* 16: 9D pat:* 17: 9D ph:* 18: 9D pat:* 19: 9D pat:* 10: 9D pat:* 10: 9D pat:* 10: 9D pat:* 11: 9D pat:* 11: 9D pat:* 11: 9D pat:* 11: 9D pat:* 11: 9D		April	46:26 ;	
table: IDENTITY NUC  Gapop 10.0 , Gapext 1.0  1: 2054640 seqs, 14551402878 residues  mber of hits satisfying chosen parameters:  DB seq length: 0  DB seq length: 0  DB seq length: 0  Cessing: Minimum Match 100%  Maximum Match 100%  Listing first 45 summaries  GanEmbl:*  1: 9b ba:*  2: 9b list:*  3: 9b list:*  5: 9b list:*  5: 9b list:*  6: 9b list:*  7: 9b list:*  8: 9b list:*  11: 9b list:*  12: 9b list:*  13: 9b list:*  14: 9b list:*  15: em list:*  16: em list:*  17: em list:*  18: em list:*  18: em list:*  22: em list:*  23: em list:*  24: em list:*  25: em list:*  25: em list:*  26: em list:*  27: em list:*  28: em list:*  29: em list:*  29: em list:*  21: em list:*  23: em list:*  23: em list:*  24: em list:*  25: em list:*  26: em list:*  27: em list:*  28: em list:*  28: em list:*  29: em list:*  29: em list:*  29: em list:*  29: em list:*  29: em list:*  29: em list:*  29: em list:*  29: em list:*  20: em list:*		US-09- 22 1 tcct	gcctcag 22	
mber of hits satisfying chosen parameters:  DB seq length: 0  DB seq length: 0  DB seq length: 200000000  Cessing: Minimum Match 100\$  Listing first 45 summaries  GenEmbl:*  1: 9D ba:*  3: 9D htg:*  4: 9D ow:*  6: 9D ph:*  9: 9D ph:*  11: 9D pat:*  12: 9D ph:*  13: 9D ph:*  14: 9D vi:*  15: 9D ph:*  16: 9D ph:*  17: 9D ph:*  18: 9D wi:*  19: 9D ph:*  10: 9D pr:*  11: 9D pt:*  12: 9D py:*  13: 9D wi:*  14: 9D vi:*  15: em ba:*  16: em hum:*  17: em hum:*  21: em ph:*  22: em ph:*  23: em ph:*  24: em ph:*  25: em ph:*  25: em ph:*  26: em htg ohus:*  27: em htg ohus:*  28: em htg ohus:*  29: em htg ohus:*  31: em htg ph:*  32: em htg ph:*  33: em htg ohus:*  34: em htg rod:*  35: em htg ohus:*  36: em htg ohus:*  37: em htg ohus:*  38: em htg ohus:*  39: em htg ohus:*  39: em htg or:*  41: em htg of hus:*  39: em htg or:*  41: em htg of hus:*  39: em htg of hus:*  41: em htg of hus:*  41: em htg of hus:*	table	IDENTI Gapop	ITY_NUC 10.0 , Gapext 1.0	
## Mark ## ## ## ## ## ## ## ## ## ## ## ## ##	earched:	205464	segs, 14551402878	
Cessing: Minimum Match Listing first  GenEmbl:*  1. gb ba:*  2. gb htg:*  3. gb pi:*  4. gb ov:*  6. gb pat:*  7. gb pi:*  10. gb co:*  11. gb pi:*  12. gb pi:*  13. gb un:*  13. gb un:*  14. gb un:*  15. gb pi:*  16. em fun:*  17. em fun:*  18. em pat:*  22. em pi:*  22. em pi:*  23. em pat:*  24. em pi:*  25. em pi:*  26. em ro:*  27. em gts:*  28. em htg lun:*  31. em htg lun:*  29. em htg lun:*  21. em co:*  22. em htg lun:*  23. em htg lun:*  24. em htg lun:*  25. em htg lun:*  26. em htg lun:*  27. em gts:*  28. em htg lun:*  39. em htg lun:*  31. em htg lun:*  32. em htg lun:*  33. em htg lun:*  34. em htg lun:*  35. em htg lun:*  36. em htg lun:*  37. em htg lun:*  38. em htg lun:*  39. em htg lun:*  39. em htg lun:*  39. em htg lun:*  30. em htg lun:*  40. em htg lun	mber o		tisfying chosen parameters:	
GenEmbl:*  1. gb ba:*  2. gb htg:*  3. gb htg:*  4. gb ov:*  5. gb ov:*  6. gb par:*  7. gb pr:*  10. gb ro:*  11. gb pr:*  12. gb pr:*  13. gb un:*  14. gb vi*  15. em ba:*  16. em fun:*  17. em ba:*  18. em pat:*  22. em ov:*  23. em pat:*  24. em pat:*  25. em pi:*  26. em ro:*  27. em gts:*  28. em lu:*  29. em htg-lun:*  31. em htg-lun:*  31. em htg-lun:*  32. em htg-lun:*  33. em htg-lun:*  34. em htg-lun:*  35. em htg-lun:*  36. em htg-lun:*  37. em htg-lun:*  38. em htg-lun:*  39. em htg-lun:*  31. em htg-lun:*  36. em htg-lun:*  37. em htg-lun:*  38. em htg-lun:*  39. em htg-lun:*  36. em htg-lun:*  36. em htg-lun:*  37. em htg-lun:*  38. em htg-lun:*  39. em htg-lun:*  30. em htg-lun:*  30. em htg-lun:*  30. em htg-lun:*  30. em htg-lun:*  30. em htg-lun:*  30. em htg-lun:*  30. em htg-lun:*  30. em htg-lun:*	ncessing	Minim Maxim Listi	Match Match G first	
	·		1:*  n:*  n:*  n:*  n:*  n:*  n:*  n:*	

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

, , , , , , , , , , , , , , , , , , ,	nordinand	866 Segn	Homo	AC091133 Homo sapi	AE001245 Treponema	Ratt	AF463492 Homo sapi	Homo	Homo	ACOUNTY HOMO BADI	D14746 Organ parts	בים מים מים	AL772420 Orvza gat	ALS89792 Homo gapi	AL031847 Human DNA	AC004963 Homo sapi	Arisaay Leishmani Araacoa womo coni	M97565 Human (clon	AY069730 Drosophil	BC030347 Mus muscu	AF214013 MUB MUBCU AF051691 Deeudomon	AE004561 Pseudomon	AE005890 Caulobact	AL357593 Leishmani	AB055101 Drosophil	AB055100 Drosophil	AB055098 Drosophil	AC1182 Drosophil AC128268 Rattus no	AC121741 Rattus no	AL138769 Human DNA	Continuation (8 of	AL669836 Mouse DNA	75	EU.	AC129925 Homo sani	AC119477 Rattue no	AC096410 Rattus no	ດຸນ				linear PAT 17-DEC-2001					t, E., Jager, E., Alexander, K.	g cancer associated antigen,
B ID	i	6 AR171866	2 AC105030	9 AC091133	1 AE001245	2 AC118983	9 AF463492	9 AKUZ1/25	9 500000	2 AC099392	11 RICG148A	9 AB061849	2 CNSOBC9Y	2 AL589792	9 HS120G22	ACOU4363	HSA336031	HUM21SEQJ	AY069730	0 BC030347	AF051693	. AE004561	AE005890	AB055099	AB055101	AB055100	AE055098 AC017132	AC128268	AC121741	AC138769 AC003042	LMFLCHR18 07	0 AL669836	AC007594	AC096	AC129	AC119	AC096	AC116771	ALIGNMENTS			1946 bp DNA	9				Tsang, S., Stockert, E	d molecule encoding
% Query Match Length Di		1946	147767	168613	12110	4844/T	2023	2002	146180	210868	352	7419	83052	132592	100518	552	818	888	1426	1727	2719	10757	15000	15267	22990	23007	61204	78.2 74169 2	83582	102818	110000	141877	109791	71110	71537	77564	97406	00158				7 from patent	1 GI:1			1 10.	T., Gure, A.,	nucleic aci
& Que Score Mat	i			7 0		00	0 0	ο α	00	00	4	4	4	σ,	* <b>4</b>	. 4	~	~ ~	N C	1 (1	N	α (	N ()	101	~	0 0	10	17.2 78	N C	v (v	α.	~ ~	v ~	~	~	O1 6	N 0	. 01					AR171866 AR171866.	Unknown.		5 - 5		Isolated the antic
Result No.	1							. eo			c 11	12	13	4 1		c 17.	18		5 2 2 2 2	22		0 t				3 7 0 3 7 0		33		35				40		24.2		Ω Ω		RESULT 1	AR171866	DEFINITION	ACCESSION VERSION	KEYWORDS SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE

FEATURES

ORIGIN

셤 ð

```
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
AC091133/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                       TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                     COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapleins circumcacure 1, Cross C. Lander, E., Ali, A., Allen, N., Salizan, L. (Dases 1 to 147767)

2 (Dases 1 to 147767)

2 (Dases 1 to 147767)

3 Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Samarta, J., Campopiano, A., Chang, J., Chazaro, B., Brown, A., Camarate, J., Campopiano, A., Chang, J., Chazaro, B., Brown, A., Calangelo, M., Collins, S., Collymore, A., Cook, A., Cohengelo, Y., Deyette, M., Orlang, J., Gandyna, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gandyna, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gandyna, S., Gord, S., Goyette, M., Graham, J., Grand-Pierre, N., Jones, C., Ramat, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Ramat, A., Kalls, C., LaRocque, K., Jones, C., Macchan, P., McKernan, K., Marquis, N., Marthews, C., Macchand, P., Major, J., Marquis, N., Maylor, J., Nguyen, C., Mencus, E., Mihonga, V., Murphy, T., Naylor, J., Nguyen, C., Norman, C.H., O'Comnor, T., O'Donnell, P., O'Neil, D., O'Neil, D., Oliver, J., Reetra, R., Fieback, M., Riley, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Santos, R., Schauer, S., Schupback, R., Santos, R., Tayls, N., Trayls, N., Trayls, N., Trayls, N., Trayls, N., Trayls, N., Ye, W.J., Young, G., Viel, R., Vo, A., Wilson, B., Wu, X., Waman, D., Ye, W.J., Young, G., Lander, M., Submitted, M., Chang, M., Chang, M., Kalber, A., and Zody, M., Zahiner, A., Vo, A., Wilson, B., Wu, X., Waman, D., Ye, W.J., Young, G., Chang, M., March, M., Chang, M., March, M., Chang, M., March, M., K., Wassillev, H., Chang, M., Submitted, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., Chang, M., C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission

Submitted (22-DEC-2001) Whitehead Institute/MIT Center for Genome Submitted (22-DEC-2001)

Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases I to 147767)

Birna, B. Musbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boqualavkry, L., Boukhgalter, B., Cock, A., Cohe, P., Debrellano, K., Dewarr, K., Diaz, J.S., Dodge, S., Cock, A., Cooke, P., Debrellano, K., Gage, D., Galagan, J., Faro, S., Faro, S., Gord, S., Grand, D., Grand-Pierre, N., Hagos, B., Gardyna, S., Gord, S., Grand, I., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jonse, C., Kamat, A., Karlas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., McCarthy, M., Meldrim, J., Manchan, P., Major, J., Mathews, C., Iuu, G., Mazlor, J., Nayen, C., Nicol, R., Norbu, C., Norman, C., Norman, V., Maylor, J., Nayen, C., Nicol, R., Norbu, C., Norman, Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P.,
                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens chromosome 17 clone CTD-2244F11 map 17, IN PROGRESS ***, 3 ordered pieces.
                                                                                                                                                                                                                      Length 1946;
                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACIOSO30.4 GI:22123404
HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 147767)
Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 17, clone CTD-2244F11
                                                                                                                                                                                                                            ;
9
                                                                                                                                                                                                                            DB
98;
                                                                                                                               ų
                                                                                                                                                                                                                                                                                        Mismatches
S 6297364-A 7 02-OCT-2001;
Location/Qualifiers
                                                                                                                               358
                                                                                                                                                                                                                            100.0%; Score 22;
100.0%; Pred. No.
                                                                                          /organism="unknown"
528 c 553 g
                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                 1 recrirececercececercae 22
                                                                                                                                                                                                                                                                                                                                                                                                          38 rccrrdcgcgcrcagccrcAG 59
                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 22; Conservative
                                                                         .1946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
             Patent: US
                                                                                                                                            ៧
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 2
AC105030/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
REFERENCE
AUTHORS
                                                                                                                                         BASE COUNT
                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
```

SOURCE

```
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Viel,R., Vo.A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Nu bubmitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome Nessearch, 320 Charles Street, Cambridge, MA 02141, USA

On Aug 6, 2002 this sequence version replaced gi:21426162.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2. (bases I to 168613)
2. (bases I, Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barren, B., Linton, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Choepel, Y., Colangelo, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC091133 168613 bp DNA linear PRI 01-JUL-2002
Homo sapiens chromosome 17, clone RP11-501C14, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces are represented as runs of N. The order of the pieces of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 22; DB 2; Length 147767;
100.0%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                  64311 64410: gap of 100 bp 64411 86773: contig of 22363 bp in length 86774 147767: contig of 60894 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          495 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birren, B., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone RP11-501C14 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="CTD-2244F11"
/clone lib="CTTD1 Human BAC"
41792 a 34009 c 33361 g 38110 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .147767
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center clone name: 2244_F_11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/chromosome="17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 130408 TCCTTGCGCGCTGCGCCTCAG 130387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC091133.11 GI:21637524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 recrrecederecederede 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 168613)
```

us-09-270-437d-11.rge

```
/map="17
                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'epeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ungure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ungure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ungure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ungure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ınsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ınsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unsure
                                                                                                                                                                                                                        FEATURES
Disaria S., Collinger A. Cooke, P. Petrelian P. Fitzhugh, A. Gage, D. Dalas J. S. Gardami, C. Gardami, C. Gardami, C. Gardami, C. Gardami, C. Gardami, C. Gardami, C. Gardami, C. Gardami, C. Gardami, C. Gardami, C. Gardami, C. Gardami, C. Gardami, C. Gardami, C. Gardami, C. Gardami, C. Gardami, C. Gardami, C. Gardami, C. Gardami, C. Gardami, C. Gardami, C. Gardami, C. Gardami, C. Marcdonald, P. Marthoy, T. Marthaga, C. Macharana, C. Marcdonald, P. Marthy, T. Marthaga, C. Macharana, C. Marcdonald, P. Marthy, T. Marylor, G. Marthy, R. Marcdonald, P. Marthy, T. Marylor, G. Marcdonald, P. Marthy, T. Marylor, G. Marcdonald, C. Marcdonald, P. Marthy, T. Marylor, G. Marcdonald, C. Marcdonald, P. Marthy, T. Marylor, G. Marcdonald, C. Marcdonald, P. Marthy, T. Marylor, G. Marthy, R. Sanner, S. Schubeck, R. Sanner, S. Schubeck, R. Sanner, S. Schubeck, R. Sanner, S. Schubeck, R. Sanner, C. Marcdonald, C. Marcdonald, C. Marthy, T. Taliana, C. A. Marcdonald, C. Marcdonald, C. Marthy, T. Taliana, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marthy, T. Taliana, C. Dannell, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Cardone, C. Dannello, C. Marcdonald, M. Tatialido, Y. W. J. Young, C. Cardonello, C. Marcdonald, P. Marcdonald, C. Cardonello, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald, C. Marcdonald,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (01-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON JUL 1, 2002 this sequence version replaced gi:21431160. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
```

COMMENT

```
------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                        Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="RP11-501C14"
/clone llb="RPC1-11 Human Male BAC"
119. 201
/rpf. family="(CA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1394. .1503
Ince="shiple clone coverage"
1569. .1573
Incte="x,0 quality SNGL region"
1592. .1904
Increaming the shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple shiple sh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="<30 quality SNGL region"
1933. 1937
/note="<30 quality SNGL region"
2002. 2007
/note="<30 quality SNGL region"
complement (3804. 4099)
/rpt family="Abusp":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1041. .1349
/rpt family="Alusx"
/rpt 1271. .1278
/note=".30 quality SNGL region"
1293. .1296
/note="<30 quality SNGL region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          456. 460
/note="<30 quality SNGL region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       484. .488
/note="<30 qual SNGL region"
                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt family="(T)n"
complement (4318. .4415)
/rpt family="U6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               family="L1M4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="AluJb"
5349. .6641
                                                                                                                                                                                                                        Center project name: 112028
Center clone name: 501_C_14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (4105, 4156)
/rpt_family="MER112"
                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ooob. .6941
/rpt_family="AluJo"
7125. .7447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255. . 519
/rpt_family="AluJb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5. .7447
t_family="AluSx"
4. .7628
t_family="AluSc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="Alusg" 5666. .6941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="AluJb" 1965. 9277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rpt_family="Alusx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'rpt_family="AluSx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="MIR"
complement (5443.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
```

```
/ remain___caute__tall
/ product="treponemal aqueous protein (tapl)"
/ product="treponemal aqueous protein (tapl)"
/ product="treponemal aqueous protein (d="AAC65699.1"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:3323036"
/ db_xref="d1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I CABARSEDCKENRTALKTLINTATHI TLIRASAI PIVGFLLKFHALAGLSYFLVAGLSV
LFLTDFIDGKI ARARRETSRVGETLDAASDYAL I GLI SALYYQSGVVPLMFFVLI ITR
LSLQTVI ACVYAL FGHPMTGSTAGGKATVAVTMLLYTLELARLLLPNLARSNSGARFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HEKESTLPKAPARRFPPVQYPPVSPDKRWILGYFSPPSMEKETAGILGSYTLFHSALV
LALSLAHGRTQVPPSSTLSFLTVIVLMHCLLFPFLVAYSREPADTTVPFKPLPEGTAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /profein id="AAC65697.1"
/db_xref="d1:3323034"
/db_xref="d1:3323034"
/translation="WYQNTNNRFERMTAAERTRLEMDVRVINKQLEAGARSAKRELGKD
/translation="WYQNTNNRFERMTAAERTRLEMDVRVINKGLEAGARSAKRELGKD
ATTAINSLAGATHQDPTAAPMQDTQFIAQMAQFSSLEQMANMSAQVEKLGTLFCNTEALQ
AVGKWYTEADNYTYRGLISAVTRADKPQVRVGSHWYEWEHVKVIADPSAS"
complement (603 . .2246)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MARASSPLSSMHSPHSLPFSAHCAARLRKKTCQSGSDASFQYKA
Khalak, H., Richardson, D., Howell, J.K., Chidambaram, M., Utterback, T., McDonald, L., Artiach, P., Bowman, C., Cotton, M.D., Fujii, C., Garland, S., Hatch, B., Horst, K., Roberts, K., Watthey, L., Weidman, J., Smith, H.O. and Venter, J.C.
Submission (Ob.-MAR-1998) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to PID:1652491 percent identity: 36.19; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to PID:2088865 percent identity: 28.12; /dentified by sequence similarity; putative" /codon start=1 /transi_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (603. .2246)
//gene="TP0729"
//note="similar to GP:2196901 percent identity: 100.00;
//note=by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                              percent identity: 100.00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'product="flagellar hook assembly scaffolding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                  identified by sequence similarity; putative" /codon start=1 /transI_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               product="conserved hypothetical protein"
protein id="AAC65698.1"
db_xref="GI:3323035"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGAEILAGFVIFTGIVEKLYLGVQHRPGRSP"
                                                                                                                                                                                                                                                              /organism="Treponema pallidum"
/db xref="taxon:160"
complement(66. .527)
/gene="TP0728"
                                                                                                                                                                                                                                                                                                                                                                                    complement (66. .527)
/gene="TP0728"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="TP0730"
2215. .3312
/gene="TP0730"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3332. .4042
/gene="TP0731"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            332. .4042
/gene="TP0731"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="TP0729"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/transl_table=
                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear BCT 16-JUL-1998
the complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fraser, C.M., Norris, S.J., Weinstock, G.M., White, O., Sutton, G.G., Dodson, R., Gwinn, M., Hickey, E.K., Clayton, R., Ketchum, K.A., Sodergren, E., Hardham, J.M., McLeod, M.P., Salzberg, S., Peterson, J., Khalak, H., Richardson, D., Howell, J.K., Chidambaram, M., Utterback, T., McDonald, L., Artiach, P., Bowman, C., Cotton, M.D., Venter, J.C. et al.

Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 12110)
Fraser, C.M., Norris, S.J., Weinstock, G.M., White, O., Sutton, G.G.,
Dodson, R., Gwinn, M., Hickey, E.K., Clayton, R., Ketchum, K.A.,
Sodergren, E., Hardham, J.M., McLeod, M.P., Salzberg, S., Peterson, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Score 22; DB 9; Length 168613;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 22; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treponema pallidum
Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
1 (bases 1 to 12110)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12110 bp DNA
Treponema pallidum section 61 of 87 of
AE001245 AE000520
AE001245.1 GI:3323033
                                                                                                          .ve67. .11138
/rpt_family="AluJo"
complement (11302. .11433)
/rpt_family="FRAM"
complement (11502. .11662)
/rpt_family="FLAM"
11653. .110c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 281 (5375), 375-388 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="AluJb"
1,6537. .16846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt family="(CA)n"
complement (15548. .15857)
/rpt family="AluSx"
complement (15870. .16050)
                                                                                                                                                                                                                                                                                                                                                                                                                                     family="AluJb"
ement(1200)
                                                                                                                                                                                                                                                                                                                                                            rpt family="Alusg"
complement(11961. .12034)
rpt family="L2"
complement(12586. .12878)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (12886. .13196)
/rpt family="Aluy"
13727. .13995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rpt_family="(GGAA)n"
4655. .1497º
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt family="L2"
16029. .16215
/rpt family="MIR"
complement(16367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="AluSx"
17040. .17157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rpt family="Alusc"
4001. .14161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            family="AluSq"
                                                         'rpt_family="AluSx"
0326. .10625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 26803 TCCTTGCGCGCTGCGCCTCAG 26782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 rectracecerraces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treponema pallidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   spirochete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98332770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9665876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                repeat_region
                                                                                                             repeat_region
                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
AE001245/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
```

ð

gene

89

gene

CDS

```
QLFSQYGFDAVFIGTGAGLPRFMNIEGEELCGVFAANDYLTRATLMKAYDTAHADTPV
YAAKSVVVVVGGGNVAVDSSRTALRLGAEQVHCLYRKTRADMTACVEEIAQAEDEGVTF
HPLCQTTRILGDEEGNVRAVVFRDCQEQIDAGERVFLPCGDAECKLAADAVIVAVGNG
SNPLMAKTTRSLAVSERGTIVVDEDQRTSIPGVWAGGDIVLGAATVIRAMGQGRRAAA
                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MFSILEKKQFSPQVFYLKVHAPDIAKNRAAGQFVLVQLDDBYAB
RIPLTIADAHADEGHIALVIQTVGAYTMRLCEKEVGDSISVVLGPLGNPTLIENVGTV
ACVAGCVGAAPLYPIAQAHRKAGNHVIVILGARNRDLIIFESERRALADELVIYTDDG
SYGRKGLYTEPLRELCKRASCPQEVVAIGPPIMMFCCAETTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALLIBYB3
175585 bp DNA linear HTG 23-APR-2002
Rattus norvegicus clone RP31-438E3 strain Brown Norway, WORKING
AC118983
                                                                                                                                                                                                                                              /note="similar to GB:L77117 PID:1592091 percent identity:
5.23, identified by sequence similarity; putative"
/codon start=1
/transI_table=11
/product=hydrogenase, gamma chain (hydG)"
/protein id="hydrogenase, gamma chain (hydG)"
/db_xref="GI:3323041"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thomas, J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="similar to GP:2293308 percent identity: 22.83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaрв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (23-APR-2002) NIH Intramural Sequencing Center, 8717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 18.8; DB 1; Length 12110;
Pred. No. 9.9e+02;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grovemont Circle, Gaithersburg, MD 20877, USA ------ Genome Center Center: NIH Intramural Sequencing Center
                                                                                                                                                        complement (8084. .8926)
                                                                                                                                                                                                    complement (8084. .8926)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC118983.1 GI:20270129
HTG; HAGS_HASBI; HTGS_DRAFT.
Rattus norvegicus
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3729 TCCCTGCGCTGCAGCCTCAG 3708
                                                                                                                                                                                                                             /gene="TP0736"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="TP0737"
9160. .10470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9160. .10470
/gene="TP0737"
                                                                                                                                                                              /gene="TP0736"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .10470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 175585)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.5#;
90:9#;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 175585)
                                                                                                                                  SINAYLAQKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCTTGCGCGCTGCGGCCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAGR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Simi
Matches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
AC118983/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 굠
                                                                /translation="MPCNTONLYOPGOKECTPMDEGRETYOPAHRAKEEKKODAHLAW
EVENKHEACELRVFHYOELESYSPRKTYRRFYTLTAPEWYIVVPHYMERAQRFFVMYR
OWRCGSQTYCTEFPGGVIDAGEHEBAARRELFEETGRRASSLAHLGTTHPNTBALLEN
RVHIFSABCTPEWYREPOLDTDEFLERCYLPVHDVYERMGRAPFDHALMAQPSFFFCGR
IRFPFCNSVRYVACSASI"

COMD, Dement (4007. 4954)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Cranel at ion="MDRALIDGKQAAHBCTARLATRVQALRAAVGTAPFLAAVLVGDD
PASCTYVAAKQRALARAHLRGETHRLPAHASHAQVLELIARLNEDARVHGILIQLPLP
AHLDAAVCKAVAPEKTVOPGFHPLLVGALFLAGGFVPCTTAGIVHLIRRAQVPLAGA
RVVIVGRSAIVGRPLAVLLASPGCDATVTLGSHTRGLADICVQADILVAALGKARFI
GAPFVRTGAVVIDVGIHHVPDATAPRGRRLGGDVDFDAVAHKVQAITPVPGGVGGWFFT
AMLIHNTLGARSYAGWIPPFRAALYADLDGRAAGDVPH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="Morterammocvoalcalspllpayssegvrevpegoepovvvay
BPIRPGDQLLKIGIVAGCQLYIAGGNGTNGSSSSGTNGNGNGKLLGGGGFHLGYEFF
TKNPSLGGGVSFECYRTTGSNYYFSVPITVNPTYTFAVGRWRIPLSLGVGLNIQSYLS
KKAPGLIAEASAGLYYQYTPDWSIGGIVAYTQLGDIASSPDKCRAVGLATIDFGVRYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MSIHLGAKGEDIAPRVLLPGDPLRARFVAERFFHNAYCYNEVRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MLGFTGTYKGYRVSYQGTGMGLPSHGIYVTELFQDYGYQKAIRVGTAGGLQEEVALKS
VVCALGAATDSAINARRFSGMHFAPTASWSLLRTAVSYADEMGTGVQYGNVISSDVFY
DESGSWRLWARYGVLAVEMETAELYTLAAKFRREALSILTISDHLVTGAVTSAQERER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="Mysvonvysdaktcdvpvesepeartyrphallobeacorlaol
OGKELKMKDRTQIPLORMRMLPPKKRSLLMQEAALGFTEQQALVESORCLNCKTKPCV
KGCPVGVPIPEFIACVQRGAFKEAVDIIKTTSLLPAICGRVCPHERQCQLQCTVGKMF
KDVSKAVSIGALERFVADWERQHGQITVPYCAPSTHKKVAVIGSGPAGLAVASDTARA
                                                                                                                                                                                                                                                                                                                                                                                             /producT="methylenetetrahydrofolate dehydrogenase (folD)"
/protein_id="AAC65701.1"
/db_xref="GI:3323038"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transI_table=11
/product="T. pallidum predicted coding region TP0733"
/protein id="AAC65708.1"
/db_xref="GI:3323045"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tocte-"similar to GP:1638807 percent identity: 57.51; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ...... samilar to GP:2244618 percent identity: 48.79; identified by sequence similarity; putative" (Codon start=1
                                                                                                                                                                                                                                                      /gene="TP0732"
/note="similar to SP:P54382 PID:1303916 GB:AL009126
percent identity: 47.14; identified by sequence
similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="hypothetical protein; identified by Glimmer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=11
/product="purine nucleoside phosphorylase (deoD)"
/proed.n_id="AAC65702.1"
/db_xref="GI:3323039"
product="conserved hypothetical protein"
protein id="AAC65700.1"
db_xref="GI:3323037"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           product="glutamate synthase (gltA) "
protein_id="AAC65703.1"
db_xref="G1:3323040"
                                                                                                                                                                                                                                  complement (4007. .4954)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (5742. .6443)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (5742. .6443)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SFTQMIEIALEAIIQ"
Complement (6525. .8081)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (6525. .8081)
                                                                                                                                                                                                                                                                                                                                                                              table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon start=1
transl table=11
                                                                                                                                                                                                            /gene="TP0732"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5050. .5709
/gene="TP0733"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5050. .5709
/gene="TP0733"
                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon start=1
transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon start=1
trans1 table=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="TP0734"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="TP0734"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="TP0735"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                putative
```

gene

CDS

```
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                               Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; vertaion 0.990319 consenus quality: 168197 bases at least Q40 consenus quality: 169738 bases at least Q30 consensus quality: 170660 bases at least Q20 Insert size: 200000; agarcse-fp Insert size: 200000; agarcse-fp Insert size: 2001001 agarcse-fp Quality coverage: 4.54x in Q20 bases; agarcse-fp Quality coverage: 5.23x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig of 12069 bp in length gap of unknown length gap of unknown length gap of unknown length gap of unknown length contig of 13791 bp in length gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gap of unknown length
contig of 5999 bp in length
gap of unknown length
contig of 747 bp in length
gap of unknown length
contig of 10389 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2278: contig of 2278 bp in length 2378: gap of unknown length 4780: contig of 2402 bp in length 4880: gap of unknown length 8217: contig of 3337 bp in length 1821; gap of unknown length 1921: gap of unknown length 1922: contig of 3504 bp in length 16465: contig of 4544 bp in length 22253: contig of 5688 bp in length 22253: gap of unknown length 22253: gap of unknown length 22253: gap of unknown length 28319: gap of unknown length 22353: gap of unknown length 22353: gap of unknown length 22353: gap of unknown length 22353: gap of unknown length 22353: gap of unknown length 22353: gap of unknown length 23353: gap of unk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 175585: contig of unknown length Location/Qualifiers 1.175.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown length
of 9857 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig of 9929 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l. .175585
/organism="Rattus norvegicus"
Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db xref="taxon:10116"
/clone="RP11-438E3"
/clone lib="RP31"
1. .278
/note="assembly_fragment"
2379. .4780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of 3863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
                                                                                                                                                              --- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  strain="Brown Norway
                                                                                                      Center project name: dcj
Center clone name: 438E03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51409:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11466:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61410
61510
71367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71467
83536
83636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123647
152338
152438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16466
16566
22254
22354
28020
28120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
```

```
Cloning and characterization of human inhibitory PAS domain protein Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF463492 2023 bp mRNA linear PRI 31-JAN-2002
Homo sapiens inhibitory PAS domain protein (IPAS) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2023)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cheng.J.O.
Direct Submission
Submitted (27-DEC-2001) Pathology, University of South Florida, Submitted (27-DEC-2001) Pathology, University of South Florida, 12901 Bruce B. Downs Blvd., MDC11, Tampa, FL 33612, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.5%; Score 18.8; DB 2; Length 175585; ilarity 90.9%; Pred. No. 4.48+02; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1812 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly fragment"
40110 c 40996 g 47398 t
                                                                                                          'note="assembly_fragment"
123647. .152337
                                                                                                                                                                                                                                                                                                                                                                                 'note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                             'note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                               note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_fragment"
113618. .123546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_fragment"
|52438. .175585
                                                                                                                                                                                                                                                                                                                                  43174. .50920 ___/note="assembly_fragment"
                                                                                                                                                                                                                                                       /note="assembly_fragment"
33112. .36974
                                                                                                                                                                                                                                                                                     'note="assembly_fragment"
                                                                                                                                                                                                                                                                                                       37075. .43073
/note="assembly_fragment"
                                                                                           note="assembly_fragment"
/note="assembly_fragment"
4881. .8217
/note="assembly_fragment
                                                                                                                                                                                                        clone_end:T7 __
vector_side:right"
                                                             vector side:right"
8318. .11821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 75043 TCCTTGCCGCTGCGGCCCCAG 75022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 recriredecerredecertag 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF463492
AF463492.1 GI:18448894
                                                                                                                                                                                                                                                                                                                                                                                                     61510. .71366
                                                                                                                                                                                                                                                                                                                                                                     .61409
                                                                                                                                                                                                                                                                                                                                                                                                                                .83535
                                                clone_end:SP6
                                                                                                                                                                                                                                          .33011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 2023)
                                                                                                                                                                                                                                                                                                                                                                                                                                   71467.
                                                                                                                                                                                                                                           28120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 20; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45269 a
                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                           misc_feature
                                                                              misc_feature
                                                                                                                   misc_feature
                                                                                                                                                                                                                                             misc_feature
                     misc_feature
                                                                                                                                                 misc_feature
                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF463492/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
```

```
/protein id="BAB5534.1"
// Drotein id="BAB5534.1"
// Drotein id="BAB5534.1"
// Lanslation="MALGLQRARSTTELRKEKSRDAARSRRSQETEVLYQLAHTLPFA
RGVSAHLDKASIMRLTIS-YLEMHLLAAGEWNQVGAGGEPLDACYLKALEGFWVLTA
RGVSAHLDKASIMRLTIS-YLEMHLLAAGEWNQVGAGGEPLQDACYLKALEGFWVVLTA
RGVSAHLDKASIMRLTIS-TRARRITANIKATWRVLNCSGHMRAYKPPVQTSPAGSPDSEPPLQC
ENCYBELIMKSGTIT-TRRRATLANIKATWRVTVCODRIAEVAGSPDDIGGSAYE
VCVHFLISQVEETGVVLSLEGTGAFLSRHSLDWKFTYCDDRIAEVAGSPDDIGGSAYE
VCVHFLISQVEETGVVLSLEGTEGNSRRPTQRGAPSQCYLTPNPGDSLDTPGPRILAFL
HPPSLSEAALAADFRRFCSPDLRRLLGPILDGASVAATRRPGVETGADLDE
ELPVGTENVHRFLTGSKOTTEAVETDLDIAQDADALDLEMLAPYISWGDDFQLNASEQL
PRAYHRPLGAVPRRRARSFHGLSPPALEPSLLPRWGSDPRLSCSSPSRGDFQLNASEQL
PRAYHRPLGAVPRRRARSFHGLSPPALEPSLLPRWGSDPRLSCSSPSRGDFGLNASEQL
GARRATLAGSSEDEDEGVELLGVRPPKRSPSPEHENFLLFPLLSLVCWGINGILMPSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BC026308

2477 bp mRNA linear PRI 08-APR-2002
Homo sapiens, hypothetical protein FLJ14033 similar to hypoxia
inducible factor 3, alpha subunit, clone MGC:26043 IMAGE:4811824,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   With-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Smail: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
http://www-shgc.stanford.edu
Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 32 Row: j Column: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2477)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (02-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.9%; Score 17.8; DB 9; Length 2082; 90.5%; Pred. No. 4.1e+03; 1.ve 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                     /tissue type="ovary, tumor tissue"
/clone lib="OVARC1"
/note="cloning vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                           13. .1911
/note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                375 t
                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="OVARC1000241"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                607
                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BC026308.1 GI:20072845
MGC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CCTTGCGCGCTGCGGCCTCAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 CCTTGCGCGCTGCAGCCCCAG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA, complete cds.
BC026308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            684 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
BC026308/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                               SOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REMARK
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein id="AAL60947.1"
// db_xref="G1:18448895"
// db_xref="G1:18448895"
// translation="MALGLQRARSTELKEKSRDAARSRRSGETEVLYGLAHTL.PFA
RGVSAHLDKASIWELTISTLENKERSTELFREKESRDAARSRRSGETEVLYGLAHTL.PFA
RGVSAHLDKASIWELTISTLENGERTLULASTHWENTLOSGENGASTERPOOTLISTREKVEAPT
ERCFSLRMKSTLTSRGRTLULASTWKTLANGSGHMARKPRAQTSPAGSPDSEPPLOC
LVLICEAIPHFGSLEPPLGRGAFLSHHSLDMKFTYCODRIAEVAGYSPDDLIGCSAYE
YIHALDSDAVSKSIHTLLSKGGAVTGQYRFLARSGGYLWTQTOATVVSGGRGPOSESI
VCVHFLISQVERETGVULSLEGTGHSRRPIGNARFORDLTGGSAYE
PPLASSEAALAADPRRFCSPDLRRLLGPILDGASVAATPSTPLATRHPQSPLSADLPD
ELPVGTENVHRLFTGGKOFTSPLDIAGDAADLDLEMLAPYISMDDFGLNASSCUL
PRAYTHR PLGAVPR FRARSFHGLSPPLENGESTLFRWGSPRSCHASSCUL
PRAYTHR PLGAVPR FRARSFHGLSPPLANGESTLERMLAPYISMDDFGLNASSCUL
PRAYTHR PLGAVPR FRARSFHGLSPPLENGESTLERMLAPYISMDDFGLNASSCUL
PRAYTHR PLGAVPR FRARSFHGLSPPLANGESTLERMGASSCUL
PRAYTHR PLGAVPR FRARSFHGLSPPLANGESTLERMLAPYISMDDFGLNASSCUL
PRAYTHR PLGAVPR FRARSFHGLSPPLANGESTLERMGASSCUL
PRAYTHR PLGAVPR FRANSFHGLSPPLANGESTLERMGASSCUL
PRAYTHR PLGAVPRAYTHR FRANSFHGLSPPLANGESTLERMGASSCUL
PRAYTHR PLGAVPRAYTHR FRANSFHGLSPPLANGESTLERMGASSCUL
PRAYTHR PLGAVPRAYTHR FRANSFHGLSPPLANGESTLERMGASSCUL
PRAYTHR PLGAVPRAYTHR FRANSFHGLSPPLANGESTLERMGASSCUL
PRAYTHR PLGAVPRAYTHR FRANSFHGLSPPLANGESTLERMGASSCUL
PRAYTHR PLGAVPRAYTHR FRANSFHGLSTRANGESTLERMGASSCUL
PRAYTHR PLANGESTLERMGASTRANGESTLERMGASSCUL
PRAYTHR PLANGESTLERMGASTLERMGASTLERMGASSCUL
PRAYTHR PLANGESTLERMGASTLERMGASTLERMGASTLERMGASTLERMGASTLERMGASTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GARKRILAQSSEDEDEGVELLGVRPPKRSPSPEHENFLLFPLSLVCWGINGILWPSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens cDNA FLJ14819 fis, clone OVARC1000241, moderately akmilar to HYPOXIA-INDUCIBLE FACTOR 1 ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isogal, T. and Octoki, T.

Direct Submission

Submission

Submission

Submission

Submission

Submission

Submission

Submission

Submission

Submission

Submission

Submission

Submission

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax.81-438-52-3986)

E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax.81-438-52-3975, Fax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Ishibashi,T., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M., Hiraoka,S., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AK027725.1 GI:14042617 oligo capping; fis (full insert sequence). Homo sapiens ovary, tumor tissue cDNA to mRNA, clone_lib:0VARC1clone:0VARC1000241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

80.9%; Score 17.8; DB 9; Length 2023;
Best Local Similarity 90.5%; Pred. No. 4.2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/product="Inhibitory PAS domain protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360 t
                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEDO human cDNA sequencing project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          593 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                  map="19q13.4" . . 2023
                                                                                                                                                                                                                                                                                                                                                                                  note="HIPAS"
                                                                                                                                                                                                                                                            gene="IPAS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CCTTGCGCGCTGCGGCCTCAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 CCTTGCGCGCTGCAGCCCCAG 33
                                                                                                                                                                                                                                                                                      27. .1925
/gene="IPAS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 699 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 2082)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWLKPTVL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401
Bource
                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
AK027725/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
```

셤 ઠે

ö

Gaps ; 0

FEATURES

```
BAC library obtained from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="predicted exon, program: grail2exons_human_1.3,
frame 2, quality: excellent, score: 81.000"
complement (5169. .5468)
/rpt_family="AluY"
5626. .5886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         frame: 0, quality: good, score: 52.00"
// frome: 10, quality: good, score: 52.000"
// frome family="Alu"
// family="Alu"
                                         /chromosome="19"
/map="19q13 2 between APOE and D19S412"
                                                                                /clone="BC29621"
/cell_line="9675K"
/cell_type="fibroblast"
/note="Lini clone name: BC82621
Research Genetics."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="LiMC/D"
complement(11536..1161)
/rpt_family="FLAM_C"
complement(1162)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="AluJo"
complement(11302, 11510, rpt_family)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (11667...11798)
/rpt_family="LiMC/D"
complement (11833...12138)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt family="Alusx"
complement (4269. .4568)
/rpt_family="Alux"
/rpt_family="Alux"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="AluSx"
complement(8575...8597)
/rpt_family="AT_rich"
complement(8598...8878)
/rpt_family="AluSx"
9477...9766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="LINE2"
complement(2629. 2921)
/rpt_family="AluJo"
          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                         .1974)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="AluSq" 3673. 3939 /rpt_family="L1" complement (4005. 420
                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="FLAM_A"
2115. .2375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'rpt_family="AluJb" 900. .8191
                                                                                                                                                                                                                                                                                   /rpt_family="L1"
1159_.1453
/rpt_family="AluSx"
1459_.1529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'rpt_family="(TA)n"
596. .781?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rpt_family="AluSx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .10258
family="AluSq"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                family="AluJb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="FLAM"
0691..10819
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="L1MB4"
2478. .2549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'rpt_family="Aludi
complement(10999.
                                                                                                                                                                                                                                                                                                                                                             1459. .1529
/rpt family="L1"
complement (1857. .
                                                                                                                                                                                                               'rpt_family="L1"
                                                                                                                                                                                                                                                             'rpt_family="L1"
:018. .1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .3655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission

Submitted (102-APR-1999) Joint Genome Institute, Lawrence Livermore
Submitted (102-APR-1999) Joint Genome Institute, CA 94551, USA
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
Map and sequence oriented from q centromere to telomere.

PAG 24476 (CIT-B-197014) to the left from
Dases 1 to 27,487 of this accession, and separated from BAC 89981
(CIT-B-158410) on the right by a gap of approximately 17 to 23 kb.
Additional chromosome 19 and sequence information may be
Additional chromosome 19 and sequence information may be
Dobtained at: http://www.bio.llnl.gov/bbrp/genome.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC007193 146180 bp DNA linear PRI 17-JUN-1999
Homo sapiens chromosome 19, BAC 82621 (CIT-B-139a18), complete
sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Bukaryota, Metazoa, Primates, Catarrhini, Hominidae, Homo.

Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

Lamerdin, J.E., McCready, P.M., Skowronski, E., Viswanathan, V.,
Lamerdin, J.E., McCready, P.M., Skowronski, E., Viswanathan, V.,
Stilwagen, S., Phan, H., Velasco, M., Do, L., Regala, W., Terry, A.,
Garries, J., Liu, S., Attix, C., Andreise, T., Trankheim, M.,
Awila, J., Liu, S., Attix, C., Andreise, T., Trankheim, M.,
Awila, J., Liu, S., Koffeld, J., Duatte, S., Lucas, S., Bruce, R.,
Thomas, P., Quan, G., Krommiller, B., Atellano, A., Sanders, C., Ow, D.,
Thomas, P., Trong, S., Kobayashi, A., Olsen, A. S. and Carrano, A.V.
Sequence analysis of a 1.9 Mb region in 19q13.2 between ApoE and
                                                                                                                                                                                                                                                                                                                                                                                                RGVSAHLDKASIMETTISYLENHENCAAGEWNQVGAGGEPLDACYLKALEGEVUNUTR
EGDMAYLSENVSKHLGLSQLELIGHSIPPTHPCDGELQDALTPQOTLSRKVYBART
ERGPSLARMSTITRSGRYLINIKAATWYLNCSGHMRAYKPPAGTSPAGSPDSEPPLOC
LVLICEAIPHGSLEEPLGRGAFLSHHSLDMKFTYCDDRIAKYAGYSPDDLIGCSAYE
YTHALDSDAVSKSIHTCMYPISPGARAATWPPADTRTPQLFIPQDALPPHLNTSSLL
                                                                                                                                                                                                                                                                                     /codon_start=1
/codon_start=1
/product="hypothetical protein FLJ14033 similar to hypoxia
/productle=factor 3, alpha subunit"
/protein_id="AAH26308.1"
/protein_id="AAH26308.1"
/db_xref="G1:20072846"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                               translation="MALGLQRARSTTELRKEKSRDAARSRRSQETEVLYQLAHTLPFA"
    This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 11968004. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 80.9%; Score 17.8; DB 9; Length 2477; Best Local Similarity 90.5%; Pred. No. 3.96+03; Indels 0; Mismatches 19; Conservative 0; Mismatches 2; Indels 0;
                                                                                              /organism="Homo sapiens"
/db_xref="LocusID:6444"
/db_xref="taxon:9606"
/clone="MGC:26043 IMAGE:4811824"
/tissue type="Brain, hippocampus"
/clone_lib="NIH_MGC_95"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PKPQGTVSFLAPSYPVPRSFSPHLPPWWP"
                                                                                                                                                                                                                      /lab host="DH10B"
/note="Vector: pBluescript"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 146180)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ccrrececerrede 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 cctriccececrecaecceae 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC007193
AC007193.1 GI:4558635
                                                                                                                                                                                                                                                                 23. .1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lamerdin, J.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D19S412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
AC007193/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
```

g à

TITLE

COMMENT

```
Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratches.

Ratche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC099392 210868 bp DNA linear HTG 17-JUL-2002
Rattus norvegicus clone CH230-160L8, *** SEQUENCING IN PROGRESS
AC09932 AC09932 AC09932. G G 1:21744099
Norway rat.
Rattus norvegicus
                                               ion complement (28526. 28705)

/rpt family="Alusc"
complement (28733. .28872)

/rpt family="Aludr"

/rpt family="Aludr"

28674. .29681

/rpt family="Aludo"

29463. .29583

/note="predicted exon, program: grail2exons_human_1.3,
frame: 2, quality: good, score: 71.000"

/rpt family="Alugo"

30336. .30634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 17.8; DB 9; Length 146180;
Pred. No. 1.18+03;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
   /rpt family="Aluu/r.u.r.
complement(18359. 28522)
/rpt family="Alusg"
complement(28526. 28705)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30336. .30634
/rpt_family="Alusq"
30646. .30779
complement (30830. .31040)
/rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 42317 CCTTGCGCGCTGCAGCCCCAG 42297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 cerrecececrececercye 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 80.9%;
Best Local Similarity 90.5%;
Matches 19; Conservative
                                               repeat_region
                                                                                                                      repeat_region
                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
AC099392
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement [14859. .15153)
/rpt family="AluSx"
15226. .15492
/rpt family="AluJo"
complement [16257. .16340)
/note="predicted exon, program: grail2exons_human_1.3,
frame: 0, quality: good, score: 63.000"
/rpt fame: 0, family: good, score: 63.000"
                                                                                                              /rpt family="rpkam"

complement (12655. 12795)

rpt family="LukCD"

complement (12806. 13106)

/rpt family="AluSx"

complement (13162. 13694)

/rpt family="AluSx"

complement (13482. 13694)

/rpt family="AluSp"

rpt family="AluSp"

rpt family="AluSp"

rpt family="AluSp"

rpt family="Ll"

complement (14099. 14105)

/rpt family="Alux"

rpt                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / 1968 ... 18273 / 1976 ... 18273 / 1976 femily="AluSq" complement (18401... 19193) / 1976 femily="AluSq" complement (1818 ... 19193) / 1976 femily="HERVH" complement (19194 ... 19193) / 1976 femily="HERVH" complement (19194 ... 19412) / 1976 femily="HERVH" complement (19031... 23647) / 1976 femily="HERVH" complement (19031... 23647) / 1976 femily="HERVH" complement (2403... 24714) / 1976 femily="HERVH" complement (2403... 24714) / 1976 femily="HERVH" complement (2403... 24714) / 1976 femily="AluSx" 25501 / 1976 femily="AluSx" 25524 ... 25509 / 1976 femily="AluSx" 25525 ... 26069 / 1976 femily="AluSx" 25525 ... 26069 / 1976 femily="AluSx" 25525 ... 26069 / 1976 femily="AluSx" 25525 ... 26069 / 1976 femily="AluSx" 26256 / 1976 femily="AluSx" 26256 / 1976 femily="AluSx" 26256 / 1976 femily="AluSx" 26256 / 1976 femily="AluSx" 26256 / 1976 femily="AluSx" 26256 / 1976 femily="AluSx" 26256 / 1976 femily="AluSx" 26256 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 / 1976 femily="AluSx" 26255 /
complement(12158. .12478)
/rpt_family="L1MC/D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rpt family="Alusg"
ompTement(16691..17060)
rpt family="THE1C"
7482..17781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rpt family="AluJo"
complement (27125, .27422)
rpt family="AluSx"
7866, .28173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rpt_family="(GAAA)n"
7968. .18273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'rpt_family="AluJo"
7782. .17870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="AluSx"
28181. .28279
       repeat_region
                                                                              repeat_region
                                                                                                                                                     repeat_region
                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
```

```
Landth Length (g of 1374 bp in length f unknown length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length (s of 2102 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bp in length
length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bo in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                           of 1262 bp in length
unknown length
of 1383 bp in length
                                                                                                                                                                                                                                                                     of 1637 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                        of 1922 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bp in length
                                                                                                                                                                                              length
bp in length
                                                                                                                                                                                                                                                                                                                            of 1484 bp in length
                                           length
bp in length
                                                                                       lèngth
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ength.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ength.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ength
                                                                                                                                                                                                                          contig of 1308 bp in l
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                       ength
                                                                                                                                             length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig of 2518 b
gap of unknown 1
contig of 1380 b
gap of unknown 1
contig of 1380 b
gap of unknown 1
contig of 1280 b
gap of unknown 1
contig of 2013 b
gap of unknown 1
contig of 2156 b
gap of unknown 1
contig of 2156 b
gap of unknown 1
contig of 2156 b
gap of unknown 1
contig of 2598 b
gap of unknown 1
contig of 2598 b
gap of unknown 1
contig of 2598 b
gap of unknown 1
contig of 2598 b
gap of unknown 1
contig of 1146 b
gap of unknown 1
contig of 2037 b
gap of unknown 1
contig of 1883 b
gap of unknown 1
contig of 1883 b
gap of unknown 1
contig of 1883 b
gap of unknown 1
contig of 1883 b
gap of unknown 1
contig of 1611 b
gap of unknown 1
contig of 2299 b
gap of unknown 1
contig of 2299 b
gap of unknown 1
contig of 2299 b
gap of unknown 1
contig of 2299 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of unknown 1 contig of 1198 b gap of unknown 1 gap of unknown 1 gap of unknown 1 contig of 2628 b gap of unknown 1 gap of unknown 1
                                                                 contig of 1512 b
gap of unknown l
contig of 1250 b
gap of unknown l
contig of 1634 b
                                                                                                                                                                         of 1634 lunknown
                   of 1251
unknown
                                                                                                                                                                                                                                                                                                                                                          unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig of
                                                                                                                                                                                                                                                                                                                                                                                contig o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig
gap of
                        contig
gap of
                                                                                                                                                                                                                                                                                contig
                                                                                                                                                                                                                                                                                                                                       contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of
                                                                                                                                                                                                       gap of
                                                                                                                                                                                                                                                                                                         gap of
                                                                                                                                                                                                                                                                                                                                                          gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73823:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78679:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82839:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61407:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78579:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58609:
58709:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62653:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67823:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69706:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2012:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56173:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65686:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37380:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44807:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51849:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54017:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61307:
                                                                                                                                                                                                                                                                              24514:
24614:
26098:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46387:
                        16673:
16773:
18285:
18385:
19635:
                                                                                                                                                   19735:
21369:
                                                                                                                                                                                                       21469:
22777:
                                                                                                                                                                                                                                                                                                                                                                                                                                      29482:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1065:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14641:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5939:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86039:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37280:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44907:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50359:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56273
                                                                                                                                                                                                                                                          22877:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72013
72113
73724
73724
776123
76223
78580
78580
82840
82840
82841
86381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37381
40009
42009
42627
44908
46388
46388
46388
46388
50360
50360
51950
51150
51150
56274
56210
56274
56210
56274
56210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62554
62654
65587
65587
67724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67824
69707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29483
29583
30966
31066
32440
32540
34642
34742
35940
36040
15323
15423
16724
16774
18286
18386
19736
21370
21470
22278
24515
24615
26099
26121
2821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission

Submitted (17-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 13, 2002 this sequence version replaced gi:18700960.

Center: Baylor College of Medicine
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: Bstimated insert size may differ from sequence length (see http://www.hgsc.bcm.tumc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 69 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be undated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                    Unpublished

2 (bases 1 to 210868)

Worley,K.C.

Direct Submission

Submitted (10-NOV-2001) Human Genome Sequencing Center, Department Submitted Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 210868)
     Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherr, G., Shen, H., Shooshari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, T., Talfrod, B., Thomas, N., Thomas, S., Warde, M., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Warden, R., Washington, C., Walliams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Weinstock, G. walliamson, A., Wleczyk, R., Wooden, S., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length
bp in length
length
bp in length
length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               length
bp in length
length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bp in length
length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
of 1610 h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown of 1416 h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
of 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
of 1368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of 1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of 1289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          븅
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig contig contig contig contig contig contig contig gap of contig gap of contig gap of contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig c
gap of t
contig c
gap of t
contig c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1434:
1534:
2658:
2758:
4174:
4274:
5456:
6845:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11066:
11166:
12215:
12315:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13612:
13712:
15322:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6945:
8313:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8314
8414
9494
9594
111067
111167
112216
12316
13316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1435
1535
2659
2759
4175
4275
5457
5557
6846
```

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

REFERENCE AUTHORS TITLE JOURNAL

TITLE JOURNAL

ሯ

```
Genum.

E 2 (bases 1 to 7419)

AS Kenmochi, N. and Shimizu, N.

Direct Submission

(AL Submitted (17-MAY-2001) Naoya Kenmochi, Miyazaki Medical College, Central Research Laboratories, 5200 Kihara, Kiyotake, Miyazaki B89-1692, Japan (B-mail:kenmochi@post.miyazaki-med.ac.jp, Tel:81-988-85-965, Fax:81-985-85-1514)

Tel:81-988-85-965, Fax:81-985-85-1514)
                    Yoshihama,M., Uechi,T., Asakawa,S., Kawasaki,K., Kato,S., Higa,S.,
Maeda,N., Minoshima,S., Tanaka,T., Shimizu,N. and Kenmochi,N.
The human ribosomal protein genes: sequencing and comparative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/product="ribosomal_protein_L22"
/protein_id="B8487.1"
/db_xref="G1:17932992"
/translation="MAPVKKLVVKGGKKKQVLKFTLDCTHPVEDGIMDAANF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.1%; Score 17.4; DB 9; Length 7419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /map="1p36.3-p36.2"
/clone 11b="Keio BAC library"
65. 187
/rpt family="MBR5A"
complement (229. .298)
/rpt family="L2"
complement (302. .386)
/rpt family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Joan (839. .850,2657. .>2761)
/gene="RPL22"
/^^^-
                                                                                           analysis of 73 genes
Genome Res. 12 (3), 379-390 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpc_family="Alueg"
complement (432)
/rpc_family="Alueg"
complement (4634, 4945)
/rpt_family="Aluex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="Alusx"
complement (4949. 5249)
/rpt_family="Aluy"
complement (5255. 5519)
/rpt_family="Aluy"
/rpt_family="Aluy"
/rpt_family="Aluy"
/rpt_family="Aluy"
/rpt_family="Aluy"
/rpt_family="Aluy"
/rpt_family="Aluy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="AluJb"
5663. .6791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="MIR3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   family="AluJb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e663. .6791
/rpt_family="AluJb"
:792. .7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  o/92. .7089
/rpt_family="Alusp"
7090. .7267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1882 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     816.7419
/gene="RPL22"
816.850
/gene="RPL22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               851. .2656
/gene="RPL22"
/number=1
2657. .2761
/gene="RPL22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2762. .>7419
/gene="RPL22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3084. .3383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      intron
                                                                                                                                                                                           AUTHORS
TITLE
JOURNAL
                                                                                                                                               MEDLINE
REFERENCE
                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon
                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOS
                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RICG148A 352 bp DNA linear STS 29-MAY-2002 Oryza Bativa (japonica cultivar-group) DNA, partial sequence of RFLP marker, clone G148, sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRI 08-MAR:2002
exons 1, 2 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D14746.1 GI:287311
STS; RFLP marker; restriction fragment length polymorphism.
Oryza sativa (japonica cultivar-group) (cultivar-sinpponbare) DNA.
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Ehrhartoideae; Oryzeae;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minobe,\gamma.
Nucleotide sequence of Sequence Tagged Site from rice RFLP marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .352
/organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon.39947"
                                                                                                                                                                                                                                                                                                                                             Ouery Match

80.9%; Score 17.8; DB 2; Length 210868;
Best Local Similarity 90.5%; Pred. No. 1e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.1%; Score 17.4; DB 11; Length 352; 94.7%; Pred. No. 1e+04; 1.1ve 0; Mismatches 1; Indels 0
92623: contig of 3090 bp in length 9723: gap of unknown length 96897: contig of 4264 bp in length 97087: gap of unknown length 99133: contig of 2046 bp in length 98233: gap of unknown length 104009: gap of unknown length 108102: contig of 4676 bp in length 108102: gap of unknown length 110791: contig of 2889 bp in length 110791: contig of 2889 bp in length 110891: gap of unknown length 110891: gap of unknown length 113718: contig of 2827 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AB061849 7419 bp DNA linear
Homo sapiens RPL22 gene for ribosomal protein L22,
Patrial cds.
AB061849
                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens DNA, clone_lib: Keio BAC library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 27677 TCCTTACGTGCTGCGGCCTCA 27697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /chromosome="12
63 c 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                        21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AB061849.1 GI:17932991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               315 rctridcececrecrect 297
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TCCTTGCGCGCTGCGGCCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TCCTTGCGCGCCTGTGGGCCT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 94.7
108 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
PROJECT ='RGP'
                                                                        96988
97088
99134
99234
103910
104010
                                                                                                                                                                                                                                                  108203
110792
110892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D14746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
RICG148A/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOURCE
                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AB061849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGIN
```

ઠે

.. 0

Gaps

ö

1; Indels

Length 83052;

407 others

ò 셤

```
ALS89792 132592 bp DNA linear HTG 10-JUL-2001
Homo sapiens chromosome 1 clone RP5-889P23 map p36.21-36.33, ***
SEQUENCING IN PROGRESS ***, 4 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 132592)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert size: 132292; sum-of-contigs
Insert size: 132129; 14.2% error; agarose-fp
Insert soverage: 11.37x in Q20 bases; sum-of-contigs Quality
coverage: 11.69x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is a not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M77815; 12% of reads
Sequencing vector: plasmid, 108752; 87% of reads
Chemistry: Dye-terminator AB1; 14% of reads
Chemistry: Dye-terminator Big Dye; 60% of reads
Chemistry: Dye-primer-amersham; 24% of reads
Chemistry: Dye-primer Big Dye; 0% of reads
Chemistry: Dye-primer Big Dye; 0% of reads
Consensus quality: 131458 bases at least Q40
Consensus quality: 131709 bases at least Q30
Consensus quality: 113165 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1332 3431; contig of 3331 bp in length 100 bp 3432 90998; contig of 87567 bp in length 9099 91098; gap of 100 bp 91099 130106; contig of 39008 bp in length 130207 132592; contig of 2386 bp in length. Location/Qualifiers
                                                                                                                    Query Match
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1;
                   /clone_lib="Monsanto"
23697 a 17081 c 17645 g 24222 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center code: SC
Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL589792.1 GI:13277194
HTG; HTGS_PHASE1; HTGS_CANCELLED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: dJ889P23
/clone="0J1410_G05"
                                                                                                                                                                                                                                                                                     Db 66870 rccrrdcccccrccrccr 66888
                                                                                                                                                                                                                                      1 TCCTTGCGCGCTGCGGCCT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lloyd, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human.
                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
AL589792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOURCE
                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (26-JUL-2002) Genoscope - Centre National de Sequencage :
Submitted (26-JUL-2002) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
Web : www.genoscope.cns.fr)
On Jul 29, 2002 this sequence version replaced gi:21535766.
IMPORTANT: This sequence is unfinished and does not necessarly represent the correct sequence is unfinished and does not necessarly represent the sequence is unfinished and the release of this data is work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage, etc.
The nucleotide sequence of this BAC clone was generated by combining Monsanto and Genoscope sequencing data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryzae; Oryzae; Oryzae; Oryzae; Oryzae; Choisne, N., Orjeda, G., Cattolico, L., Demange, N., Wincker, P., Segurens, B., Pelletier, E., Scarpelli, C., Salanoubat, M., Oryza sativa chromosome 12 sequencing Oryza sativa chromosome 12 sequencing
                                                                                                                                                                                                                                                            CNSO8C9Y 83052 bp DNA linear HTG 27-JUL-2002 Oryza sativa chromosome 12 clone OJ1410_G05, *** SEQUENCING IN PROCRESS ***, 5 ordered pieces.
                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contige Composition:
14140 bp contig from 14241 to 29139
14899 bp contig from 14241 to 29139
1207 bp contig from 29240 to 36446
10841 bp contig from 36547 to 47387
35565 bp contig from 47488 to 83052.

* NOTE: This is a "working draft" sequence. It currently
* consists of 5 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* This contig of 11140 bp in length
                                            Gaps
                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29240 36446: contig of 7207 bp in length
36447 36546: gap of 100 bp
36447 47387: contig of 10841 bp in length
47388 47487: gap of 108 bp
47488 83052: contig of 35565 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14141 14240: gap of 100 bp 11 length 14241 29139: contig of 14899 bp in length 29140 29239: gap of 100 bp
                                            Indels
                                               ä
                      4e+03;
                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Oryza sativa"
/cultivar="Nipponbare"
/sub_species="japonica"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                         AL772420
AL773420.2 GI:22003296
HTG, HTGS PHASE2; HTGS_ACTIVEFIN.
Oryza sativa
Oryza sativa
                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome="12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contigs composition :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 83052)
                                                                                                                                     771 CCTTGCGCGCTGCGGCTC 789
                      94.78;
                                                                                                      2 ccrrececerrececrrc 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .83052
                        Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3enoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                            RESULT 13
                                                                                                                                                                                                                                                                     CNS08C9Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
```

```
The true left end of clone RP5-889P23 is at 90508 in this
The true right end of clone RP1-20208 is at 100 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="match: GSS: Em:AF046498"
49180. 49534
/note="single clone region. short insert library only"
complement(57981. 58764)
/note="match: GSS: Em:AF158011"
/note="match: GSS: Em:AF158011"
/note="match: GSS: Em:AR158011"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64797. .64811
/note="Single clone region. short insert library only"
68250. .68620
70460. .70622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(112106. .112211,116809. .116933,123047. .123132)
/note="match: GSS: Em:AQ634365"
complement(join(112121. .112215,116809. .116936))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anote="match: GSS: Em:AQ202845"
[12126. .112224 .11222 .116936]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="match: GSS: Em:AF046385"
join(112145. .112211,116809. .116936)
/note="match: GSS: Em:AQ634370"
complement(in[112150. .112211,116809. .116933,
123047. .123172)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="match: STS: Em:AF191963"

complement (79556. 79740)

complement (79558. Em:AQ541496"

complement (79315. 80319)

/note="match: STS: Em:HSA052WG1"

complement (89942. 86372)

/note="match: STS: Em:G22706"

complement (86963. 8732)
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="match: GSS: Em:AQ270793"
25588. .26045
/note="match: GSS: Em:AQ214655"
25694. .25967
                                                                                                                                                                                                                                                                                                 note="match: GSS: Em: AQ716455"
                                                                                                                                                                                                                                                                                                                       1816. .9229
note="match: GSS: Em:AQ239786"
                                                                                                                                                                                                                                                                                                                                                                                       /note="match: GSS: Em:AQ678815"
18389. .18823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="match: STS: Em:G21080"
complement (74554. .74895)
/note="match: GSS: Em:AQ097224"
complement (79470. .79747)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="match: GSS: Em:AQ097494"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="match: GSS: Em:AQ133445"
45297. .45591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="match: GSS: Em:AQ191756"

/note="match: GSS: Em:AQ191756"

/note="match: GSS: Em:AQ191756"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="match: GSS: Em:AQ698012"
88780. .89285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="match: GSS: Em:AQ121434"
94030. 94434
/note="match: GSS: Em:BB9150"
94030. 94405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="match: GSS: Em:AQ008338"
94054. .94464
/note="match: GSS: Em:AQ010380"
                                                                                                                            /organisme"Homo sapiens"
/db_xrefe"taxon:9606"
/chromosome="1"
/map="p36.21-36.33"
/clone="RP1-120G22"
/clone="RP1-120G22"
/clone="RP1-130G22"
                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112126. .112224
                                                                                                                                                                                                                                                                                                                                                                   .0012. .10541
                 sequence. T
sequence. T
sequence.
                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                             source
                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission

Submitted (20-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 183, UK. E-mail enquirles: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Jul 22, 2000 this sequence version replaced gi:9368784.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the corresponding to the overlapping clone name. Note that the corresponding to the overlapping clone, as we submit sequence submission only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em., EMBL; Sw.: SWISSPROT; Tr., TREMBL; Wp.: WORNPEP; Information the WORNPEP database can be found at thtp://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence chromosome 1, constructed by the Sanger Centre Chromosome 1 mapping chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping thtp://www.sanger.ac.uk/HGP/Chr1

RP1-120G22 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further upcamens.
                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRI 21-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata; Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 166518)

                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VECTOR: pCYPAC2
IMPORTANT: This sequence is not the entire insert of clone
RP1-120G22 It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true right end of clone RP1-120G22 is at 166518 in this
                                                                                                                                                                                                                                                                                                                                                                 79.1%; Score 17.4; DB 2; Length, 132592; 94.7%; Pred. No. 1.7e+03; ative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human DNA sequence from clone RP1-120G22 on chromosome 1p36.21-36.33, complete sequence.
                                                                                                                                                                                                                                                                                                         300 others
                                                                                                                                                  ture 3432. .90998 ...
ture 13099. ...
130106 ...
iture 130207. .132992 ...
iture 130207. .132992 ...
7.0010e="8880mbly_fragment:03330."
7.0010e="8880mbly_fragment:03380."
26843 a 36833 c 36775 g 31841 t 30
                                                                                                        . .3331
note="assembly_fragment:00799"
db_xref="taxon:9606"
                                           /map="p36.21-36.33"
/clone="RP5-889P23"
                                                                                       clone_lib="RPCI-5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL031847.17 GI:9369286
                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 CCTTGCGCGCTGCGGCCTC 20
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 94.7°
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wray, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human.
                                                                                                           misc_feature
                                                                                                                                                      misc_feature
                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ношо
                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
HS120G22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
```

COMMENT

ઠે

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 94.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0;
/note="match: GSS: Em:AQ489599"
complement(113100. .113712)
/note="match: GSS: Em:AQ477048"
complement(113105. .113715)
/note="match: GSS: Em:AQ477048"
113710. .114090
/note="match: GSS: Em:AQ434216"
/note="match: GSS: Em:AQ434216"
/note="match: GSS: Em:AQ434216"
/note="match: GSS: Em:AQ434216"
/note="match: GSS: Em:AQ434216"
/note="match: GSS: Em:AQ432216"
/note="match: GSS: Em:AQ432217"
/note="match: GSS: Em:AQ47297 Em:AQ351276"
/note="match: GSS: Em:AQ47297 Em:AQ351276"
/note="match: GSS: Em:AQ482227"
/note="match: GSS: Em:AQ482227"
/note="match: GSS: Em:AQ4365"
/note="match: GSS: Em:AQ4365"
/note="match: GSS: Em:AQ4365"
/note="match: GSS: Em:AQ634365"
/note="match: GSS: Em:AQ002260"
/note="match: GSS: Em:AQ002260"
/note="match: GSS: Em:AQ002260"
/note="match: GSS: Em:AQ002260"
/note="match: GSS: Em:AQ002260"
/note="match: GSS: Em:AQ002260"
/note="match: GSS: Em:AQ002260"
/note="match: GSS: Em:AQ002260"
/note="match: GSS: Em:AQ002260"
/note="match: GSS: Em:AQ002260"
/note="match: GSS: Em:AQ002260"
/note="match: GSS: Em:AQ002260"
/note="match: GSS: Em:AQ002260"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature 144105. 144488

misc_feature 7,00ce="match: GSS: Em:AQ231956"

misc_feature 7,00ce="match: GSS: Em:AQ672446"

misc_feature 152031. 152510

Misc_feature 152031. 152510

Anote="match: GSS: Em:AQ672446"

misc_feature 152031 152510

Anote="match: GSS: Em:AQ234353"

DRIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="single clone region"
44105. 144499
note="match: GSS: Em:AQ231959"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                   misc_feature
                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                misc_feature
                                                                                                         misc_feature
```

Search completed: April 18, 2003, 06:20:58 Job time : 508 secs

Db 110222 ccrridcicciccridciccic 110240

2 ccrrececereceecre 20

ð

```
April 18, 2003, 04:12:35; Search time 98 Seconds (without alignments) 505.551 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
|SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
|SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
|SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | SIDS2/39C3Gata/geneseq/geneseqn-embl/NA1991.DAT:+
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:+
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:+
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:+
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:+
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:+
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:+
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:+
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:+
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:+
| SIDS2/gcdata/geneseq/geneseqn-embl/NA1997.DAT:+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:+
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:+
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:+
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:+
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:+
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:+
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:+
| SIDS2/gcgdata/geneseqn-embl/NA1989.DAT:+
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:+
| SIDS2/gcdgata/geneseq/geneseqn-embl/NA1989.DAT:+
| SIDS2/gcdgata/geneseq/geneseqn-em
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDS2/gcgdata/geneseq/genesegn-emb1/NA1998.DAT:
/SIDS2/gcgdata/geneseq/genesegn-emb1/NA1999.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.
GenCore version 5.1.4 ps 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2185239 seqs, 1125999159 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 tecttgegegetgeggeeteag 22
                                                                                                                                                                                                                                                                   OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N_Geneseq_101002:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-270-437D-11
22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	PCR primer for DNA. An alternative for Human secreted pro	DNA encoding novel DNA encoding novel Human cDNA sequenc Human immune/haema Drosophila melanog
SUMMARIES	ΩI	AAZ36157 AAZ36153 AAC27338 AAH07034	AAS68110 AAS73402 AAH14706 AAK63986 ABL29179
	DB	22122	32233
de	Query re Match Length DB I	22 1946 139 711	1785 1785 2082 464 1217
	Query	100.0 100.0 80.9 80.9	80.9 80.9 78.2 78.2
	Score	22 22 17.8 17.8	17.8 17.8 17.2 17.2
	Regult No.	00 40 m 41	n n n n

Drosophila melanog Human breast cance Human breast cance Human breast tumou Polynucleotide seq Human enclase 3 (be Human golynucleotide Human polynucleotide Human chan polynucleotide Human polynucle	CDNA polyn polyn ane-bo DNA e DNA e CRN CBNA Carbo secre secre secre polyn polyn	AAAA MAMAX
23 ABL29178 22 AAS47110 24 ABC95145 20 AAX20553 20 AAX30553 20 AAX39556 22 AAS41291 22 AAS41291 22 AAS408526	22 AAH06824 22 AAI53862 22 AAI53862 22 AAI53862 22 AAS6600 22 AAS6600 22 AAS6600 22 AAI1456 22 AAI14539 22 AAI14539 20 AAZ00477 20 AAZ00477 22 AAI61259 22 AAI61260 22 AAI65473	21 AAC10004 22 AAC61146 22 AAF66068 22 AAF66313 22 AAH07664 22 AAH07830 23 AAS74508 23 AAS74508 24 AAF19377 29 AAV19377 29 AAV19377 20 AAV19281
3408 462 462 462 10461 13308 151 333 762	764 1580 1620 1759 1759 1875 1885 1931 1932 1940 1940	2008 6008 6008 6008 7009 24009 25009 25009
80000004444		733.6 733.6 733.6 733.6
	444444444444444444	10000000000000000000000000000000000000
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2,000000000000000000000000000000000000	-

## ALIGNMENTS

BP.

AAZ36157 standard; DNA; 22

Cancer associated antigen; KOC-1; cancer; vaccine; CT7; PCR primer; ss. PCR primer for DNA encoding cancer associated antigen KOC-2. Chen Y, Gure A, Tsang S, Stockert E, (LUDW-) LUDWIG INST CANCER RES. 99WO-US05766, 98US-0061709 11-FEB-2000 (first entry) 17-APR-1998; Homo sapiens. 16-MAR-1999; WO9954738-A1 28-OCT-1999. Synthetic. AAZ36157; 

old LJ;

Knuth A,

Jager E,

Nucleotides representing cancer-associated genes, used to develop products for the diagnosis, monitoring and treatment of cancers

WPI; 2000-013284/01.

a saponin,

or vaccine composition with an adjuvant, e.g. a cytokine, granulocyte macrophage-colony stimulating factor (GM-CSF)

Sequence 1946 BP; 502 A; 528 C; 553 G; 358 T; 5 other;

ö

Gaps

ö

0; Indels

Length 1946;

100.0%; Score 22; DB 21; 100.0%; Pred. No. 2.5;

100.08;

Similarity

Ma. Local S... 22;

Matches

ò

ö

Query Match

ន្តដូន

Conservative

0; Mismatches

1 TCCTTGCGCGCTGCGGCCTCAG 22

```
The present sequence represents an alternative form of a cancer associated antigen gene designated KOC-2. The specification also describes a cancer associated antigen designated CT7. The CT7 by Dolynucleotide was isolated from SK-MEL-37 melanome cells. The CD7 polyneptide has some homology with MAGE-10, limited to about 210 carboxy terminal amino acids. The amino terminal of the protein has a repetitive pattern, with repeats rich in serine, proline, glutamine and leucine, and an almost invariable core of the peptide given in AAV43877. The CT7 polypeptide can be processed to peptides which provoke lysis by polypeptide can be processed to peptides and polypeptides can be used for cycloptic cells. The polynucleotides and polypeptides can be used for treating a cancerous condition and screening for or diagnosing cancerous conditions. The cancer associated antigens can be used as an immunogenic
                        per primers AAZ36157-58 were used to amplify a cancer associated antigen gene designated KOC-2. The specification also describes a cancer associated antigen designated CT7. The CT7 polymuclecitide was isolated from SK WEL-37 melanoma cells. The polypeptide has some homology with terminal of the protein has a repetitive pattern, with repeats rich in terminal of the protein has a repetitive pattern, with repeats rich in the peptide given in AAX43877. The CT7 polypeptide can be processed to the peptides which provoke lysis by cytolytic T cells. The polymuclecides and polypeptides can be used for treating a cancerous condition and antigens can be used for treating a cancerous condition and antigens can be used an animumogenic or vaccine composition with an adjuvant, e.g. a cytokine, a saponin, or granulocyte macrophage-colony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Old LJ;
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An alternative form of DNA encoding cancer associated antigen KOC-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotides representing cancer-associated genes, used to develop products for the diagnosis, monitoring and treatment of cancers
                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Knuth A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cancer associated antigen; KOC-2; cancer; vaccine; CT7; ss.
                                                                                                                                                                                                                                                                                                                                                               DB 21; Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                    0; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gure A, Tsang S, Stockert E, Jager E,
                                                                                                                                                                                                                                                                                                                                                                   Score 22; DB 2
Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                          Sequence 22 BP; 1 A; 9 C; 7 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 55; Page 42; 44pp; English.
Claim 108; Page 13; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ36153 standard; DNA; 1946 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCTTGCGCGCTGCGGCCTCAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 recriecececrececercae 22
                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0061709.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US05766.
                                                                                                                                                                                                                                                                         adjuvant, e.g. a cytokine, a stimulating factor (GM-CSF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-013284/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09954738-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-OCT-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ36153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ36153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is one of a large number of 5' ESTS derived from mRNAs encoding secreted proteins. No ORP has yet been conclusively identified within the present sequence. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oilgo-dT primed CDNA ilbraries. Such ESTS are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTS are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTS are also used in diagnostic, forensic, gene therapy and chromsome mapping procedures.
                                                                                                                                                                                         ; expressed sequence tag; secreted protein; cDNA isolation; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 17.8; DB 21; Length 139;
Pred. No. 1.5e+02;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 139 BP; 26 A; 44 C; 54 G; 14 T; 1 other;
                                                                                                                                                                Human secreted protein 5' EST, SEQ ID NO: 31413
                                                                                                                                                                                                                                                                                                                                                                                                                                  Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID 31413; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                          AAC27338 standard; cDNA; 139 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 ccrrececerieceecrcae 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30
80.9%;
90.5%;
                                                                                                                                                                                                                                                                                                                                          21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                                                                                                                                                                                                                         99US-0122487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 cciricciccicicaciccad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 90.5
les 19; Conservative
                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                         (GEST ) GENSET
                                                                                                                                                                                                      Human; 5' EST;
gene therapy;
                                                                                                                                                                                                                                                                                                                                                                             26-FEB-1999;
                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                  EP1033401-A2.
                                                                                                                                          06-OCT-2000
                                                                                                                                                                                                                                                                                                                06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                              AAC27338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                   RESULT 3
                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
 셤
```

```
The present invention describes primer sets for synthesising 5602

full-length cDNAs defined in the specification. Where a primer set

comprises: (a) an oligo-dT primer and an oligomuclectide complementary

to the complementary strand of a polynuclectide which comprises one of

coligonuclectide comprises at least 15 nuclectides; or (b) a combination

of an oligonuclectide comprises as least 15 nuclectides; or (b) a combination

complementary strand of a polynuclectide which comprises a 5'-end

complementary strand of a polynuclectide which comprises a 5'-end

sequence and an oligonuclectide comprising a sequence complementary to a

complementary strand of a polynuclectide which comprises and the combination of

complementary strand of a polynuclectide strand of sequence of sequence of an oligonuclectide comprises as 1'-end sequence, where the

complementary strand of sequence is selected from those defined in

the 5'-end sequence 3'-end sequence is selected from those defined in

the specification. The primer sets can be used in antisense therapy and

the specification and/or diagnosis of the abnormality of the proteins encoded by

the full-length cDNAs. The primers are also useful for the

complementary full-length cDNAs. The primers are also useful for the

the full-length cDNAs. The primers allow obtaining of the full-length

complementary sull-length cDNAs. The primers and low obtaining of the full-length

AMH13613 to AMH18742 represent human cDNA sequences; AMH13618 and

AMH13613 to AMH18742 represent human cDNA sequences; AMH13618
                                                                                                                                                                                                            Human, primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB95893 represent human amino acid sequences, and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer sets for synthesizing polynuclectides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saito K, Ya
, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 711 BP; 149 A; 239 C; 209 G; 111 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID 3869; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isogai T, Nishikawa T, Hayashi K, S, Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                        Human cDNA clone (5'-primer) SEQ ID NO:3869.
RESULT 4
AAH07034/c
ID AAH07034 standard; cDNA; 711 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-AUG-1999; 99JP-0300253
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
                                                                                                                                                                                                                                                                                                                                                                                    28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JUN-2000; 2000JP-0241899
                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                   EP1074617-A2.
                                                                                                                                                                                                                                                             Ното варіеля
                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JUL-1999;
                                                                                                                             26-JUN-2001
                                                                                                                                                                                                                                                                                                                                           07-FEB-2001
                                                                                     AAH07034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ota T,
```

```
ô
                                                           Gaps
                                                           .
0
Query Match

80.9%; Score 17.8; DB 22; Length 711;
Best Local Similarity 90.5%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0;
```

```
Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                              DNA encoding novel human diagnostic protein #3914.
                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID No 3914; 103pp; English.
                                             BP.
                                           AAS68110 standard; cDNA; 1785
39 CCTTGCGCGCTGCAGCCCCAG 19
                                                                                                                                                                                                                                                             Tang YT;
                                                                                                                                                                                                               31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                              30-MAR-2001; 2001WO-US08631.
                                                                            13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                             WPI; 2001-639362/73.
P-PSDB; ABG03923.
                                                                                                                                                                                                                                                            Drmanac RT, Liu C,
                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                           WO200175067-A2.
                                                                                                                                           Homo sapiens.
                                                                                                                                                                             11-OCT-2001.
                                                            AAS68110;
                                   AAS68110/c
                          RESULT 5
```

The invention relates to isolated polymucleotide (I) and propertide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PER) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or treat disease states involving (II). (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) and (II) are useful in medical considers involving aberrant protein expression or biological activity. (I disorders involving aberrant protein expression or biological activity. (I disorders involving aberrant protein expression or biological activity. (I disorders involving aberrant protein expression or biological activity. (I disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences the invantion.

Che polymore coding sequences of the invantion.

Che sequence data for this patent did not appear in the printed of the coding sequence in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

Score 17.8; DB 23; Length 1785; Pred. No. 1.5e+02; 0; Mismatches 2; Indels 0; 855 CCTTGCGCGCTGCAGCCCCAG 835 2 CCTTGCGCGCTGCGGCCTCAG 22 sch 11 Similarity 90.5%; 19; Conservative ( Query Match Best Local Similarity Matches 19; Conservat à

Sequence 1785 BP; 416 A; 497 C; 517 G; 355 T; 0 other;

ö

Gaps

ô

2 CCTTGCGCGCTGCGGCCTCAG 22

Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

Human cDNA sequence SEQ ID NO:12421.

26-JUN-2001

AAH14706;

Homo sapiens. EP1074617-A2.

```
AAH14706/c
ID AAH14706 standard; cDNA; 2082 BP.
            The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapphing, and in recombinant production of (II). (II) in the state also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) and (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in capponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences haskelly-hasyster reates to assess biodiversity amino acid sequence data for this patent did not appear in the printed sequence the invalidation, but was obtained in electronic format directly from WIPO
                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.9%; Score 17.8; DB 23; Length 1785; 90.5%; Pred. No. 1.5e+02; ive 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1785 BP; 355 A; 517 C; 497 G; 416 T; 0 other;
                                                                                                                       DNA encoding novel human diagnostic protein #9206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID No 9206; 103pp; English.
                                          AAS73402 standard; cDNA; 1785 BP.
                                                                                                                                                                                                                                                                                                                                                                Tang YT
                                                                                                                                                                                                                                                                                                31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US08631
                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                 Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 19; Conser
                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; ABG09215
                                                                                                                                                                                                                    WO200175067-A2
                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                 Drmanac RT,
                                                                                                  13-FEB-2002
                                                                                                                                                                                                                                              11-OCT-2001
                                                                         AAS73402;
                      RESULT 6
```

primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -

Claim 8; SEQ ID 12421; 2537pp + CD ROM; English.

Yamamoto J; T;

Saito K, , Otsuki

Ota T, Isogai T, Nishikawa T, Hayashi K, S Ishii S, Sugiyama T, Wakamatsu A, Nagai K,

WPI; 2001-318749/34.

2000JP-0118776

27-AUG-1999; 11-JAN-2000; 29-JUL-1999;

99JP-0300253

28-JUL-2000; 2000EP-0116126

07-FEB-2001

02-MAY-2000; 2000JP-0183767 09-JUN-2000; 2000JP-0241899

(HELI-) HELIX RES INST.

```
The present invention describes primer sets for synthesising 5602

(ill-length cDNAs defined in the specification. Where a primer set

(ill-length cDNAs defined in the specification. Where a primer set

(inl-length cDNAs defined in the specification where the

(inl-length cDNAs defined in the specification, where the

(inl-length comprises at least 15 nucleotides, or (b) a combination

(inl-length comprises at least 15 nucleotides) or (b) a combination

(inl-length comprises at least 15 nucleotides) or (b) a combination

(inl-length comprises at least 15 nucleotides as 5'-end

(inl-length comprises at least 15 nucleotides and the compination of

(inl-length comprises at least 15 nucleotides and the combination of

(inl-length comprises at least 15 nucleotides and the combination of

(inl-length comprises at least 15 nucleotides and the combination of

(inl-length comprises at least 15 nucleotides and the combination of

(inl-length comprises at least 15 nucleotides and the compination of

(inl-length comprises at least 15 nucleotides and the compination of

(inl-length comprises at least 15 nucleotides and the compination of

(inl-length comprises at least 15 nucleotides and the compination of

(inl-length comprises at least 15 nucleotides and the compination of

(inl-length comprises at least 15 nucleotides and the compination of

(inl-length comprises at least 15 nucleotides and the compination of

(inl-length comprises at least 15 nucleotides and length for the primers are also useful for the

(inl-length companies)

(inl-length companies)

(inl-length companies)

(inl-length companies)

(inl-length companies)

(inl-length companies)

(inl-length companies)

(inl-length companies)

(inl-length companies)

(inl-length companies)

(inl-length companies)

(inl-length companies)

(inl-length companies)

(inl-length companies)

(inl-length companies)

(inl-length companies)

(inl-length companies)

(inl-length companies)

(inl-length companies)

(inl-length companies)

(inl-length companies)

(inl-length companie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17.8; DB 22; Length 2082;
Pred. No. 1.5e+02;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2082 BP; 416 A; 684 C; 607 G; 375 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   °,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTTGCGCGCTGCGGCCTCAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ccircececrecaecceae 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  represent oligonucleotide of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

931 ccrrdcdcdcrdcadcccdad 951 CCTTGCGCGCTGCGGCCTCAG 22

> a ઠે

N

19; Conservative

ö

Gaps

0

```
2000US - 024696
2000US - 0241785
2000US - 0241785
2000US - 0241787
2000US - 0241809
2000US - 0241809
2000US - 0241806
2000US - 024617
2000US - 0246475
2000US - 0246476
2000US - 0246476
2000US - 0246576
2000US - 0246525
2000US - 0246525
2000US - 0246525
2000US - 0246525
2000US - 0246525
2000US - 0246525
                                                                                                                                                                                                                                                                                                                                                   2000US-0246532.
2000US-0246609.
2000US-0246610.
                                                                                                                                                                                                                                                                                                                                                                         2000US-0246611.
2000US-0246613.
2000US-0249207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0249300.
2000US-0250160.
2000US-0250391.
                                                                                                                                                                                                                                                                                                                                                                                              2000US-0249208
                                                                       Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ss.
                                                        Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:9046
RESULT 8
AAK63986/c
ID AAK63986 standard; CDNA; 464 BP.
                                                                                                                                      17-JAN-2001; 2001WO-US01354
                                                                                                                                                                                                                                                                                      2000US-0224518
2000US-0224519
                                         06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                             000US-0225758
                                                                                                          WO200157182-A2
                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                           -AUG-2000;
                                                                                                                         09-AUG-2001
                             AAK63986;
```

23-MAR-2001; 2001WO-US09231.

2000US-0251030

```
incomparation in this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA (ABBS7737-ABB72072).
                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster genomic polynucleotide SEQ ID NO 39007.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 17.2; DB 23; Length 1217;
Pred. No. 2.78+02;
0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 39010; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1217 BP; 301 A; 328 C; 358 G; 230 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Myers EW;
                                                                                                                                               Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1066 TCCTTCTGCGCTGCAGCCTCAG 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     멾.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL29178 standard; DNA; 3408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 78.2%;
Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 recrisedecerecederad
                                   23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pharmaceutical; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams M,
                                                                                                                                                   Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PEKE ) PE CORP NY.
                                                                                                                                                                                              WPI; 2001-656860/75.
                                                                                                       (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200171042-A2.
                                                                                                                                                                                                                                                                                         interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABL29178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

c amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)

c activity, and can be used in gene therapy and vaccine production. (II)

c proteins and polynucleotides may be used in the prevention, diagnosis and

c treatment of diseases associated with inappropriate (I) expression. For

c expression by rectifying mutations or deletions in a patient's senome

cc expression by rectifying mutations or deletions in a patient's senome

cc that affect the activity of (I) by expressing inactive proteins or to

c supplement the patients own production of (I). Additionally, (I)

c supplement the patients own product the secreted (I), by inserting

cc polynucleotides may be used to produce the secreted (I), by inserting

cc protein. (I) proteins and polynucleotides may be used to prevent,

cancers and cancer metastess of haematopoietic-derived cells. AAK64703

cc cancers and cancer metastess of haematopoietic-derived cells. AAK64703

cc cancers and cancer metastess of haematopoietic-derived cells. AAK64703

concers and cancer metastess of haematopoietic antigen genomic

concers and cancer metastess of haematopoietic antigen genomic

concers and cancer metastess of haematopoietic antigen genomic

concers from the present invention. AAK64922 to AAK64550 and AAM82169

crepresent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster genomic polynucleotide SEQ ID NO 39010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 78.2%; Score 17.2; DB 22; Length 464;
Best Local Similarity 86.4%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 9046; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 464 BP; 131 A; 115 C; 110 G; 107 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200 rcchrecerecrecedecerere 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL29179 standard; DNA; 1217 BP
                                                                                                                                                                                                                                                                                                                               Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 recriredecerrecedecreage 22
                                                                                                08-DEC-2000; 2000US-0251856.
08-DEC-2000; 2000US-0251868.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251999.
08-DEC-2000; 2000US-0251990.
                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                               2000US-0251479
                                                                                                                                                                                                                                      05-JAN-2001; 2001US-0259678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila; developmental
pharmaceutical; gene; ds.
                                                                                                                                                                                                                                                                                                                               Rosen CA, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                         2001-483426/52
                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAM91205
                                                        05-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-2002
```

ö

Gaps

ö

New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell

WPI; 2001-656860/75.

Drosophila melanogaster.

ABL29179

RESULT

셤

8

WO200171042-A2

interactions

įs

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and insectle. The interactions in higher evkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511); expressed DNA equence. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences. Claim 1; SEQ ID NO 39007; 21pp + Sequence Listing; English. Sequence 3408 BP; 945 A; 779 C; 790 G; 894 T; 0 other; (ABB57737-ABB72072).

Gaps ö Length 3408; Indels Query Match 78.2%; Score 17.2; DB 23; Best Local Similarity 86.4%; Pred. No. 2.6e+02; Matches 19; Conservative 0; Mismatches 3; 1 TCCTTGCGCGCTGCGGCCTCAG 22 ઠે g

2257 rccrrccccrccaccrcas

AAS47110/c ID AAS47110 standard; cDNA; 462 BP. AAS47110; 

18-DEC-2001 (first entry

ss; breast cancer protein; tumour; cancer; cytostatic; Human breast cancer cDNA clone 14382, gene therapy. Human;

WO200179286-A2. Homo sapiens.

25-OCT-2001

12-APR-2001; 2001WO-US12164

17-APR-2000; 2000US-0551621. 08-JUN-2000; 2000US-0590751. 22-JUN-2000; 2000US-0604287. 20-JUL-2000; 2000US-0620405.

(CORI-) CORIXA CORP

Mitcham JL, Dillon DC, Jiang Y,

Harlocker SL,

Xu J,

Breast Tumour Proteins and nucleic acids useful for the prevention, diagnosis and treatment of breast cancer -WPI; 2001-611721/70.

Claim 37; Page 193; 297pp; English.

The invention relates to isolated breast tumour proteins and nucleic acids that encode them, including immunogenic fragments of the proteins. Also included are expression vectors expressing the proteins, transformed cells and antibodies raised against the proteins or an antigen presenting cell expressing the protein. The protein and an antigen presenting cell expressing the protein. The protein and diseases associated with inappropriate breast tumour protein expression, i.e. breast tumours and breast cancer e.g by gene therapy. The nucleic acids and their complements may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in

samples, and therefore which patients may be in need of restorative therapy. The proteins, nucleic acids and antibodies may be used in assays to identify modulators (e.g. antagonists) of breast tumour protein expression and activity. The antibodies and antagonists may also be used to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the proteins in samples (e.g. by enzyme linked immunosorbant assay (ELISA)) and in other immuno-purification diagnostic techniques. The present sequence is a CDNA from a breast tumour cDNA library isolated by subtractive hybridisation against a normal breast cDNA library. 886666666668888888

Sequence 462 BP; 124 A; 108 C; 118 G; 99 T; 13 other;

Gaps ö 76.4%; Score 16.8; DB 22; Length 462; 90.0%; Pred. No. 4e+02; ive 0; Mismatches 2; Indels 0 Local Similarity 90.0 Query Match Best Loca Matches

ö

91 TCTTTGCTCGCTGCGGCCTC 72 1 recriecececrececere ઠે 유

ô

7680/c AAF17680 standard; cDNA; 462 RESULT 12 AAF17680/

13-MAR-2001 (first entry) AAF17680;

Human breast cancer associated 14382 coding sequence.

Human; breast cancer associated gene; vaccine; diagnosis; therapy; ss.

Homo sapiens

WO200060076-A2

12-OCT-2000

15-FEB-2000; 2000WO-US05308 02-APR-1999;

99US-0285480. 99US-0339338. 99US-0389681. 99US-0433826. 03-NOV-1999; 23-JUN-1999; 02-SEP-1999; 

(CORI-) CORIXA CORP.

Xu J, Harlocker SL; Mitcham JL, Dillon DC, WPI; 2001-122627/13. Yuqiu J,

An isolated polypeptide useful for the treatment and diagnosis of tumors e.g. breast cancer comprises at least an immunogenic portion of a breast tumor protein -

Claim 66; Page 138; 238pp; English.

The present invention provides the coding sequences and some protein sequences of proteins associated with breast cancer in humans. These sequences can be used in the diagnosis and treatment of cancers, particularly breast tumours.

Sequence 462 BP; 124 A; 108 C; 118 G; 99 T; 13 other;

Gaps ö 76.4%; Score 16.8; DB 22; Length 462; 90.0%; Pred. No. 4e+02; 1.ve 0; Mismatches 2; Indels 0. Best Local Similarity .... Matches 18; Conservative

ô

1 TCCTTGCGCGCTGCGGCCTC 20

ઠે 셤

91 rérridérédédédédésésés 72

BP.

(first entry)

97US-0050667. 98WO-US13041

```
New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis
                                                                                                                                                Treponema pallidum infection; syphilis; Borrelia infection; animal; enzyme production; ds.
                                                                                                                   Polynucleotide sequence from the genome of Treponema pallidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 491-497; 1150pp; English
                         AAX20553 standard; DNA; 10461
                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-081273/07.
                                                                                                                                                                                                         rreponema pallidum.
                                                                                                                                                                                                                                                                                                           23-JUN-1998;
                                                                                                                                                                                                                                                                                                                                            24-JUN-1997;
                                                                                                                                                                                                                                           409859034-A2
                                                                                            05-MAY-1999
                                                                                                                                                                                                                                                                            30-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                             Fraser CM;
                                                             AAX20553;
RESULT 14
AAX20553/c
                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated polymucleotides ([1] - [IV) encoding breast cancer antiqens SYN22A12, SYN22A2, B722P and B726P (4 of 172 cDNA cancer antiqens SYN22A12, SYN22A2, B722P and B726P (4 of 172 cDNA sequences included in the specification). Also included are isolated comprising sequences with 90 % identity to (1)-IV), an expression vector comprising the cDNAs, a host cell transformed with the expression vector and a diagnostic kit comprising 2 oligomuclectide primers or probes, where 1 of the oligomuclectide primers or probes, where 1 of the oligomuclectide primers or probes, where 1 of the oligomuclectide primers or probes; where 1 of the oligomuclectide sequences with 90 % compression and B726P peptides they encode can be used as diagnostic markers, as models for the development of human therapeutic targets.

CC markers, as models for the development of human therapeutic targets of in the identification of therapeutic proteins, and serve as targets of the development of human therapeutic proteins. And serve as targets of the development of human therapeutic general that may be used for the treatment of breast cancer. In particular, they may be transfected (using a vector) into a host cell that may be cultured to express the breast cancer antigens may then be used in the production of antibodies against SYN22A12, BYN22A2, BY33P and B726P, which in turn configuration of breast cancer. Short 10 nucleotide sequences of (1) to (IV) may be used as primers and probes in hybridisation and amplification creations for the detection of SYN22A12, SYN22A2, B723P and B726P in the cancer. The present sequence is a breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acids encoding breast cancer antigens SYN22A12, SYN22A2, . B723P and B726P, useful for the prevention, diagnosis and treatment of breast cancer -
                                                                                                                                                                                             Human; 88; breast cancer; cytostatic; gene therapy; SYN22A12; SYN22A2;
B723P; B726P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.4%; Score 16.8; DB 24; Length 462; 90.0%; Pred. No. 4e+02; rive 0; Mismatches 2; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 462 BP; 124 A; 108 C; 118 G; 99 T; 13 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Column 147-148; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xu J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitcham JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specific cDNA of the invention.
                                                                      ABK95145 standard; cDNA; 462 BP.
                                                                                                                                                                        Human breast tumour cDNA 14382.
                                                                                                                                                                                                                                                                                                                                                         98US-0222575
                                                                                                                                                                                                                                                                                                                                                                                        98US-0222575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yuqiu J, Dillon DC,
                                                                                                                                                                                                                                                                                                                                                                                                                         (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-478446/51
                                                                                                                                                                                                                                                                                          US6387697-B1.
                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                           28-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                          28-DEC-1998;
                                                                                                                                             24-SEP-2002
                                                                                                                                                                                                                                                                                                                          14-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                            ABK95145;
                                            RESULT 13
ABK95145/
```

```
AAX20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrella infections in animals, and for the production of biosynthetic products such as enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enolase 3(beta, muscle); ENO3; single nucleotide polymorphism;
                                                                                                                                                                                    Gaps
                                                                                                                                                  Length 10461;
                                                                                                                                                                                    ö
                                                                                                                  Sequence 10461 BP; 2325 A; 3411 C; 2493 G; 2213 T; 19 other;
                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "this sequence contains introns"
                                                                                                                                                  76.4%; Score 16.8; DB 20;
90.0%; Pred. No. 3.9e+02;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; haplotype analysis; isogene; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human enolase 3 (beta, muscle) isogene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                            ВÞ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "ENO3"
                                                                                                                                                                                                                                                        6012 ccrecececrecaectrcae 5993
                                                                                                                                                                                                                                                                                                                                          AAK98531 standard; DNA; 13308
                                                                                                                                                                                                                           22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/product=
                                                                                                                                                                                                                                                                                                                                                                                                          16-APR-2002 (first entry)
                                                                                                                                                                                                                         3 CTTGCGCGCTGCGGCCTCAG
                                                                                                                                                            Query Match
Best Local Similarity 90.00
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                               AAK98531;
                                                                                                                                                                                                                                                                                                           RESULT 15
AAK98531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
```

ö

Gaps ö

> 20 72

1 recrisededecere rcrirecrescresescre

à g

91

ö

```
/*tag= b
4092.4176
4092.4176
/*tag= c
/number= "1"
4177.5056
/*tag= d
/*tag= d
/*tag= d
/*tag= d
/*tag= d
/*tag= d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= 1
replace(5357,C)
/*tag= 1
replace(5366,C)
/*tag= k
5371..5532
/*tag= 1
/*tag= 1
/*tag= 1
                                                                                                                                                                                                                                             /*tag= 6
5057.5152
/*tag= f
/number= "2"
5153.5312
/*tag= g
/number= g
/number= g
/number= "2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= m
/number= "4"
replace(5542,C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= w
7867.8203
/*tag= x
/number= "7"
replace(8181,G)
     (3640,C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*tag= 0 /*t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= aa
8406..8834
/*tag= ab
/number= "8"
replace(8423,C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *tag= n
eplace(5547,C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eplace (7790,G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eplace (8332,G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= 8
7337.7559
7463= 1
7500.7668
7560.7668
7609.7866
7669.7866
7669.7866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= y
8204..8405
/*tag= z
/number= "8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= ac
8835..8943
allele
                                                                                                                                     intron
                                                                                                                                                                                                                   allele
                                                                                                                                                                                                                                                                                                                                                         intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              allele
                                                       exon
                                                                                                                                                                                                                                                                          exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   allele
                                                                                                                                                                                                                                                                                                                                                                                                                                          exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon
```

```
The present invention provides the protein, cDNA and genomic sequences of a human enolase 3 (beta, muscle) isogene containing a number of single nucleotide polymorphisms (SNPS). The sequences can be used to identify the haplotype of an individual and identify whether particular haplotypes are linked to certain diseases. The present sequence is the ENO3 gene.
                                                                                                                                                                                                                                                                                                                                                                                           Novel genetic variants of enclase 3, (beta, muscle) gene useful in studying expression and function of the protein, and for screening drugs to treat disorders of glycolytic pathway .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13308 BP; 2874 A; 3775 C; 3758 G; 2901 T; 0 other;
                                                                                                                                                                                                                                                                                                                                          Koshy B, Parks KE;
                                   /*tag= ae
/number= "9"
replace(8951,C)
                                                                                                                                                                           /*tag= aj
/number= "11"
replace(9431,G)
/*tag≈ ak
                                                                                                                                             eplace (9154,G)
                                                                                    /*tag= ag
/number= 10"
9152.9239
/*tag= ah
/number= 10"
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; Fig 1; 90pp; English.
                                                                                                                                                                                                                                                                                                                  (GENA-) GENAISSANCE PHARM INC
                                                                                                                                                                                                                                                                         02-JUL-2001; 2001WO-US20952.
                                                                                                                                                                                                                                                                                              30-JUN-2000; 2000US-215236P.
  /*tag= ad / number= "98944..9092
                                                                   /*tag= af
9093..9151
                                                                                                                                                        /*tag= ai
9240..9309
                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-154721/20.
P-PSDB; AAM48922.
                                                                                                                                                                                                                                                                                                                                         Duda A, Finkel K,
                                                                                                                                                                                                                              WO200202579-A2
                                                                                                                                                                                                                                                    10-JAN-2002.
                       intron
                                                      allele
                                                                                                          intron
                                                                                                                                          allele
                                                                                                                                                                                               allele
                                                                                                                                                              exon
                                                                            exon
```

1405 ccgrccccccccccc 1424 21 2 CCTTGCGCGCTGCGGCCTCA ઠ

ö

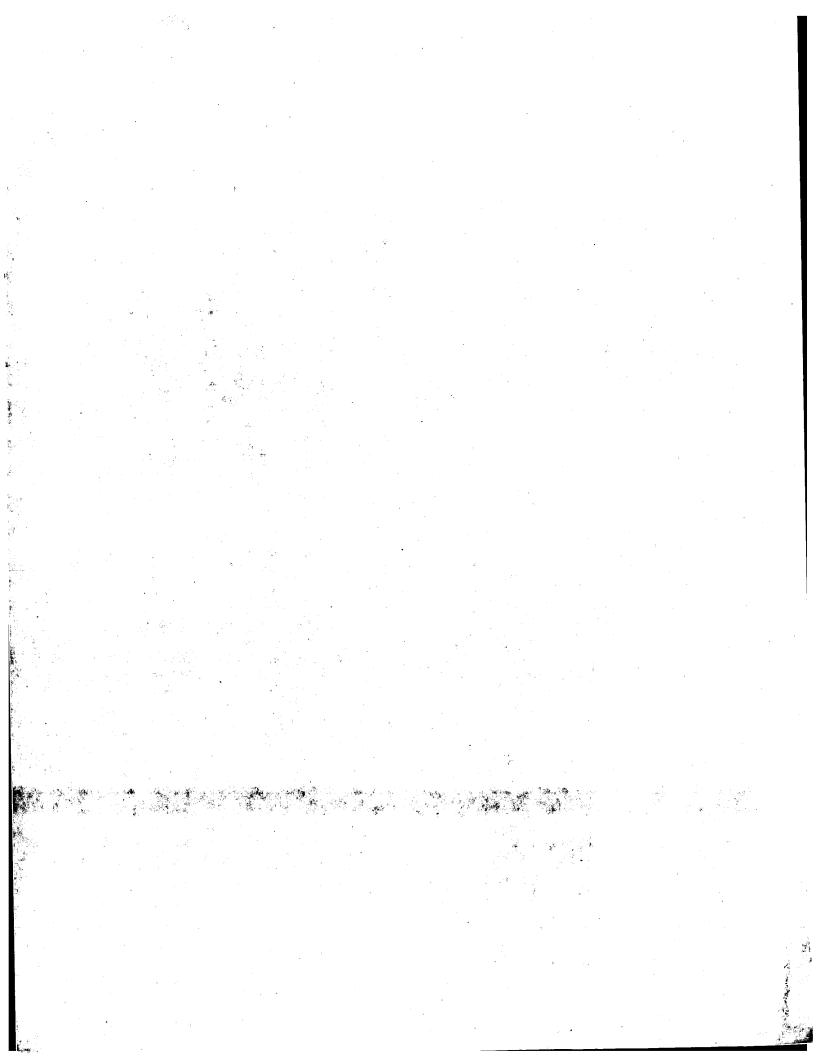
Gaps

76.4%; Score 16.8; DB 24; Length 13308; 90.0%; Pred. No. 3.9e+02; Live 0; Mismatches 2; Indels 0;

Query Match Best Local Similarity 90.0 Matches 18; Conservative

Search completed: April 18, 2003, 05:45:23 Job time : 103 secs

exon



Sequence 39, Appl Sequence 31, Appl Sequence 11, Appl Sequence 10, Appl Sequence 10, Appl Sequence 1, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 50, Appl Sequence 50, Appl Sequence 50, Appl Sequence 50, Appl Sequence 50, Appl Sequence 50, Appl Sequence 50, Appl Sequence 50, Appl

US-09-528-706-104
US-09-452-239-39
US-09-452-239-39
US-09-318-191-33
US-08-45-239-41
US-08-35-742-1
US-08-35-742-1
US-08-35-09323-1
US-08-35-09323-1
US-08-385-2
US-08-399-385-2
US-08-999-385-2
US-08-999-385-50
US-08-997-362-50
US-08-997-362-50
US-08-997-362-50
US-08-997-362-50
US-08-977-500-50
US-08-977-500-50
US-08-973-970-50
US-08-973-970-50
US-08-973-970-50
US-08-973-970-50
US-08-973-970-50
US-08-973-970-50
US-08-973-970-50
US-08-973-970-50

4 4 222444 222444 2233444 223344 223344 223344 223344 23344 4334 4334 4334 4344 4344 4344 4344 4344 4344 4344 4344 4344 4344

```
Appl
Appl
Appli
Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                  April 18, 2003, 04:53:41; Search time 21.5 Seconds (without alignments) 313.809 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1
Sequence 6
Sequence 6
Sequence 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Issued_Patents NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

7_cgn2_6/ptodata/1/ina/6A_COMB.seq:*

1: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-222-575-165
US-09-222-575-165
US-09-230-225B-3
US-08-465-965-16
US-08-465-965-16
US-08-264-861A-11
PCT-US95-07784-11
US-08-264-88-6
US-08-264-88-6
US-08-28-488-6
US-09-299-68A-6
US-08-738-172-1
US-08-738-172-1
US-08-738-172-1
US-08-738-172-1
US-08-738-172-1
US-08-738-172-1
US-08-738-172-1
US-08-738-172-1
US-08-738-172-1
US-08-738-173-1
US-08-178-13-1
US-09-282-305-7
US-09-282-305-7
US-09-282-305-7
US-09-282-305-7
                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                 441362 seqs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                               1 tccttgcgcgctgcggcctcag 22
                                                                                   - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                          IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                US-09-270-437D-11
22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2462
2462
37444
783
783
11150
11263
2936
                                                                                                                                                                                                                                                      Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
116.8
                                                                                     OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database
                                                                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22221084221088765
74654321088768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        00000000
```

```
Sequence 7, Application US/09061709B

Sequence 7, Application US/09061709B

Sequence 7, Application US/09061709B

Sequence 7, Application US/09061709B

Sequence 7, Application US/0906170B

Sequence 7, Application Yournament of Application Solam

APPLICANT: Gare, Ali

APPLICANT: Tangy Solam

APPLICANT: Tangy Solam

APPLICANT: Tangy Solam

APPLICANT: Tangy Applicant And Alexander

APPLICANT: Old, Lloyd J.

TITLE OF INVENTION: LODGet And Uses Thereof

TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof

CURRENT APPLICATION NUMBER: US/09/061,709B

CURRENT APPLICATION NUMBER: US/09/061,709B

SEQ ID NO 7

LENGTH: 1946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 1946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09608917A
| Patent No. 6409648
| GENERAL INFORMATION:
| APPLICANT: The Regents of the University of California
| APPLICANT: Campisi, Judith
| APPLICANT: Campisi, Judith
| APPLICANT: Kim, Sahn.Ho
| TITLE OF INVENTION: TEF1 Binding Protein
| TITLE REFERENCE: LBNL IB 1317
| CURRENT APPLICATION NUMBER: US/09/608,917A
| CURRENT PILING DATE: 2000-06-30
| NUMBER OF SEQ ID NOS: 4
| SEQ ID NOS: 4
| SEQ ID NO 3
| LENGTH: 1704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 22; DB
Pred. No. 0.44
; Mismatches
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Sc
100.0%; Pr
:ive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 TCCTTGCGCGCTGCGGCCTCAG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 22, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
US-09-608-917A-3
                                                                                    JS-09-061-709-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-061-709-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
```

24, Appl 13, Appl 7, Appli 1, Appli 1, Appli 584, App 1, Appli 1, Appli 1, Appli

Sequence Sequence Sequence

Sequence 1 Sequence 7 Sequence 1

Sequence 1 Sequence 2 Sequence 2

423 1588 1588 1672

584,

Sequence 104, App Sequence 104, App

US-09-370-700-1 JS-08-516-859A-104 US-09-586-472-104

5919 80161 80161 391 391

ò 셤

```
Sequence 3. Application US/09230225B

Sequence 3. Application US/09230225B

Fatent No. 6403362

GENERAL INFORMATION:
APPLICANT: Moijs Seike Kaisha, Ltd.
APPLICANT: Moijs Jateuki for the Mass Production of Proteins or Peptides by Microo TITLE OF INVENTION: Of the Genus Humicola
TITLE OF INVENTION: Of the Genus Humicola
FILE REFRENCE: VX990054

CURRENT APPLICATION NUMBER: US/09/230,225B

CURRENT FILING DATE: 1999-03-03

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3

LENGTH: 2409
                                                                                                                                                                           ö
                                                                                                                                                                           Gaps
                                                                                                                                                                           ö
                                                                                                                                 DB 4; Length 462;
                                                                                                                                                                             2; Indels
                                                                                                                                 Query Match 76.4%; Score 16.8; E Best Local Similarity 90.0%; Pred. No. 67; Matches 18; Conservative 0; Mismatches
OTHER INFORMATION:
NAME/KEY misc feature
LOCATION: (688) (653)
OTHER INFORMATION: Cleavage site Smal
NAME/KEY: misc feature
LOCATION: (1253). (1259)
OTHER INFORMATION: Cleavage site BamH1
                                                                                                                                                                                                                           1 recrireçececrecere 20
                                                                                                                                                                                                                                                  91 TCTTTGCTCGCTGCGGCCTC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Humicola insolens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
COCATION: (1816)..(1989)
THER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Intron
(1990)..(2044)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Intron
LOCATION: (1762)..(1815)
OTHER INFORMATION:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS (2045)..(2095)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Intron
GCCATION: (1030)..(1141)
STHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ION: (1142)..(1761)
INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ION: (536)..(1029)
INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: sig_peptide
LOCATION: (389)..(457)
OTHER INFORMATION:
NAME/KEY: mat_peptide
LOCATION: (458)..()
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AME/KEY: Intron
OCATION: (478)..(535)
THER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCATION: (458)..(477)
THER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OCATION: (1990)..
                                                                                                                                                                                                                                                                                                                                            RESULT 4
US-09-230-225B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IAME/KEY:
                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-09-222-575-165/C
; Sequence 165, Application US/09222575
; Patent No. 6387697
; GENERAL INFORMATION:
    APPLICANT: Vidiu, Jiang
; APPLICANT: Mitcham, Jennifer L.
    APPLICANT: Mitcham, Jennifer L.
    APPLICANT: Mitcham, Jennifer L.
    APPLICANT: Mitcham, Jennifer L.
    APPLICANT: Mitcham, Jennifer L.
    APPLICANT: Mitcham, Jennifer L.
    APPLICANT: Mitcham, Jennifer L.
    APPLICANT: Mitcham, Jennifer L.
    APPLICANT: Mitcham, Jennifer L.
    APPLICANT: Mitcham, Jennifer L.
    APPLICANT: Mitcham, Jennifer L.
    APPLICANT: Mitcham, Jennifer L.
    APPLICANT: Mitcham, Jennifer L.
    TITLE OF INVENTION: and Methods for Their Use
    TITLE PEPLICATION NUMBER: US/09/222,575
    CURRENT FILING DATE: 1998-12-28
    NUMBER OF SEQ ID NOS: 174
    SOFTWARE: FastSEQ for Windows Version 3.0
    SEQ ID NO 165
    LENGTH: 462
                                                                            FEATURE:
NAME/KEY: misc feature
| LOCATION: (1687)..(1687)
| CTHER INFORMATION: "n" represents "A" because it is in the poly A tail of the CDNA
| US-09-608-917A-3
                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                  Length 1704;
                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (399)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (405)
                                                                                                                                                                                                  78.2%; Score 17.2; I ilarity 86.4%; Pred. No. 45; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ör
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JTHER INFORMATION: Where n is a, C, g or NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ör
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                מ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (198)

THER INFORMATION: Where n is a, c, g

NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEI: MOSILICAL-DATE
LOCATION: (222)
OTHER INFORMATION: Where n is a, c,
NAME/KEY: modified base
LOCATION: (243)
OTHER INFORMATION: Where n is a, c,
NAME/KEY: modified base
LOCATION: (278)
OTHER INFORMATION: Where n is a, c,
NAME/KEY: modified base
LOCATION: (357)
OTHER INFORMATION: Where n is a, c,
NAME/KEY: modified base
LOCATION: (385)
OTHER INFORMATION: Where n is a, c,
NAME/KEY: modified base
LOCATION: (385)
OTHER INFORMATION: Where n is a, c,
NAME/KEY: modified base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ϋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ϋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ບັ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Where n is a, NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Where n is a, NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Where n is a, NAME/KEY: modified base
                                                                                                                                                                                                                                                                                                                                     319 rcchrececechecrecece 340
                                                                                                                                                                                                                                                                                          1 TCCTTGCGCGCTGCGGCCTCAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: modified_base_
LOCATION: (10)
                                                                                                                                                                                                                           Best Local Similarity
Matches 19; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Human
                                    TYPE: DNA
ORGANISM: mouse
                                                                                                                                                                                                                Query Match
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 15.8; DB 2; Length 3744; Pred. No. 1.7e+02; 0; Mismatches 2; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INCORNATION:
APPLICANT: Tuomanen, Elaine
APPLICANT: Tuomanen, Elaine
APPLICANT: Tuomanen, Elaine
APPLICANT: Tuomanen, Elaine
TITLE OF INVENTION: Antibody Recognizing Endothelial Cell
TITLE OF INVENTION: Ligand for Leukocyte CR3
TITLE OF INVENTION: Ligand for Leukocyte CR3
VUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack
STATE: New Jersey
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1..3744

PUBLICATION INFORMATION:
AUTHORS: Delisse-Gathoye, et al.
TITLE: Cloning, Partial Sequence, Expressions, and
TITLE: Antigenic Analysis of the Filamentous
TITLE: Hemagglutinin Gene of Bordatella Pertussis
JOURNAL: Infection and Immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: CLASSIFICATION: CLASSIFICATION: S14
ATTORNEY/AGENT INFORMATION: NAME: Jackson, David REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELEPHONE: 201-487-1684
INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS: LENGTH: 3744 base pairs TYPE: nucleic acid TYPE: nucleic acid TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16, Application US/08465965
Patent No. 5968512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 3050 rccrrccccccccx 3032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.8%;
89.5%;
                                      30-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TCCTTGCGCGCTGCGGCCT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 89.5 Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAGES: 2895-2905

DATE: September-1990

US-08-348-353-16
                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-08-465-965-16/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                       Query Match 73.6%; Score 16.2; DB 4; Length 2409; Best Local Similarity 85.7%; Pred. No. 1.2e+02; Matches 18; Conservative 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16, Application US/08348353
Patent No. 593217
GENERAL INPORMATION:
APPLICANT: Tuomanen, Elaine
APPLICANT: Tuomanen, Elaine
APPLICANT: Tuomanen, Elaine
APPLICANT: Magure, Robert
ITILE OF INVENTION: Ligand for Leukocyte CR3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: New Jersey
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description: Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 71.8%; Score 15.8; DB 4; Length 1471; Best Local Similarity 89.5%; Pred. No. 1.76+02; Matches 17; Conservative 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,353
                    LOCATION: (1505)...(1510)
CTHER INFORMATION: Cleavage site BglII
MAME/KEY: misc feature
LOCATION: (1643)...(1648)
OTHER INFORMATION: Cleavage siteStul
US-09-230-2258-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/09492985
Patent No. 6376240
                                                                                                                                                                                                                                                                                                                                                                                         886 cctrcheccrccccccc 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       650 ccrrdcccccccc 632
                                                                                                                                                                                                                                                                                                                                         2 CCTTGCGCGCTGCGGCCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 CCTTGCGCGCTGCGGCCTC 20
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; SEQ ID NO 11
; LENGTH: 1471
; TYPE: DNA
; ORGANISM: mouse
US-09-492-985-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-492-985-11/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-348-353-16/c
                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
```

ö

```
2895-2905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tille.
JOURNAL: Ins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tuomanen, Elaine
APPLICANT: Tuomanen, Elaine
APPLICANT: Tuomanen, Elaine
APPLICANT: Masure, Robert
TITLE OF INVENTION: Ligand for Leukocyte CR3
TITLE OF INVENTION: Ligand for Leukocyte CR3
TITLE OF INVENTION: Ligand for Leukocyte CR3
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack Avenue
CITY: Hackensack Avenue
CITY: Hackensack Avenue
CITY: Hackensack Avenue
CONTRY: U.S.A.
ZIP: 07601
COMPUTER: READABLE FORM:
COMPUTER: IBM FC COMPALIBLE
COMPUTER: Patentin Release #1.0, Version #1.25
CURRATION DATH:
CURRENT APPLICATION DATH:
PELLING DATH:
PELLING DATH:
PELLING DATH:
PUBLICATION NUMBER: US/08/465,966
FILLING DATH:
PELLING DA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 3744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE: Cloning, Partial Sequence, Expressions, and TITLE: Antigenic Analysis of the Filamentous TITLE: Hemenglutinin Gene of Bordatella Pertussis JOURNAL: Infection and Immunity VOLUME: 58 ISSUE: 9 ISSUE: 9 ISSUE: 9 PAGES: 2895-2905 DATE: September-1990
                                                               Query Match

71.8%; Score 15.8; DB 2;
Best Local Similarity 89.5%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 2;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/03725
FILING DATE: 04-MAY-1992
FILING DATE: 04-MAY-1992
FILING DATE: 04-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/348,353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-08-465-966-16/c
; Sequence 16, Application US/08465966
; Patent No. 6015560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3050 †cciriccccccccccc 3032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 recrrecederecect 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
```

```
CLASSICONION: 424

PRICA PRICATION DEATH.

PRICA PRICATION DEATH.

PRICA PRICATION NUMBER: CPT/US29/03725

PILING DATE: 3.444/1994

PRICA PRICATION NUMBER: CPT/US29/03725

PILING DATE: 04-MA-1992

CLASSICONION: 444

PRICA PRICATION NUMBER: CPT/US29/03725

PRICA PRICATION NUMBER: CPT/US29/03725

PRICA PRICATION: 444

PRICA PRICATION NUMBER: CPT/US29/03725

PRICA PRICATION: 444

PRICA PRICATION: 444

APPLICATION NUMBER: 66/700-1-097CIPIDIV2

REFERENCE CHARACTERISTICS: 104-14-1644

NAME: 201-14-1644

INFORMATION NUMBER: 66/700-1-097CIPIDIV2

PRICA PRICA PRICATION: 444

PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRICA PRI
```

```
RESULT 11
US-08-264-861A-10/C

i Sequence 10. Application US/08264861A

i Patent No. 5622866

j GENERAL INFORMATION:
APPLICANT: MOTAMEDI, HAIDEH
ITLE OF INVENTION: CONSTRUCTION OF INTEGRATIVE AND REPLICATIVE EXPRESSION
ITLE OF INVENTION: VECTORS FOR STREPTOMYCES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEB: J. SEDS:
ADDRESSEB: J. BEDS:
CITY: RAHWAY

CITY: RAHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                   ö
                                                                                                                                                             Length 783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.9%; Score 15.6; DB 1; Length 1150; larity 81.8%; Pred. No. 2.16+02; Conservative 0; Mismatches 4; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
PCT-US95-07784-10/c
SCT-US95-07784-10/c
SCHERAL INFORMATION:
APPLICANT: MOTAMEDI, HAIDEH
HAPPLICANT: SHAFIEE, ALI
TITLE OF INVENTION: EXPRESSION CASSETTES USEFUL IN
                                                                                                                                                    Score 15.6; DB 5;
Pred. No. 2.1e+02;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                        401 TCCTTGCGGGCCGCGCGTCCG 380
                                                                                                                                                                                                                                                        1 TCCTTGCGCGCTGCGGCCTCAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     462 recrrécédecedecédece 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-CHITICAL: NO
                                                                                                                                  Query Match 70.99
Best Local Similarity 81.89
Matches 18, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 18; Conser
                                                         ; ANTI-SENSE: NO
PCT-US95-07784-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-264-861A-10
                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application PC/TUS9507784
GENERAL INFORMATION:
APPLICANT: MOTHABDI, HAIDEH
APPLICANT: SHAFIES, ALI
TITLE OF INVENTION: EXPRESSION CASSETTES USEFUL IN
TITLE OF INVENTION: CONSTRUCTION OF INTEGRATIVE AND REPLICATIVE EXPRESSION
TITLE OF INVENTION: VECTORS FOR STREPTOMYCES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSE: J. ERIC THIES
STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
CITY: RAHWAY
CITY: RAHWAY
COUNTRY: USA
ZIP: 07065
COMPUTER: BP C COMPATIBLE
COMPUTER: TEMPE: Flopy disk
COMPUTER: TEMPE: Flopy disk
COMPUTER: TEMPE: Flopy disk
COMPUTER: TEMPE: Flopy disk
COMPUTER: TEMPE: Flopy disk
COMPUTER: TEMPE: PC-DOS/MS-DOS
SOFTWARE: PREABLICATION DATA:
APPLICATION NUMBER: PCT/US95/07784
CLASSIFICATION:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: J9132
FELECPHONE: (908) 554-4720
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGRAL OF SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGRAL OF SEQ ID NO: 11:
STRANDEDNESS: SINGle
TYPE: NUCLEIC CACITY
CONTACT: UNKNOWN
                     SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 70.9%; Score 15.6; DB 1; Best Local Similarity 81.8%; Pred. No. 2.1e+02; Matches 18; Conservative 0; Mismatches 4;
SOFTWARE: Patentin Kulling
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,861A
FILING DATE: 23-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: THIES, J. ERIC
REGISTRATION NUMBER: 35,382
REFRENCE/DOCKET NUMBER: 19132
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 11:
ENGTH: 783 base pairs
TENTANDEDNESS: 81ngle
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    401 TCTTGCGGCGCGGCGTCCG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TCCTTGCGCGCTGCGGCCTCAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US95-07784-11/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

ô

```
Score 15.4; DB 2; Length 1263; Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,689A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
FILING DATE: Filed Herewith ...
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 9F-0241 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Phillip R.
APPLICANT: Lal, Preeti
APPLICANT: Cal, Preeti
APPLICANT: Oli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN SERINE
TITLE OF INVENTION: CARBOXYEEPTIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICALLER
PILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 86,749
REFERENCE/DOCKET NUMBER: PF-0;
TELECOMMUNICATION INFORMATION:
TELECHONE: 415-85-0555

TELEPHONE: 415-85-0555

TELEPHONE: 415-85-0556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09299689A Patent No. 6379913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                         TELEPHONE: 412-9160.

TELEPHONE: 412-9160.

INPORMATION FOR SEQ ID NO: 6. SEQUENCE CHARACTERISTICS:

LENGTH: 1263 base pairs

TYPE: nucleic acid

STRANUBUSS: single

TOPOLLGY: linear

IMMEDIATE SOURCE:

LIBRARY: COLNCRT01

CLONE: 770469
US-08-928-488-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TCCTTGCGCGCTGCGGC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 recriececececedes 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 31/-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
            CONSTRUCTION OF INTEGRATIVE AND REPLICATIVE EXPRESSION VECTORS FOR STREPTOMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5; Length 1150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                  COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC Compatible
COMPUTER: EN PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07784
FILING DATE:
CLASSIFICATION NUMBER: PCT/US95/07784
FILING DATE:
NAME: THIES J. ERIC
NAME: THIES J. ERIC
NAME: 19132
REGERENCE/DOCKET NUMBER: 19132
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                             ADDRESSEE: J. ERIC THIES
STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
CITY: RAHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS SOFFWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/828,488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: CA ALCO COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 15.6; DE pred. No. 2.1e+ 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN SERINE
TITLE OF INVENTION: CARBOXYPEPTIDASE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08828488 Patent No. 592551
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             462 recrrécédedecédedecres 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 5EQUENCE CHARACTERISTICS: LENGTH: 1150 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 70.9%;
Best Local Similarity 81.8%;
Matches 18; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                  TITLE OF INVENTION: CON
TITLE OF INVENTION: VEC
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: DANTI-SENSE: NO PCT-US95-07784-10
                                                                                                                                                                                   STATE: NJ
COUNTRY: USA
ZIP: 07065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-08-828-488-6
                                                                                                                                                                                   STATE: N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
```

Gaps

ö

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

70.0%; Score 15.4; DB 4; Length 1263;
Best Local Similarity 94.1%; Pred. No. 2.56+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
70.0%; Score 15.4; DB 2; Length 2936;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08738172
| Patent No. 5939557
| GENERAL INFORMATION:
| APPLICANT: Stast, Joseph APPLICANT: Davis, Maria
| APPLICANT: Davis, Maria
| TITLE OF INVENTION: THERMOSTABLE ALKALINE PHOSPHATASES NUMBER OF SEQUENCES: 1
| CORRESPONDENCE ADDRESS: ADDRESSEE: Lyon & Lyon STREET: 633 Weet Fifth Street CITY: Los Angeles STREET: Suite 4700
| CITY: Los Angeles STARE: California COUNTRY: U.S.A.
| ZIP: 90071-2066 |
| COMPUTER RADABLE FORM: MEDIUM TYPE: 315 "Diskette, 1.44 Mb MEDIUM TYPE: 315 "Diskette, 1.44 Mb MEDIUM TYPE: 315 "Diskette, 1.44 Mb MEDIUM TYPE: 180 "COMPUTER: IBM COMPACIAL IBM P.C. DOS 5.0 SOFTWARE: WORD PATECT 5.1
| CURRENT APPLICATION DATE: US/08/738,172 |
| FILING DATE: FILING DATE: US/08/738,172 |
| FILING DATE: FILING DATE: US/08/738,172 |
| FILING DATE: FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,172 |
| FILING DATE: US/08/738,173 |
| FILING DATE: US/08/738,173 |
| FILING DATE: US/08/738,173 |
| FILING DATE: US/08/738,173 |
| FILING DATE: US/08/738,173 |
| FILING DATE: US/08/738,173 |
| FILING DATE: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION: A35
CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/06,965
FILING DATE: October 27, 1995
APPLICATION NUMBER: 08/465,003
FILING DATE: December 20, 1995
APPLICATION NUMBER: 08/26,1995
APPLICATION NUMBER: 08/29,329
FILING DATE: May 10, 1994
APPLICATION NUMBER: 08/29,329
FILING DATE: May 10, 1994
ATTORNEY/AGENT INFORMATION:
RECISTRATION NUMBER: 08/29,329
ATTORNEY/AGENT INFORMATION:
RECISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
RELEPHONES: (213) 489-1600
TELEPHONES: (213) 489-1600
TELEPHONES: (213) 955-0440
INFORMATION FOR SEQ ID NO: 1:
LENGTH: 2936 base pairs
ITYRE: NOCCASE ACID STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STRANDED STR
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: COLNCRT01
; CLONE: 770469
US-09-299-689A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 recrrececerecee 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 TCCTTGCGCGCGCGGG 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-08-738-172-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

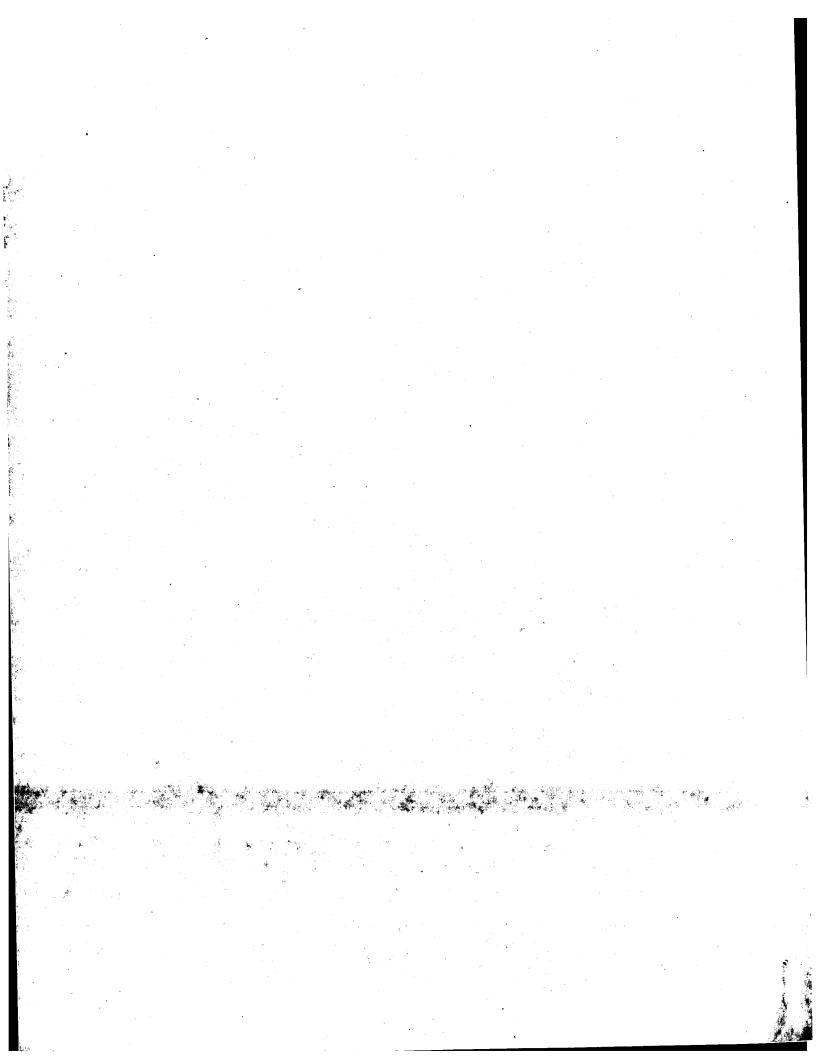
ö

Gaps

ö

```
CGGC 17
                  1111 TCCATGCGCG
```

Search completed: April 18, 2003, 07:34:29 Job time : 27.5 secs



```
RESULT 2
US-09-960-352-11656/c
'Sequence 11656, Application US/09960352
'Patent No. US20020137139A1
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TCCTTGCGCGCTGCGCCTCAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 TCCTTGCGCGCTGCGGCCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-899-651-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Si
Matches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 165, App
Sequence 165, App
Sequence 165, App
Sequence 165, App
Sequence 27, Appl
Sequence 180, App
Sequence 180, App
Sequence 180, App
Sequence 180, App
Sequence 180, App
Sequence 180, App
Sequence 180, App
Sequence 180, App
Sequence 180, App
Sequence 180, App
Sequence 180, App
Sequence 180, App
Sequence 180, App
Sequence 180, App
Sequence 181, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Appli
Sequence 11656, A
                                                                                                                                         April 18, 2003, 06:35:31; Search time 91.3333 Seconds (Without alignments) 241.975 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/DSO6_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
11: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
11: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0 US-09-899-651-7

0 US-09-960-352-11656

US-00-604-287A-165

0 US-09-604-287A-165

12 US-09-393-338-165

14 US-09-998-187-27

9 US-09-998-180

9 US-09-999-180

9 US-09-999-180

9 US-09-991-181-180

9 US-09-991-181-180

9 US-09-991-687-180

                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                              639749 seqs, 502280978 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                            US-09-270-437D-11
22
1 tccttgcgcgctgcggcctcag 22
                                                                                        OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                   IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     score:
                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
1166.8
11
                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                               Title:
Perfect :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database
                                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  00000
```

```
Sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I sequence I 
           Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence
US-10-175-737-151

US-09-99-667-180

US-10-173-706-151

US-10-175-722-151

US-10-176-482-151

US-10-176-482-151

US-10-176-913-151

US-10-180-552-151

US-10-180-557-151

US-09-990-438-180

US-09-990-438-180

US-09-990-66-180

US-09-997-66-180

US-09-997-66-180

US-10-174-572-151

US-10-174-572-151

US-10-174-582-151

                      თთთთთთთთთთთთ

      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
      C
```

## ALIGNMENTS

```
Sequence 7, Application US/09899651

Factor No. US20020111470A1

Factor No. US20020111470A1

FARENERAL INFORMATION:

APPLICANT: Chen, Yao-Tseng

APPLICANT: Tsang, Solam

APPLICANT: Stockert, Elisabeth

APPLICANT: Stockert, Elisabeth

APPLICANT: Stockert, Elisabeth

APPLICANT: Stockert, Elisabeth

APPLICANT: Stockert, Elisabeth

APPLICANT: Stockert, Islanbeth

APPLICANT: Orger, Elke

APPLICANT: Orger, Elke

APPLICANT: Orger, Elke

APPLICANT: Nath, Alexander

APPLICANT: Orger, Elke

APPLICANT: Orger, Elke

APPLICANT: Orger, Elke

APPLICANT: Orger, Elke

APPLICANT: Orger, Elke

CURRENT APPLICATION NUMBER: US/09/661, 709

FILE REFERENCE: LUD 5538

CURRENT FILING DATE: 1998-04-17

SEQ ID NO 7

LENGTH: 1946

TYDE: DANA

TYDE: DANA

TYDE: DANA

TYDE: DANA

TYDE: DANA

TYDE: DANA

TYDE: DANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 22; DB 10; Length 1946; 100.0%; Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
```

ô

```
Sequence 165, Application US/0933938A;
Sequence 165, Application US/0933938A;
Patent No. US20020102602A1
GENERAL INFORMATION:
APPLICANT: Vidiu, Jiang
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: MIVENTION: COMPOSITIONS FOR THE REATMENT AND TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.470CZ
CURRENT FILIAG DATE: 1999-06-23
CURRENT FILIAG DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 315
SOFTWARE: PREESEQ for Windows Version 3.0
SEQ ID NO 165
SEQ ID NO 165
                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.4%; Score 16.8; DB 10; Length 462; 90.0%; Pred. No. 62; tive 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                         DB 10;
                                                                                                                                                                                                                                                                                                                                                                    76.4%; Score 16.8; I
90.0%; Pred. No. 62;
tive 0; Mismatches
FILE REFERENCE: 210121.470C7
CURRENT APPLICATION NUMBER: US/09/604,287A
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 489
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 165
LENGTH: 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 165, Application US/10007805
Patent No. US20020150581A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1)...(462)
; OTHER INFORMATION: n = A,T,C or G US-09-339-338-165
                                                                                                                                                                               TYPE: DNA

| ORGANISM: Homo sapien
| PEATURE:
| NAME/KEY: misc_feature
| LOCATION: (1)...(462)
| OTHER INFORMATION: n = A,T,C or G

US-09-604-287A-165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xu, Jiangchun
Harlocker, Susan L.
Hepler, William T.
Henderson, Robert A.
Fanger, Gary R.
Vedvick, Thomas S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Jiang, Yuqiu
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 recrirececerrececere 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 recrirececeriececere 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 rcrrrdcrcdcrdcdccrc 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 76.4
Query Match
Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
US-10-007-805-165/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-09-339-338-165/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGIH: 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                 APPLICANT: Byatt, John C.
APPLICANT: Machialagan, Wagappan
APPLICANT: Mathialagan, Wagappan
TITLE OF INVENTION: WUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: WUSCLE AND FAT DEPOSITION
FILLE REFERENCE: 15511.06/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 11656
LENGTH: 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: misc_feature
; LOCATION: 10, 33, 36, 49, 198, 222, 243, 278, 357, 385; 399, 405, 437
; OTHER INFORMATION: n = A,T,C or G
US-10-076-622-165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 165, Application US/09604287A

Patent No. US20020064872A1

GENERAL INFORMATION:
APPLICANT: Jiang, Yuqiu
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 76.4%; Score 16.8; DB 10; Length 386; Best Local Similarity 90.0%; Pred. No. 64; Aismatches 18; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 9; Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 165, Application US/10076622

Sequence 165, Application US/10076622

Publication No. US20030023036A1

GENERAL INFORMATION:
APPLICANT: Houghton, Raymond L.
APPLICANT: Bleath, Paul R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TF
TITLE OF INVENTION: COMPOSITIONS OF BREAST CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
CURRENT APPLICATION UNMERR: US/10/076,622

CURRENT FILING DATE: 2002-02-13

NUMBER OF SEQ ID NOS: 627

SOSTWARE: FREESEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                            TYPE: DNA CRGANISM: Bos taurus CTPER INFORMATION: Clone ID: 50-LIB3057-003-Q1-K1-E10 US-09-960-352-11656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 76.4%; Score 16.8; I Best Local Similarity 90.0%; Pred. No. 62; Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCTTGCGCGCTGCGGCCTC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91 TCTTTGCTCGCTGCGCCTC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     326 ccrréccédcrécéccich 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 CCTTGCGCGCTGCGGCCTCA 21
                                  APPLICANT: Warren, Wesley C. APPLICANT: Tao, Nengbing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
US-09-604-287A-165/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
```

ö

```
R APPLICATION NUMBER: 60/088212
R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088217
R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/086555
R PILING DATE: 1998-06-09
                                                                                                                                                                                                                                                                                   Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                                                              Paoni, Nicholas F.
                                                                                                                                                                                 Napier, Mary A.
                                                                                                                                                                                                                   Pan,James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature

: LOCATION: 10, 33, 36, 49, 198, 222, 243, 278, 357, 385, 399, 405, 437

: OTHER INFORMATION: n = A,T,C or G

US-10-007-805-165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27, Application US/09808387
Sequence 27, Application US/09808387
GENERAL INFORMATION:
APPLICANT: Kaia Palm
APPLICANT: Centines Research
TITLE OF INVENTION: MAMMALIAM NEURALIZED FAMILY OF
TITLE OF INVENTION: MAMMALIAM NEURALIZED FAMILY OF
TITLE OF INVENTION: MAMMALIAM NEURALIZED FAMILY OF
TITLE OF INVENTION: MAMMALIAM NEURALIZED FAMILY OF
TITLE OF INVENTION: MAMMALIAM NEURALIZED FAMILY OF
TITLE OF INVENTION: MAMMALIAM NEURALIZED FAMILY OF
TITLE OF INVENTION: MAMMALIAM NEURALIZED FAMILY OF
TITLE OF INVENTION NUMBER: US/09/808,387
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 48
SEG ID NOS: 48
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID NOS: 40
SEG ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16.4; DB 10; Length 1641;
Pred. No. 74;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match

76.4%; Score 16.8; DB 12; Length 462;
Best Local Similarity 90.0%; Pred. No. 62;
Matches 18; Conservative 0; Mismatches 2; Indels 0
                                  APPLICANT: Durham, Margarita
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: ADD DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.470C10
CURRENT PEPLICATION NUMBER: US/10/007,805
CURRENT FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 593
SOFTWARE: PSELSEQ FOR Windows Version 4.0
LENGTH: 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 180, Application US/09992598
Fatent No. US200201660384A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Beter, Kevin P.
APPLICANT: Botsein, David
APPLICANT: Beter, Kevin P.
APPLICANT: Beter, Application Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Contr
APPLICANT: McNeill, Patricia D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 rccrrgcgcgcrgcggccrc 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 TCTTTGCTCGCTGCGGCCTC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 74.5%;
Best Local Similarity 94.4%;
Matches 17; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1011 TCCTGGCGCGCTGCGGCC 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TCCTTGCGCGCTGCGGCC 18
                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; SEQ ID NO 27
| LENGTH: 1641
| TYPE: DNA
| ORGANISM: Rat
US-09-808-387-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-992-598-180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -09-808-387-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
```

```
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPLICATION NUMBER: 60/090435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090252
FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LING DATE: 1998-06-23
PLICATION NUMBER: 60/090429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 806680/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LICATION NUMBER: 60/089948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/089952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATION NUMBER: 60/090246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/090349
FILING DATE: 1998-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLICATION NUMBER: 60/090355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATION NUMBER: 60/090431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LICATION NUMBER: 60/089947
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/088876
FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/089105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLING DATE: 1998-06-17
PPLICATION NUMBER: 60/089599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LING DATE: 1998-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60/089653
                                                                                                                                                                                             FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088826
FILING DATE: 1998-06-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60/089440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/089512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILING DATE: 1998-06-16
PPLICATION NUMBER: 60/089514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60/089532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ICATION NUMBER: 60/089538
                                          FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088742
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088810
                                                                                                                                                                                                                                                                     ICATION NUMBER: 60/088858
                                                                                                                                             FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/08824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LING DATE: 1998-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1998-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1998-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1998-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1998-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LING DATE: 1998-06-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 998-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LING DATE: 1998-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LING DATE: 1998-06-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LING DATE: 1998-06-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1998-06-1
                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1998-06-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LING DATE: 1998-06-.
PLICATION NUMBER: 60
                                                                                                                                                                                                                                                                                               FILING DATE: 1998-06-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH PRICH
```

PRIOR FILING DATE: 1938-06-24

PRIOR APPLICATION NUMBER: 60/090542

PRIOR APPLICATION NUMBER: 60/090542

PRIOR PILING DATE: 1938-06-24

PRIOR PILING DATE: 1938-06-25

PRIOR APPLICATION NUMBER: 60/090576

PRIOR APPLICATION NUMBER: 60/090578

PRIOR PILING DATE: 1938-06-25

PRIOR PILING DATE: 1938-06-25

PRIOR PILING DATE: 1938-06-25

PRIOR PILING DATE: 1938-06-25

PRIOR PILING DATE: 1938-06-25

PRIOR PILING DATE: 1938-06-26

PRIOR PILING DATE: 1938-06-26

PRIOR PILING DATE: 1938-06-26

PRIOR PILING DATE: 1938-06-26

PRIOR PILING DATE: 1938-06-26

PRIOR PILING DATE: 1938-06-26

PRIOR PILING DATE: 1938-06-26

PRIOR PILING DATE: 1938-06-26

PRIOR PILING DATE: 1938-06-26

PRIOR PILING DATE: 1938-06-26

PRIOR PILING DATE: 1938-06-26

PRIOR PILING DATE: 1938-06-26

PRIOR PILING DATE: 1938-06-26

PRIOR PILING DATE: 1938-06-26

PRIOR PILING DATE: 1938-06-26

PRIOR PILING DATE: 1938-06-26

PRIOR PILING DATE: 1938-07-01

PRIOR PILING DATE: 1938-07-01

PRIOR PILING DATE: 1938-07-01

PRIOR PILING DATE: 1938-07-01

PRIOR PILING DATE: 1938-07-01

PRIOR PILING DATE: 1938-07-02

PRIOR PILING DATE: 1938-07-02

PRIOR PILING DATE: 1938-07-02

PRIOR PILING DATE: 1938-07-02

PRIOR PILING DATE: 1938-07-02

PRIOR PILING DATE: 1938-07-02

PRIOR PILING DATE: 1938-07-02

PRIOR PILING DATE: 1938-07-02

PRIOR PILING DATE: 1938-07-02

PRIOR APPLICATION NUMBER: 60/09183

PRIOR PILING DATE: 1938-07-02

PRIOR APPLICATION NUMBER: 60/09183

PRIOR PILING DATE: 1938-07-02

PRIOR APPLICATION NUMBER: 60/09182

PRIOR PILING DATE: 1938-07-02

PRIOR APPLICATION NUMBER: 60/09182

PRIOR PILING DATE: 1938-07-03

PRIOR PILING DATE: 1938-07-04

PRIOR PILING DATE: 1938-07-07

PRIOR PILING DATE: 1938-07-07

PRIOR APPLICATION NUMBER: 60/09183

PRIOR PILING DATE: 1938-07-07

PRIOR APPLICATION NUMBER: 60/09183

PRIOR PILING DATE: 1938-07-07

PRIOR PILING DATE: 1938-07-07

PRIOR PILING DATE: 1938-07-07

PRIOR PILING DATE: 1938-07-07

PRIOR PILING DATE: 1938-07-07

PRIOR PILING DATE: 1938-07-07

PRIOR PILING DATE: 1938-07-07

PRIOR PILING DATE: 1938-07-07

PRIOR PI

Oy 5 TGGGGGTGGGGCTCAG 22

Db 98 TGGGGCTGCTGCTCAG 115

ö

GEOUGH 180
Sequence 180, Application US/09989293A
patent No. US20020177164A1
GENERAL INFORMATION:
APPLICANT: Ashkenati,Avi J.
APPLICANT: Baker,Kevin P.
APPLICANT: Bester,Kevin P.
APPLICANT: Bester, David
APPLICANT: Beston, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Mary E.
APPLICANT: Gerber, Mary E.
APPLICANT: Gedber, Panspeter
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi,J.Christopher
APPLICANT: Grimaldi,J.Christopher
APPLICANT: Grimaldi,J.Christopher
APPLICANT: Grimaldi,J.Christopher
APPLICANT: Grimaldi,J.Christopher
APPLICANT: Grimaldi,J.Christopher
APPLICANT: Grimaldi,J.Christopher
APPLICANT: Grimaldi,J.Christopher
APPLICANT: Grimaldi,J.Christopher
APPLICANT: Grimaldi,J.Christopher
APPLICANT: Grimaldi,J.Christopher
APPLICANT: Grimaldi,J.Christopher
APPLICANT: Grimaldi,J.Christopher
APPLICANT: Grimaldi,J.Christopher
APPLICANT: Grimaldi,J.Christopher
APPLICANT: Grimaldi,J.Christopher
APPLICANT: Grimaldi,J.Christopher
APPLICANT: Grimaldi,J.Christopher
APPLICANT: Grimaldi,J.Christopher
APPLICANT: Grimaldi,J.Christopher
APPLICANT: Grimaldi,J.Christopher
APPLICANT: Grimaldi,J.Christopher
APPLICANT: Grimaldi,J.Christopher
APPLICANT: Grimaldi,J.Christopher
APPLICANT: Grimaldi,J.Christopher
APPLICANT: Grimaldi,J.Christopher
APPLICANT: Grimaldi,J.Christopher
APPLICANT: Grimaldi,J.Christopher

Paoni, Nicholas F

```
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/08824
PRIOR PILING DATE: 1998-06-10
PRIOR PILING DATE: 1998-06-10
PRIOR PILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/08861
PRIOR APPLICATION NUMBER: 60/08861
PRIOR PILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/08976
PRIOR PILING DATE: 1998-06-12
PRIOR PILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089105
PRIOR PILING DATE: 1998-06-16
PRIOR PILING DATE: 1998-06-16
PRIOR PILING DATE: 1998-06-16
PRIOR PILING DATE: 1998-06-16
PRIOR PILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR PILING DATE: 1998-06-16
PRIOR PELING DATE: 1998-06-17
PRIOR PELING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1998-06-23
RIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PLICATION NUMBER: 60/090431
PRIOR PLICATION NUMBER: 60/090435
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NA APPLICATION NUMBER: 6/090246

R FILING DATE: 1998-06-22

R APPLICATION NUMBER: 60/090252

R FILING DATE: 1998-06-22

R APPLICATION NUMBER: 60/090254

R FILING DATE: 1998-06-22

R APPLICATION NUMBER: 60/090349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NA APPLICATION NUMBER: 60/090445

R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090472

R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090535

R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090542
FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60/090557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/
FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR
PRIOR
PRIOR
                                                                       APPLICANT: Name, Daniel A.
APPLICANT: Watanabo, Colin K.
APPLICANT: Watanabo, Colin K.
APPLICANT: Watanabo, Colin K.
APPLICANT: Watanabo, Colin K.
APPLICANT: Watanabo, Colin K.
APPLICANT: Watanabo, Colin K.
APPLICANT: Suno, Tabuda Emain I.
TITLE OF INVENTION: Secreted and fransmembrane Polypeptides and Nucleic Title Of Invention Mayors: 105/11/20
FILE REFERENCE: P2730PLCGG and MAYORS: 105/11/20
FILE REPRENCE: P2730PLCGG
FILE REPLICATION WADRES: 6/06250
FILE REDIG PLICATION WADRES: 6/06250
FILE REPRENCE: 1997-11-12
FILE REPRENCE: 1997-11-12
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 1997-11-13
FILE REPRENCE: 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088810
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
```

```
TITLE OF INVENTION: Secreted and Transmembrane. Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730PIC61
CURRENT APPLICATION NUMBER: US/09/989,735
CURRENT APPLICATION NUMBER: 60/049787
PRIOR PILING DATE: 1997-06-16
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PAPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-24
PRIOR PILING DATE: 1997-11-24
PRIOR PILING DATE: 1997-11-24
PRIOR PILING DATE: 1997-11-24
PRIOR PILING DATE: 1998-02-25
PRIOR PILING DATE: 1998-02-25
PRIOR PILING DATE: 1998-02-25
PRIOR PILING DATE: 1998-02-25
PRIOR PILING DATE: 1998-02-25
PRIOR PILING DATE: 1998-02-25
PRIOR PILING DATE: 1998-03-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR PELING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-09
PRIOR FILING DATE: 1998-06-09
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/08873
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRIUN FILLING LALLS: 129 COOL OF PRIOR FILLING DATE: 1998-06-04
PRIOR FILLING DATE: 1998-06-04
PRIOR FILLING DATE: 1998-06-04
PRIOR FILLING DATE: 1998-06-04
PRIOR PILLING DATE: 1998-06-04
PRIOR PILLING DATE: 1998-06-04
PRIOR PILLING DATE: 1998-06-04
PRIOR PAPLICATION NUMBER: 60/088167
PRIOR PLING DATE: 1998-06-05
PRIOR PLING DATE: 1998-06-05
PRIOR PILLING DATE: 1998-06-05
PRIOR PILLING DATE: 1998-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/087759
FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/084600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/087106
FILING DATE: 1998-05-28
APPLICATION NUMBER: 60/087607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/088021
FILING DATE: 1998-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/088025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1998-06-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1998-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 16.4; DB 9; Length 1759;
Pred. No. 73;
0; Mismatches 1; Indels 0,
                                          PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 180, Application US/09989735 Publication No. US20020193299A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grimaldi,J.Christopher
Gurney,Austin L.
Kljavin,Ivar J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         errara, Napoleone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     loy, Margaret Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 rececerrecrecione 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stewart, Timothy
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gerritsen, Mary E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s rececerrececercae 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lapier, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Godowski, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ong, Sherman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

```
PRIOR PLINKO DATE: 1998-06-11
PRIOR PRICATION WARBER: 60/089105
PRIOR PRICATION WARBER: 60/089105
PRIOR PRICATION WARBER: 60/089105
PRIOR PRICATION WARBER: 60/089105
PRIOR PLINKO DATE: 1998-06-11
PRIOR PLINKO DATE: 1998-06-16
PRIOR PLINKO DATE: 1998-06-16
PRIOR PLINKO DATE: 1998-06-16
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PLINKO DATE: 1998-06-17
PRIOR PRILIKO DATE: 1998-06-17
PRIOR PRILIKO DATE: 1998-06-17
PRIOR PRILIKO DATE: 1998-06-17
PRIOR PRILIKO DATE: 1998-06-17
PRIOR PRILIKO DATE: 1998-06-17
PRIOR PRILIKO DATE: 1998-06-17
PRIOR PRILIKO DATE: 1998-06-17
PRIOR PRILIKO DATE: 1998-06-17
PRIOR PRILIKO DATE: 1998-06-17
PRIOR PRILIKO DATE: 1998-06-17
PRIOR PRILIKO DATE: 1998-06-17
PRIOR PRILIKO DATE: 1998-06-17
PRIOR PRILIKO DATE: 1998-06-17
PRIOR PRILIKO DATE: 1998-06-17
PRIOR PRILIKO DATE: 1998-06-17
PRIOR PRILIKO DATE: 1998-06-17
PRIOR PRILIKO DATE: 1998-06-17
PRIOR PRILIKO DATE: 1998-06-17
PRIOR PRILIKO DATE: 1998-06-17
PRIOR PRILIKO DATE: 1998-06-17
PRIOR PRILIKO DATE: 1998-06-17
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITLE OF INVENTION: Acids Encoding the Same ILE REFERENCE: P2730PIC19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 9; Length 1759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16.4; DP
Pred. No. 73;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATION NUMBER: US/09/990,444
PRIOR FILING DATE: 1998-06-25
PRIOR PLING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/99
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grimaldi, J. Christopher
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USOD.

US-09-990-44.

I Sequence 180, Apr.

Publication No. US2002.

GENERAL INFORMATION:

APPLICANT: Baker Kevin P.

"ICANT: Botstein, David
"". Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 74.5%;
Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 recederecrecreating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 TGCGCGCTGCGGCCTCAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fong, Sherman
Gerber, Hanspeter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gerritsen, Mary E
Goddard, Audrey
Godowski, Paul J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pan, James
Paoni, Nicholas F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kljavin, Ivar J.
Napier, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

60/0 60/0	PELLING DATE: 1998- APPLICATION NUMBER PILING DATE: 1998- APPLICATION NUMBER PILING DATE: 1998- APPLICATION NUMBER PILING DATE: 1998- APPLICATION NUMBER FILING DATE: 1998- APPLICATION NUMBER FILING DATE: 1998- APPLICATION NUMBER PILING DATE: 1998- APPLICATION NUMBER PILING DATE: 1998 APPLICATION NUMBER PILING DATE: 1998 APPLICATION NUMBER APPLICATION NU

PRIOR APPLICATION NUMBER: 60/089512
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-22
PRIOR PPLICATION NUMBER: 60/09045
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PELICATION NUMBER: 60/09045
PRIOR PILING DATE: 1998-06-24
PRIOR PELICATION NUMBER: 60/09045
PRIOR PILING DATE: 1998-06-24
PRIOR PELICATION NUMBER: 60/09045
PRIOR PILING DATE: 1998-06-24
PRIOR PELICATION NUMBER: 60/09045
PRIOR PILING DATE: 1998-06-24
PRIOR PELICATION NUMBER: 60/09045
PRIOR PILING DATE: 1998-06-24
PRIOR PELICATION NUMBER: 60/09045
PRIOR PILING DATE: 1998-06-24
PRIOR PELICATION NUMBER: 60/09065
PRIOR PELING DATE: 1998-06-24
PRIOR PELICATION NUMBER: 60/09065
PRIOR PELING DATE: 1998-06-25
PRIOR PELICATION NUMBER: 60/09065
PRIOR PELING DATE: 1998-06-25
PRIOR PELICATION NUMBER: 60/09065
PRIOR PELING DATE: 1998-06-25
PRIOR PELICATION NUMBER: 60/09065
PRIOR PELING DATE: 1998-06-25
PRIOR PELICATION NUMBER: 60/09065
PRIOR PELING DATE: 1998-06-25
PRIOR PE

```
FRICK ALLING DATE: 1998 -02-25

PRIOR FILING DATE: 1998 -03-20

PRIOR FILING DATE: 1998 -03-20

PRIOR PLING DATE: 1998 -03-20

PRIOR PLING DATE: 1998 -03-20

PRIOR PLING DATE: 1998 -05-07

PRIOR PLING DATE: 1998 -05-07

PRIOR PLING DATE: 1998 -05-07

PRIOR PLING DATE: 1998 -05-08

PRIOR PLING DATE: 1998 -05-08

PRIOR PLING DATE: 1998 -05-02

PRIOR PLING DATE: 1998 -06-02

PRIOR PAPLICATION NUMBER: 60/087609

PRIOR PAPLICATION NUMBER: 60/087609

PRIOR PAPLICATION NUMBER: 60/087509

PRIOR PLING DATE: 1998 -06-02

PRIOR PLING DATE: 1998 -06-04

PRIOR PLING DATE: 1998 -06-04

PRIOR PLING DATE: 1998 -06-04

PRIOR PLING DATE: 1998 -06-04

PRIOR PLING DATE: 1998 -06-04

PRIOR PLING DATE: 1998 -06-04

PRIOR PLING DATE: 1998 -06-04

PRIOR PLING DATE: 1998 -06-04

PRIOR PLING DATE: 1998 -06-04

PRIOR PLING DATE: 1998 -06-04

PRIOR PLING DATE: 1998 -06-04

PRIOR PLING DATE: 1998 -06-04

PRIOR PLING DATE: 1998 -06-04

PRIOR PLING DATE: 1998 -06-04

PRIOR PLING DATE: 1998 -06-05

PRIOR PLING DATE: 1998 -06-05

PRIOR PLING DATE: 1998 -06-05

PRIOR PLING DATE: 1998 -06-05

PRIOR PLING DATE: 1998 -06-05

PRIOR PLING DATE: 1998 -06-05

PRIOR PRILING DATE: 1998 -06-05

PRIOR PLING DATE: 1998 -06-05

PRIOR PRILING DATE: 1998 -06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR APPLICATION NUMBER: 60/088738
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R APPLICATION NUMBER: 60/08810
R FILING DATE: 1998-06-10
R PILING DATE: 1998-06-10
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/08824
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/08858
R APPLICATION NUMBER: 60/08858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1998-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730PICG9 CURRENT APPLICATION NUMBER: US/09/989,730 CURRENT FILING DATE: 2001-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 9; Length 1759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
74.5%; Score 16.4; I
Best Local Similarity 94.4%; Pred. No. 73;
Matches 17; Conservative 0; Mismatches
PHOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/09163
PRIOR APPLICATION NUMBER: 60/09178
PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
                                                            CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR PILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR PILING DATE: 1997-111-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PILING DATE: 1997-111-13
PRIOR PILING DATE: 1997-111-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Godowski, Paul J.
Grimaldi, J. Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98 receceraciones 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roy, Margaret Ann
Stewart, Timothy A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 TGCGCGCTGCGGCCTCAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gurney, Austin L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Napier, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumas, Danie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-989-730-180
```

ઠે

```
APPLICATION NUMBER: 60/090862
ATMING DATE: 1998-06-26
APPLICATION NUMBER: 60/090863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090690
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090696
FILING DATE: 1998-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/091544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLICATION NUMBER: 60/090535
LING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/090542
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090557
FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LICATION NUMBER: 60/090540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPLICATION NUMBER: 60/090676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LING DATE: 1998-06-24
PLICATION NUMBER: 60/090435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LING DATE: 1998-06-24
PLICATION NUMBER: 60/090472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLICATION NUMBER: 60/090429
LING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATION NUMBER: 60/090444
G DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATION NUMBER: 60/090445
                                                                                                                                                                                                                                                                                                                                                                                                                                                ING DATE: 1998-06-23
LICATION NUMBER: 60/090355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LICATION NUMBER: 60/090431
                                                                                                                                                                                                                                                                                                                                                                                                                           60/090349
                                                                                                                                                                                                                                            LING DATE: 1998-06-19
PLICATION NUMBER: 60/089948
                                                                                                                                                                                                                                                                                                                                                         ICATION NUMBER: 60/090252
                                                                                                                                                                                                                                                                                                                                                                                           60/090254
                                                                                                                                                                                                                                                                                                                           60/090246
                                                                        FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089653
FILING DATE: 1998-06-17
                                                                                                                                                                                                                            60/089947
                                                                                                                                                                                                                                                                               FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089952
          TLING DATE: 1998-00-1,
PPLICATION NUMBER: 60/089599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            998-06-24
                                                                                                                                                                                                          NG DATE: 1998-06-18
ICATION NUMBER: 60/
                                                                                                                                                                                                                                                                                                                                                                                                            1998-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1998-06-23
                                                                                                                                                                                                                                                                                                           FILING DATE: 1998-06-19
                                                                                                                                             1998-06-
PRIOR A
PRIOR F
PRIOR F
PRIOR P
PRIOR P
PRIOR P
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
PRIOR F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR
```

```
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C14 CURRENT APPLICATION NUMBER: US/09/990,436 CURRENT FILING DATE: 2001-11-14
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                 Length 1759;
                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                          DB 9;
                                                                                                                                                                                                                                                                                        Query Match

74.5%; Score 16.4; E
Best Local Similarity 94.4%; Pred. No. 73;
Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR PELLING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-12
PRIOR PLING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065710
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-13
                                                                                                          DR FILING DATE: 1998-07-02
DR APPLICATION NUMBER: 60/091978
DR FILING DATE: 1998-07-07
DR APPLICATION NUMBER: 60/091982
DR FILING DATE: 1998-07-07
DR APPLICATION NUMBER: 60/092182
DR FILING DATE: 1998-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 180, Application US/09990436 Publication No. US20020198148A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60/083322
ION NUMBER: 60/091519
ATE: 1998-07-02
                                                                FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roy, Margaret Ann
                                                                                                                                                                                                                                                                                                                                                                                                                               98 rececerrecrecerra
                                                                                                                                                                                                                                                                                                                                                                                     s rececerrecedecricae 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ashkenazi, Avi J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Napier, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stewart,
                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
PRIOR APPLICATION NUMBER: 60/084600
PRIOR PLICATION NUMBER: 60/08106
PRIOR PLICATION NUMBER: 60/08106
PRIOR PLICATION NUMBER: 60/08106
PRIOR PLICATION NUMBER: 60/08107
PRIOR PLILING DATE: 1998-66-02
PRIOR PLILING DATE: 1998-66-03
PRIOR PLILING DATE: 1998-66-03
PRIOR PLILING DATE: 1998-66-03
PRIOR PLILING DATE: 1998-66-03
PRIOR PLILING DATE: 1998-66-04
PRIOR PLILING DATE: 1998-66-04
PRIOR PLILING DATE: 1998-66-04
PRIOR PLILING DATE: 1998-66-04
PRIOR PLILING DATE: 1998-66-04
PRIOR PLILING DATE: 1998-66-04
PRIOR PLILING DATE: 1998-66-04
PRIOR PLILING DATE: 1998-66-04
PRIOR PLILING DATE: 1998-66-04
PRIOR PLILING DATE: 1998-66-04
PRIOR PLILING DATE: 1998-66-04
PRIOR PLILING DATE: 1998-66-04
PRIOR PLILING DATE: 1998-66-04
PRIOR PLILING DATE: 1998-66-04
PRIOR PLILING DATE: 1998-66-04
PRIOR PLILING DATE: 1998-66-04
PRIOR PLILING DATE: 1998-66-04
PRIOR PLILING DATE: 1998-66-04
PRIOR PLILING DATE: 1998-06-04
PRIOR PLILING DATE: 1998-06-01
PRIOR PLILING DATE: 1998-06-01
PRIOR PLILING DATE: 1998-06-01
PRIOR PLILING DATE: 1998-06-01
PRIOR PLILING DATE: 1998-06-01
PRIOR PLILING DATE: 1998-06-01
PRIOR PLILING DATE: 1998-06-01
PRIOR PLILING DATE: 1998-06-01
PRIOR PLILING DATE: 1998-06-01
PRIOR PLILING DATE: 1998-06-01
PRIOR PLILING DATE: 1998-06-01
PRIOR PLILING DATE: 1998-06-01
PRIOR PLILING DATE: 1998-06-01
PRIOR PLILING DATE: 1998-06-01
PRIOR PLILING DATE: 1998-06-01
PRIOR PLILING DATE: 1998-06-01
PRIOR PLILING DATE: 1998-06-01
PRIOR PRILING DATE
```

PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-18
PRIOR PELICATION NUMBER: 60/08961
PRIOR FILING DATE: 1998-06-18
PRIOR PILICATION NUMBER: 60/08901
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-22
PRIOR PILING DATE: 1998-06-22
PRIOR PILING DATE: 1998-06-22
PRIOR PILING DATE: 1998-06-22
PRIOR PILING DATE: 1998-06-22
PRIOR PILING DATE: 1998-06-22
PRIOR PILING DATE: 1998-06-22
PRIOR PILING DATE: 1998-06-22
PRIOR PILING DATE: 1998-06-22
PRIOR PILING DATE: 1998-06-23
PRIOR PILING DATE: 1998-06-23
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-2

g ઠે

```
PRIOR AFFILIAND MANBER: 60/08824
PRIOR APPLICATION NUMBER: 60/08824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/08826
PRIOR PILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-11
PRIOR FILING DATE: 1998-06-11
PRIOR FILING DATE: 1998-06-11
PRIOR PILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/08861
PRIOR PILING DATE: 1998-06-12
PRIOR PILING DATE: 1998-06-16
PRIOR PILING DATE: 1998-06-16
PRIOR PILING DATE: 1998-06-16
PRIOR PILING DATE: 1998-06-16
PRIOR PILING DATE: 1998-06-16
PRIOR PILING DATE: 1998-06-16
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/088738
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088742
FILING DATE: 1998-06-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088810
                                                                                                                                                                                                                                                                                                                                                                                                 APPLING DATE: 1998-06-04
APPLICATION NUMBER: 60/088326
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088167
PILING DATE: 1998-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/088212
FILING DATE: 1998-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/088217
FILING DATE: 1998-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/088655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/088734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/088202
FILING DATE: 1998-06-05
                                                           FILING DATE: 1998-06-03
APPLICATION NUMBER: 60/088021
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088025
                                                                                                                                                                                                         FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088028
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088029
                                                                                                                                                                                                                                                                                                         FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088030
                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088033
                                                                                                                                                           FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1998-06-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1998-06-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Mucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Mucleic TITLE OF INVENTION: Acids Encoding the Same TITLE OF INVENTION: Acids Encoding the Same TITLE REFERENCE: P2730PIC53
CURRENT APPLICATION NUMBER: US/09/991,181
CURRENT FILING DATE: 2001-11-16
PRIOR PILING DATE: 1997-06-16
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-24
PRIOR PILING DATE: 1997-11-24
PRIOR PLING DATE: 1997-11-24
PRIOR PLING DATE: 1997-11-24
                                                                                                                                                                                                       ö
                                                                                                                                                                                                            Gaps
                                                                                                                                                           DB 9; Length 1759;
                                                                                                                                                                                                            1; Indels
                                                                                                                                                             ; Score 16.4; DB; Pred. No. 73; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1998-02-25
APPLICATION NUMBER: 60/078910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087609
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 180, Application US/09991181
Publication No. US20020197615A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/083322
                    PRIOR PILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR PILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Grimaldi,J.Christopher
Gurney,Austin L.
Kljavin,Ivar J.
APPLICATION NUMBER: 60/091978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JLING DATE: 1998-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1998-03-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1998-05-28
                                                                                                                                                                     Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ferrara, Napoleone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              erritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aoni, Nicholas F
                                                                                                                                                                                                                                                                                                                      98 recederacracraca 115
                                                                                                                                                                                                                                                                     s rececerrecescercies 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rber, Hanspeter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baker, Kevin P.
Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wapier, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Godowski, Paul
                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-09-991-181-180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR
PRIOR
PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
```

ô

```
PRIOR APPLICATION NUMBER: 60/08998
PRIOR PLILING DATE: 1998-06-19
PRIOR PELING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/080524
PRIOR PELING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090246
PRIOR PELING DATE: 1998-06-22
PRIOR PELING DATE: 1998-06-23
PRIOR PELING DATE: 1998-06-23
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-03
PRIOR PELING DATE:
```

APELICANT: Thumas, Daniel
APELICANT: Thumas, Daniel
APELICANT: Thumas, Daniel
APELICANT: Thumas, Daniel
APELICANT: Watanabe, Colin K.
APELICANT: William I.
APELICANT: Manage P. Mickey
APELICANT: Mood, William I.
TILLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
CURRENT FILING DATE: 1997-10-14
PRIOR APELICATION NUMBER: US/0993,687
CURRENT FILING DATE: 1997-0-17
PRIOR PELICATION NUMBER: 60/06250
PRIOR PELICATION NUMBER: 60/06250
PRIOR PELICATION NUMBER: 60/06211
PRIOR APELICATION NUMBER: 60/06311
PRIOR APELICATION NUMBER: 60/06311
PRIOR APELICATION NUMBER: 60/06311
PRIOR APELICATION NUMBER: 60/06311
PRIOR PELING DATE: 1997-11-14
PRIOR APELICATION NUMBER: 60/08312
PRIOR PELING DATE: 1998-10-25
PRIOR FILING DATE: 1998-0-25
PRIOR PELING DATE: 1998-0-25
PRIOR PELING DATE: 1998-0-6-0
PRIOR PELING DATE: 1998-0-6-0
PRIOR PELING DATE: 1998-0-6-0
PRIOR PELING DATE: 1998-0-6-0
PRIOR PELING DATE: 1998-0-6-0
PRIOR PELING DATE: 1998-0-6-0
PRIOR PELING DATE: 1998-0-6-0
PRIOR PELING DATE: 1998-0-6-0
PRIOR PELING DATE: 1998-0-6-0
PRIOR PELING DATE: 1998-0-6-0
PRIOR PELING DATE: 1998-0-6-0
PRIOR PELING DATE: 1998-0-6-0
PRIOR PELING DATE: 1998-0-6-0
PRIOR PELING DATE: 1998-0-6-0
PRIOR PELING DATE: 1998-0-6-0
PRIOR PELING DATE: 1998-0-6-0
PRIOR PELING DATE: 1998-0-6-0
PRIOR PELING DATE: 1998-0-6-0
PRIOR PELING DATE: 1998-0-6-0
PRIOR PELING DATE: 1998-0-6-0
PRIOR PELING DATE: 1998-0-6-0 Gaps ö Score 16.4; DB 9; Length 1759; Pred. No. 73; 0; Mismatches 1; Indels 0; RESULT 15
US-09-993-687-180
; Sequence 180, Application US/09993687
; Publication No. US20020198149A1
; RENERAL INFORMATION:
; APPLICANT: Ashkenai, Avi J.
; APPLICANT: Baker, Kevin P.
nopilCANT: Botstein, David Goddard, Audrey Godowski, Paul J. Grimaldi, J.Christopher FILING DATE: 1998-06-03 APPLICATION NUMBER: 60/088021 FILING DATE: 1998-06-04 Query Match 74.5%; Best Local Similarity 94.4%; Matches 17; Conservative Roy, Margaret Ann Stewart, Timothy A Tumas, Daniel Ferrara, Napoleone 5 TGCGCGCTGCGGCCTCAG 22 Pan, James Paoni, Nicholas F. Wapier, Mary A. Fong, Sherman ò g

DB 9; Length 1759; 74.5%; Score 16.4; D 94.4%; Pred. No. 73; ive 0; Mismatches PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090252
PRIOR APPLICATION NUMBER: 60/090254
PRIOR APPLICATION NUMBER: 60/090254
PRIOR APPLICATION NUMBER: 60/090254
PRIOR APPLICATION NUMBER: 60/090349
PRIOR PILING DATE: 1998-06-23
PRIOR PELLING DATE: 1998-06-23
PRIOR PELLING DATE: 1998-06-23
PRIOR PILING DATE: 1998-06-23
PRIOR PILING DATE: 1998-06-23
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090540
PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR APPLICATION NUMBER: 60/090695
PRIOR APPLICATION NUMBER: 60/090695
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-03
PRIOR PILING DATE: 1998-07-03
PRIOR PILING DATE: 1998-07-03
PRIO Query Match
Best Local Similarity 94.4
Matches 17; Conservative

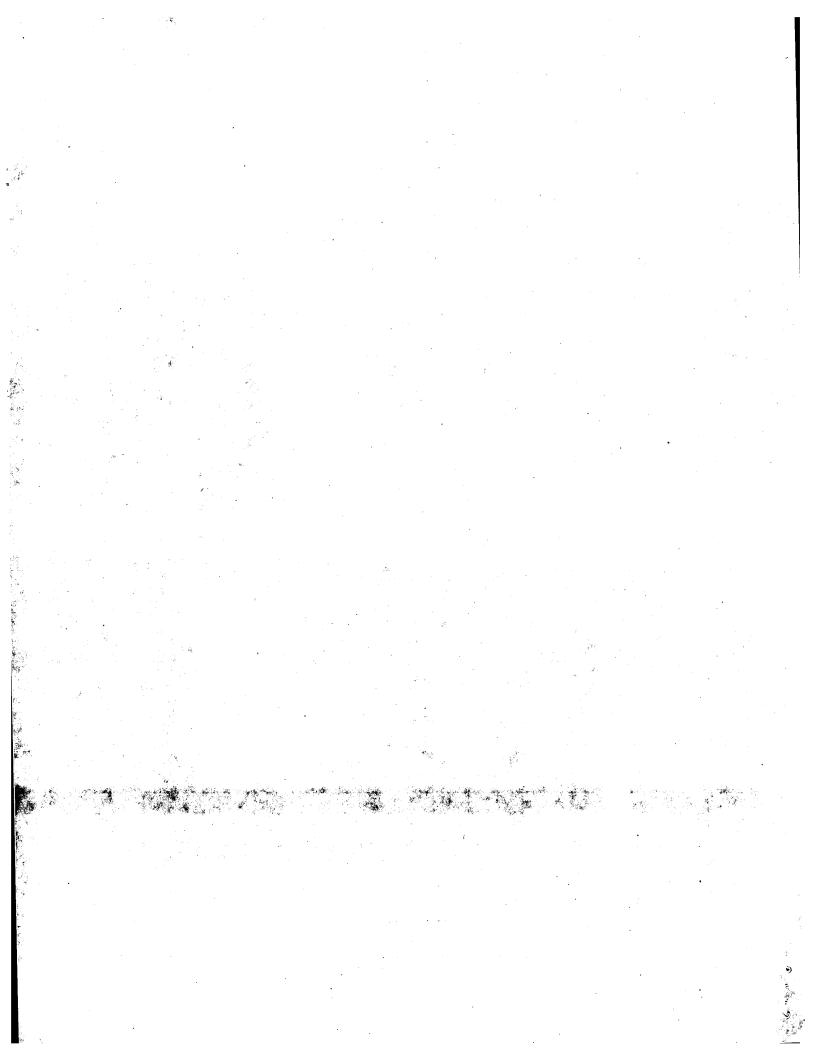
ö

ö

Indels

94.48;

8 g



```
April 18, 2003, 05:48:17 ; Search time 1211 Seconds (without alignments) 456.759 Million cell updates/sec
                                                                                                                                                                                                                                                                                      1/pna/USO39A_COMB. seq:
1/pna/USO39A_COMB. seq:
1/pna/USO39A_COMB. seq:
1/pna/USO39A_COMB. seq:
1/pna/USO39B_COMB. seq:
1/pna/USO39B_COMB. seq:
1/pna/USO39D_COMB. seq:
1/pna/USO39D_COMB. seq:
1/pna/USO39D_COMB. seq:
GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/1/pna/vazzz_
/cgn2_6/ptodata/1/pna/US102A_COMB.seq:
/cgn2_6/ptodata/1/pna/US102B_COMB.seq:
                                                                                                                                                                               24791104 seqs, 12571243825 residues
                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                     - nucleic search, using sw model
                                                                                                                           1 tecttgegegetgeggeeteag 22
                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                   US-09-270-437D-11
22
                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                    Title:
Perfect score:
                                                                                                                                                Scoring table:
                                      OM nucleic
                                                                                                                          Sequence:
                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                     Database
                                                            Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	DB	a a	Description
-	22	100.0	1946	16	US-09-270-437-7	fack t contained
7	22	100.0	1946	33	13-09-89-651-7	מסשימשט יי שהודיות
m	18.8	85	270	2	118-09-535-806-2020	-
4	18		7,7	2 -	110-00-417 600-26762	sequence 28/82,
		9	7.	9 6	US-09-41/-50/-8435	Sequence 8435, A
ים	B (	81.8	445	27	US-09-696-664A-7808	Sequence 7808, A
ם ט	18	81.8	445	9	US-60-161-619-7647	Seguence 7647. A
0	18	81.8	1166	42	US-10-219-999-7854	Semience 7854
တ	17.8	80.9	214	7	US-08-369-881-2595	T T T T T T T T T T T T T T T T T T T
o O	17.8	80.9	214	œ	US-08-408-872-939	Semience 630 ann
c 10	17.8	80.9	214	20	US-09-535-896-13145	Company 13176
c 11	17.8	80.9	283	14	US-09-050-817-727	Compace 13143,
c 15	17.8	80.9	283	9	TIS-00-270-8400	Sequence 121, App
,,	4	0	000	;	10 00 110 010 010	seduence 135409,
			263	7	US-09-540-210B-7050	Sequence 7050, A
# f	P:/T	80.9	283	48	US-60-043-792-727	Seguence 727, Ap
c I2	17.8	80.9	301	φ	US-08-221-623A-3280	Sequence 3280. Ap
c 16	17.8	80.9	301	9	US-08-221-623B-3280	Semience 3280 An
c 17	17.8	80.9	301	9	US-08-221-623D-3280	Semience 3280 An
18	17.8	80.9	432	18	US-09-436-762A-13454	Semience 13454
c 19	17.8	80.9	473	19	US-09-528-409-68226	Semience 68226
c 50	17.8	80.9	473	35	US-09-933-524-68226	Semience 68226
c 21	17.8	80.9	473	32	US-09-933-524A-68226	
						· />22>> >>::::::::::::::::::::::::::::::

```
RESULT 4
US-09-417-507-8435/c
US-09-417-507-8435, Application US/09417507
; GENERAL INFORMATION:
APPLICANT: KEITH G. WEINSTOCK ET AL.
TITLE OF INVENTION: FUNIGATUS FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: FUNIGATUS FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF PRIB9-10
; FILE REFERENCE: PATH99-10
; CURRENT APPLICATION NUMBER: US/09/417,507
; CURRENT PILING DATE: 1999-10-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Delegemene, Angelo M.
APPLICANT: Delegemene, Angelo M.
APPLICANT: Stuart, Suan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Milahy, Sara J.
APPLICANT: Mulahry, Sara J.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Naughton, POLYNUCLEOTIDES ENCODING OR REGULATING HYDROLASES
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING HYDROLASES
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING HYDROLASES
CURRENT APPLICATION NUMBER OF 244
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 46268
SOFTWARE: PERL Program
SEQ ID NO 28782
LENGTH: 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                        Gaps
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer TITLE OF INVENTION: Associated TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof FILE REFERENCE: LUD 5538
CURRENT APPLICATION NUMBER: US/09/899,651
CURRENT PILING DATE: 2001.07-06
PRIOR APPLICATION NUMBER: US/09/061,709
PRIOR APPLICATION NUMBER: US/09/061,709
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 7
LENGTH: 1946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .<del>.</del>
                                                                                                                                                                                                                                                                                                                                                                      o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 270;
                                                                                                                                                                                                                                                                                                                              100.0%; Score 22; DB 33; Length 1946; 100.0%; Pred. No. 38; 0; Indels 0; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 90.9%; Pred. No. 9.1e+02;
Matches 20; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: hu00928771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ), LOCATION: 88
), OTHER INFORMATION: a, t, c, g, or other
US-09-535-896-28782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-535-896-28782
Sequence 28782, Application US/09535896
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 İCCİTGCGCGCCGCGGCİCAG 47
                                                                                                                                                                                                                                                                                                                                                                                                                   1 rectracecerracecercas 22
                                                                                                                                                                                                                                                                                                                                                                                                                                              38 TCCTTGCGCGCTGCGCCTCAG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 rccrrcccccrcccccrcAG
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                       TYPE: DNA
CRGANISM: Homo sapiens
FEATURE:
US-09-899-651-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/09270437A

GENERAL INFORMATION:
APPLICANT: Chen, Yao-Tseng
APPLICANT: Gure, Ali
APPLICANT: Gure, Ali
APPLICANT: Gure, Ali
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Jager, Elke
APPLICANT: Old, Lloyd
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Antige
TITLE OF INVENTION: Antigens Per Se, And Uses Thereof
TITLE OF INVENTION: Antigens Per Se, And Uses Thereof
TITLE CONTENT APPLICATION UNMBER: US/09/270,437A
CURRENT FILING DATE: 1999-03-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                        Sequence 3114, Ap Sequence 1241, Ap Sequence 12421, A Sequence 12421, A Sequence 12421, A Sequence 72, Appl Sequence 22, Appl Sequence 2100, Ap Sequence 2100, Ap Sequence 7723, Ap Sequence 7723, Ap Sequence 7723, Ap Sequence 17, Appl Sequence 17, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 110, Ap Sequence 110, Ap Sequence 110, Ap Sequence 110, Ap Sequence 110, Ap Sequence 110, Ap Sequence 110, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 22; DB 16; Length 1946; larity 100.0%; Pred. No. 38; Conservative 0; Mismatches 0; Indels 0
                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/09899651
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gure, Ali
Tsang, Solam
Stockert, Elisabeth
Jager, Elke
Knuth, Alexander
Old, Lloyd J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TCCTTGCGCGCTGCGCCTCAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 rccrrdcdcdcrdcddccrchd 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Chen, Yao-Tseng
                                                                                                                                                                                                                                                      6454
11288
14860
37518
37518
                                 711
1785
1785
2041
2082
2687
2840
2840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-899-651-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-270-437-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-270-437-7
                                                                                                                                                                                                                                                                                                                                                          17.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
```

ö

```
Gaps
                                                                                                                                                                                                                                                                                APPLICANT: Cao, Yongwel
APPLICANT: Cao, Yongwel
APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Kovalle, Gregory J.
APPLICANT: Liu, Jingdong
APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT:
FILE REFERENCE: 38-10(52726)C
CURRENT APPLICATION NUMBER: US 10/10/219,999
CURRENT FILING DATE: 2002-08-15
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-15
NUMBER OF SEQ ID NOS: 63520
SEQ ID NO 7854
LENGTH: 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wilde, Craig G.
APPLICANT: Wilde, Craig G.
APPLICANT: Bills, Pamela Kay
APPLICANT: Bills, Pamela Kay
APPLICANT: Bills, Pamela Kay
APPLICANT: Bills, Pamela Kay
APPLICANT: Pham, Mino Phi,
TITLE OF INVENTION: HUMAN CARDIAC CELL-DERIVED POLYNUCLEOTIDES
NUMBER OF SEQUENCES: 3690
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3330 Hillview Drive
CITY: Palo Alto
                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1166;
                 Score 18; DB 60; Length 445;
Pred. No. 1.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Word Perfect 6.0/6.1/MS-DOS
                                                                                                                                                                                                                                               Sequence 7854, Application US/10219999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-369-881-2595/c; Sequence 2595, Application US/08369881; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
CERATING SYSTEM: PC-DGS/MS-DOS
SOFTWARE: Word Perfect 6.0/6.1/
81.8%; Scc...
100.0%; Pre
0;
                                                                                                                           355 CCTTGCGCTGCGGCCT 338
                                                                                                   2 CCTTGCGCGCTGCGGCCT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 404 ccrrececerececri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTTGCGCGCTGCGGCCT 19
           Query Match
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 81.8
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION:
US-10-219-999-7854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                       US-10-219-999-7854/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
                                                                                                à
                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                         US-09-696-664A-7808/C
; Sequence 7808, Application US/0969664A
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Dubois, Patrice
; APPLICANT: Mandeco, Debbie A.
; APPLICANT: Masucci, James D.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(51721)B
; CURRENT APPLICATION NUMBER: US/09/696,664A
; PRIOR APPLICATION NUMBER: US 60/161,619
; PRIOR FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 17472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7647, Application US/60161619
GENERAL INFORMATION:
APPLICANT: Abad, Mark S.
APPLICANT: Andersen, Scott E.
APPLICANT: Dubois, Patrice
APPLICANT: Manadeo, Debbie A.
APPLICANT: Masucci, James D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(51721)A
CURRENT APPLICATION NUMBER: US/60/161,619
CURRENT FILING DATE: 1999-10-26
NUMBER OF SEQ ID NOS: 7685
SEQ ID NO 7647
                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                          Length 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.8%; Score 18; DB 27; Length 445; 100.0%; Pred. No. 1.98+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                 Indels
                                                                                                                                                 Query Match 85.5%; Score 18.8; DB 18; Best Local Similarity 90.9%; Pred. No. 8.7e+02; Matches 20; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: LIB3279-048-P1-K1-E7
US-09-696-664A-7808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: LIB3279-048-P1-K1-E7
US-60-161-619-7647
                                                                                                                                                                                                                                                                              497 récrrécécaérécerécitése 476
                                                                                                                                                                                                                                    1 TCCTTGCGCGCTGCGGCCTCAG 22
; NUMBER OF SEQ ID NOS: 44312
; SEQ ID NO 8435
; LENGTH: 525
; TYPE: DNA
; ORGANISM: A.fumigatus
US-09-417-507-8435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             355 CCTTGCGCGCTGCGGCCT 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 CCTTGCGCGCTGCGGCT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 18, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
US-60-161-619-7647/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH
                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠ
```

```
APPLICANT: Stuve, Laura L.

APPLICANT: Stuart, Susan G.

APPLICANT: Itc, Laura V.

APPLICANT: Akerblom, Ingrid E.

APPLICANT: Delegeane, Angelo M.

APPLICANT: Noughton, Rebecca E.

APPLICANT: Klingler, Tod M.

APPLICANT: Klingler, Tod M.

TITLE OF INVENTION: POLYMUCLEOTIDES AND POLYPEPTIDES DERIVED FROM TITLE OF INVENTION: HUMAN FETAL KIDNEY

NUMBER OF SEQUENCES: 2115
                                                        80.9%; Score 17.8; DB 8;
90.5%; Pred. No. 2.4e+03;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-00-050-817-727/c
; Sequence 727, Application US/09050817
GENERAL INFORMATION:
APPLICANT: Geoding, Douglas H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 rccrrdcdgdcrdcddcrch 137
                                                                                                                                                                           157 recrrécégecrécégecrek 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
                                                                                                                                         1 TCCTTGCGCGCTGCGGCCTCA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 recriecececrececerca
                                                            Query Match
Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                          US-08-408-872-939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wilde, Craig G.
APPLICANT: Wilde, Craig G.
APPLICANT: Bills Pamela K.
APPLICANT: Bills Pamela K.
APPLICANT: Hills Pamela K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: CARDIAC CELL-DERIVED POLYNUCLEOTIDES AND TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 1954
CORRESPONDENCE ADDRESS:
ADDRESSE: INCYTR PITTE.
STREFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                               Query Match

80.9%; Score 17.8; DB 7; Length 214;
Best Local Similarity 90.5%; Pred. No. 2.4e+03;
Matches 19; Conservative. 0; Mismatches 2; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: INCYTE PHARMACEUTICALS, INC. STREET: 3330 HILLVIEW AVENUE CITY: PALO ALTO STATE: CALIFORNIA
CIASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Barbara J. Luther
REGISTRATION NUMBER: 39.54
REFERENCE/DOCKET NUMBER: PD0019 US
TELECOMMUNICATION INFORMATION:
TELEPRAN: 415-855-0555
TELEFAX: 415-855-0557
INFORMATION FOR SEQ ID NO: 2595:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 base pairs
TYPE: nucleic acid
STRANDENNESS: single
""DOLOGY: linear
CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LUTHER, BARBARA J.
REGISTRATION NUMBER: 33554
REFERENCE/DOCKET NUMBER: PD-0
TELECOMMUNICATION INFORMATION:
TELEFAN: (415) 852-0555
INFORMATION FOR SEQ ID NO: 939:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 rccrrcccccccccccc 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TCCTTGCGCGCTGCGGCCTCA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 214 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: 187978
                                                                                                                                                                                                                                                                                      TOPOLOGY: linea
MOLECULE TYPE: CD
IMMEDIATE SOURCE:
CLONE: 187978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-408-872-939/c
                                                                                                                                                                                                                                                                                                                                                               US-08-369-881-2595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING HYDROLASES FILE REBERENCE: PD-1003 CIP
CURRENT FILING DATE: 2000-03-24
CURRENT FILING DATE: 2000-03-24
CURRENT FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 46268
SOOTWARE: PERL Program
SEQ ID NO 13145
TYPR: ...
                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 214;
Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: hu00824962
NAME/KEY: unsure
LOCATION: 16, 59, 104, 106, 126, 170, 194, 196, 200
CHER INFORMATION: a, t, c, g, or other
US-09-535-896-13145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

80.9%; Score 17.8; DB 20;
Best Local Similarity 90.5%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 2;
```

us-09-270-437d-11.rnpm

```
THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION NAMES OF THE SECTION SECTION NAMES OF THE SECTION SECTION NAMES OF THE SECTION SECTION NAMES OF THE SECTION SECTION NAMES OF THE SECTION SECTION NAMES OF THE SECTION SECTION NAMES OF THE SECTION SECTION NAMES OF THE SECTION SECTION NAMES OF THE SECTION SECTION NAMES OF THE SECTION SECTION NAMES OF THE SECTION SECTION NAMES OF THE SECTION SECTION NAMES OF THE SECTION SECTION NAMES OF THE SECTION SECTION NAMES OF THE SECTION SECTION SECTION NAMES OF THE SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/040,431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR
PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-270-849B-135409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.9%; Score 17.8; DB 14; Length 283; illarity 90.5%; Pred. No. 2.4e+03; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 80.9%; Score 17.8; DB 16; Length 283; Best Local Similarity 90.5%; Pred. No. 2.48+03; Matches 19; Conservative 0; Mismatches 2; Indels 0;
                              OPERMING SYSTEM: PC-DOS/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,817
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/043,792
FILING DATE:
APPLICATION NUMBER: 60/043,792
FILING DATE:
ATTORNEY/ACENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: 39,132
REFERENCE/DOCKET NUMBER: 9D-0355P
TELECPHONE: (415) 845-4166
INFORMATION FOR SEQ ID NO: 727:
SEQUENCE CHARACTERISTICS:
LENGTH: 283 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
US-09-270-849B-135409/C
'S GEQUENCE 135409, Application US/09270849B
'GENERAL INFORMATION:
'APPLICANT: Swimmer et al.'
'TITLE OF INVENTION: INSect genome survey devices
'FILE REFERENCE:
'CURRENT APPLICATION WUMBER: US/09/270,849B
'CURRENT APPLICATION WUMBER: 1999-03-17
'NUMBER OF SEQ ID NOS: 195450
'SOFTWARE: PatentIn Ver. 2.0
'SEQ ID NO 135409
'LENGTH: 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7050, Application US/09540210B GENERAL INFORMATION:
APPLICANT: Scalhamer, Jeffrey J. APPLICANT: Delegeane, Angelo M. APPLICANT: Stuart, Susan G. APPLICANT: Stuart, Laura L.
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 cerrececerecaececes 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 CCTTGCGCGCTGCGGCCTCAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 cércécécéciécésécéres s7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ## ACLECULE TYPE: CDNA

## MOLECULE TYPE: CDNA

## MMEDIATE SOURCE:

## CLONE: 2991071H1

US-09-050-817-727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-540-210B-7050/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
```

```
..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-221-623A-3280/c

i Sequence 3280, Application US/08221623A

GENERAL INFORMATION:
TITLE OF INVENTION: Human Genes, Sequences, and Expression
TITLE OF INVENTION: Products

NUMBER OF SEQUENCES: 3319
CORRESPONDENCE ADDRESS:
ADDRESSEE: Olstein
STREET: & Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

80.9%; Score 17.8; DB 48; Length 283;
Best Local Similarity 90.5%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6; Length 301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 5.0
SOFTWARE: ASCIT Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,623A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.9%; Score 17.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot
REGISTRATION NUMBER: 24,025
REPERENCE/POCKET UNBER: 325800-73
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 994-1700
                                                                              ALTOKUNIA AGEAL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL THE ANGEL 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 CCTTGCGCGCTGCGCCTCAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47 cerriecececrecaececeae 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (201) 994-1744
INFORMATION FOR SEQ ID NO: 3
              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) MOLECULE TYPE: CDNA

) IMMEDIATE SOURCE:

) CLONE: 2991071H1

US-60-043-792-727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gooding, Douglas H.
APPLICANT: Stuve, Laura L.
APPLICANT: Stuve, Laura L.
APPLICANT: Stuve, Laura Y.
APPLICANT: Stuve, Laura Y.
APPLICANT: Akerblom, Ingrid E.
APPLICANT: Belegeane, Angelo M.
APPLICANT: Naughton, Rebeca E.
APPLICANT: Kingler, Tod M.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM TITLE OF INVENTION: POLYNUCLEOTIDES, INC.
STREET: 3174 PORTER DRIVE
COUNTRY: USA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

80.9%; Score 17.8; DB 21; Length 283;
Best Local Similarity 90.5%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Word Perfect 6.1 for Windows/MS-DOS 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: hu00436211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , NAME/KEY: unsure
, LOCATION: 266-267
, OTHER INFORMATION: a, t, c, g, or other
US-09-540-210B-7050
PRIOR FILING DATE: March 5, 1997
PRIOR APPLICATION NUMBER: 09/041,894
PRIOR APPLICATION NUMBER: 06/040,199
PRIOR APPLICATION NUMBER: 06/040,199
PRIOR PILING DATE: March 14, 1997
PRIOR PELING DATE: March 14, 1997
PRIOR PILING DATE: March 30, 1998
PRIOR FILING DATE: March 30, 1998
PRIOR PILING DATE: May 8, 1998
PRIOR PILING DATE: May 8, 1998
PRIOR PILING DATE: May 8, 1998
PRIOR PILING DATE: May 29, 1997
PRIOR PILING DATE: June 30, 1998
PRIOR PILING DATE: June 30, 1998
PRIOR PILING DATE: June 30, 1998
PRIOR PILING DATE: June 30, 1998
PRIOR PILING DATE: June 30, 1998
PRIOR PILING DATE: June 30, 1998
PRIOR PILING DATE: June 30, 1998
PRIOR PILING DATE: June 9, 1997
PRIOR APPLICATION NUMBER: 06/049,975
PRIOR APPLICATION NUMBER: 06/049,975
PRIOR PILING DATE: June 13, 1997
NUMBER OF SEQ ID NOS: 35654
SEQ ID NO 7050
LENGTH: 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/60/043,792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: Word Perfect 6.1 f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 CCTTGCGCGCTGCGGCCTCAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 ccrrececerecaececeae 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
```

g ð

0; Gaps Best Local Similarity 90.5%; Pred. No. 2.3e+03; Matches 19; Conservative 0; Mismatches 2; Indels

ö

g ઠે

Search completed: April 18, 2003, 09:35:44 Job time : 1214 secs

							- 1
			4				l
				•			1
						•	
			•				
	4. · · · ·			•			
							- 1
*			•				
taget C						•	
4			·.				ļ
	•						
Ç.							
4 1 6				•			
in the second							
							•
					•	•	
						•	
5 <del>.</del>							
	•				*		
	en en en en en en en en en en en en en e					en en en en en en en en en en en en en e	4
	**			200	4		131
W.,		. ·				* * * * * * * * * * * * * * * * * * * *	
<b>1</b>							
				,			
	<b>x</b>					,	d.
				a c			
•							
•			· whi				
						***	
						3. • • • • • • • • • • • • • • • • • • •	
							<del>,</del>
							<del>,</del>

Н

25, Appl 25, Appl 32171, A 180, App 181, App 151, App 151, App 151, App 151, App 151, App 151, App

Sequence 3 Sequence 4 Sequence 5 Sequence 5 Sequence 5 Sequence 1

151, App 18030, A 8, Appli 26844, A 24, Appl 24, Appl

Sequence Seq

Sequence 14079, A Sequence 871, App

Sequence.

us-09-270-437d-11.rnpn

```
APPLICANT: Gure, Ali
APPLICANT: Gure, Ali
APPLICANT: Tsang, Solam
APPLICANT: Tsang, Solam
APPLICANT: Stockert, Elisabeth
APPLICANT: Jager, Elisabeth
APPLICANT: Jager, Elisabeth
APPLICANT: Jager, Elisabeth
APPLICANT: Old, Lloyd J.
ITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Antiger
ITLE OF INVENTION: Antigens Per Se, And Uses Thereof
ITLE REFERENCE: LUD 5538.1
ICURRENT PRILIG DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 09/061,709
PRIOR FILING DATE: 1998-04-17
ILBNGHR OF SEQ ID NOS: 23
SEQ ID NO 11
ILBNGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 22; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 22; Conservative 0; Mismatches 0; Indels
             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-US-Z/U-43/U-7

Sequence 7, Application US/09270437D

Sequence 7, Application US/09270437D

SERERAL INFORMATION:

APPLICANT: Chen, Yao-Tseng

APPLICANT: Gure, All

APPLICANT: Stockert, Elisabeth

APPLICANT: Jager, Elke

APPLICANT: Knuth, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/09270437D
, GENERAL INFORMATION:
, APPLICANT: Chen, Yao-Tseng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TCCTTGCGCGCTGCGGCCTCAG 22 1 TCCTTGCGCGCTGCGGCCTCCAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-270-437D-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FEATURE:
US-09-270-437D-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
US-09-270-437D-7
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Appl
Sequence 7, Appli
Sequence 318, App
Sequence 31974,
Sequence 219774,
Sequence 19, Appl
Sequence 6708, Ap
Sequence 2261, Ap
Sequence 2261, Ap
Sequence 2851, Ap
Sequence 5851, Ap
Sequence 5851, Ap
Sequence 252, App
Sequence 252, App
Sequence 252, App
Sequence 252, App
Sequence 2670, Ap
Sequence 6577, Ap
Sequence 61013, Ap
Sequence 61013, Ap
Sequence 61013, Ap
                                                                                              April 18, 2003, 06:35:28; Search time 245.167 Seconds (without alignments) 400.770 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pending_Patents_NA_New:*

1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*

3: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*

4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*

5: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*

6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*

7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*

8: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*

9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*

9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*

10: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*

11: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*
      GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                             58972.97 seqs, 2233080881 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                               OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                 1 tecttgegegetgeggeeteag 22
                                                                                                                                                                                                                               IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                 US-09-270-437D-11
22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0 22 5

100.0 1946 5

100.0 1236069

80.9 136069

80.9 1006 1

79.1 15251 7

79.1 15251 7

78.2 423 11

78.2 1231 9

78.2 1231 9

78.2 1231 9

78.2 1231 9

78.2 1231 9

78.2 1230 9

78.2 1230 9

76.4 2626 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
Match Length DB
                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                  Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
```

Database :

Seguence:

Run on:

Searched:

ö

Gapa

ö

16.8 16.8 16.8 16.8

ö

Gaps

```
APPLICANT: Rosen, et. al.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 100
FILE REFERENCE: PO-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Remaining Prior Application data removed - See File Wrapper or PALM. WUMBER OF SEQ ID NOS: 244538
SEQ ID NO 219774
LENGTH: 301
                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                      Length 139;
                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                         Score 17.8; DB 6;
Pred. No. 3.2e+02;
                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (14)...(14)
OTHER INFORMATION: n is equal to a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (25)...(25)
OTHER INFORMATION: n is equal to a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/912,293
CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: 08/103,744
PRIOR FILING DATE: 1993-08-09
PRIOR APPLICATION NUMBER: 09/249,651
PRIOR FILING DATE: 1999-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-912-283-219774/c
; Sequence 219774, Application US/09912293
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1993-06-09
PRIOR FILING DATE: 1993-08-09
PRIOR PILING DATE: 1994-02-18
PRIOR PILING DATE: 1994-02-18
PRIOR PILING DATE: 1994-02-18
PRIOR PILING DATE: 2001-05-18
PRIOR PILING DATE: 1994-02-15
PRIOR PILING DATE: 1994-02-15
PRIOR FILING DATE: 1994-03-11
PRIOR FILING DATE: 1994-03-11
PRIOR FILING DATE: 1994-03-31
PRIOR FILING DATE: 1994-03-31
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 09/741,830
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 09/813,155
PRIOR PILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 08/104,507 PRIOR FILING DATE: 1993-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         equal to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       equal to
                                                                                                                                                                                                                                                                                                                                                                 so ccrrecececrecaececae 30
                                                                                                                                                                                                                           Query Match 80.9%;
Best Local Similarity 90.5%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                      CCTTGCGCGCTGCGGCCTCAG
                                                                                        FEATURE:
NAME/KBY: misc_feature
LOCATION: 106
COTHER INFORMATION: s=g or c
US-09-513-999C-31413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (9)...(9)
OTHER INFORMATION: n is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ION: (16)..(16)
INFORMATION: n is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (37)..(37)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
SEQ ID NO 31413
LENGTH: 139
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OCATION:
                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 318, Application US/09948128
GENERAL INFORMATION:
CETAIG
TITLE OF INVENTION: COLLECTION OF SINGLE NUCLECTIDE POLYMORPHISM (SNP8) LOCATED ON CH
TITLE OF INVENTION: COLLECTION OF DETECTION, AND USES THEREOF
FILE REFERENCE: CL001294
CURRENT APPLICATION NUMBER: US/09/948,128
CURRENT FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 465
           APPLICANT: Old, Lloyd J.

TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Antige
TITLE OF INVENTION: Antigens Per Se, And Uses Thereof
TITLE OF INVENTION: LUD 5538.1

CURRENT APPLICATION NUMBER: US/09/270,437D
CURRENT FILING DATE: 1999-03-16
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 23
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Duclert, A. APPLICANT: Glordano, J.Y. APPLICANT: Glordano, J.Y. TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. TITLE OF INVENTION: ESPERSE CURRENCE: 59.US2.REG CURRENT APPLICATION NUMBER: US/09/513,999C CURRENT FILING DATE: 2000-02-24 PRIOR APPLICATION NUMBER: US 60/122,487 PRIOR PRIOR DATE: 1999-02-26 NUMBER OF SEQ ID NOS: 36681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 22; DB 5; Length 12360069;
Pred. No. 5.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5; Length 1946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 22;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 10941150 rccrrdcccccrdccccrcrd 10941129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 31413, Application US/09513999C GENERAL INFORMATION:
APPLICANT: Duras Milne Edwards, J.B. APPLICANT: Onclert, A. APPLICANT: Giordano, J.Y.
                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: CDS
LOCATION: 1622,1702,1771,1809,1833
CTHER INFORWATION: unsure of nucleotide
US-09-270-437D-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (1)...(12360069)
; OTHER INFORMATION: n = A,T,C or G
US-09-948-128-318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 recridededergedecercag 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TCCTTGCGCGCCTCAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 recrirecececiecececercae 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%;
Matches 22; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: NUMBER OF SEQ ID NOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
US-09-513-999C-31413/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 318
LENGTH: 12360069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
US-09-948-128-318/c
                                                                                                                                                                                                                                                   LENGTH: 1946
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
```

```
US-09-949-016-14274

Sequence 14274, Application US/09949016

Sequence 14274, Application US/09949016

GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR PILICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-01-0-03

PRIOR PILING DATE: 2000-01-0-03

NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gape
                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1200;
                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                      Query Match 80.9%; Score 17.8; DB 1; Best Local Similarity 90.5%; Pred. No. 3.2e+02; Matches 19; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.1%; Score 17.4; DB 8; 94.7%; Pred. No. 4.8e+02; ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ISHIKAWA, UUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
FILE REFERENCE: 249-26
CURRENT PILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
FILING PAPLICATION NUMBER: UP 2001-272697
NUMBER OF SEQ ID NOS: 15109
ENGYPH: 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-156-761-6708/c; Sequence 6708, Application US/10156761; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                 2 CCTTGCGCGCTGCGCCTCAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 cciriecececienececene 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      668 TCCTTGCGCGCCGCGCT 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 94.7
Matches 18; Conservative
                                                                                          TYPE: DNA
ORGANISM: CG164521-01
FEATURE:
                                                                                                                                                                                     ; NAME/KEY: CDS
; LOCATION: (24)..(995)
PCT-US02-38821-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: CDS
; LOCATION: (1)..(1200)
US-10-156-761-6708
                             SEQ ID NO 19
LENGTH: 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRESENT. 19/C

| Sequence 19, Application PC/TUS0238821
| Sequence 19, Application PC/TUS0238821
| Sequence 19, Application PC/TUS0238821
| APPLICANT: CLREGEN COTP. et al. |
| TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS C TITLE OF INVENTION: THE SAME POLYNOR CLREAT FOR THE SAME POLYNOR CONTRENT FILING DATE: 2002-12-03
| PRIOR APPLICATION NUMBER: 60/341,477
| PRIOR FILING DATE: 2002-03-17 |
| PRIOR PLICATION NUMBER: 60/341,477 |
| PRIOR PLICATION NUMBER: 60/341,540 |
| PRIOR PLICATION NUMBER: 60/341,540 |
| PRIOR PLICATION NUMBER: 60/341,540 |
| PRIOR PLICATION NUMBER: 60/341,540 |
| PRIOR PLICATION NUMBER: 60/341,540 |
| PRIOR PLICATION NUMBER: 60/342,592 |
| PRIOR PLICATION NUMBER: 60/343,744 |
| PRIOR PLICATION NUMBER: 60/344,903 |
| PRIOR PLICATION NUMBER: 60/344,903 |
| PRIOR PLICATION NUMBER: 60/344,903 |
| PRIOR PLICATION NUMBER: 60/344,903 |
| PRIOR PLICATION NUMBER: 60/340,901 |
| PRIOR PLICATION NUMBER: 60/340,901 |
| PRIOR PLICATION NUMBER: 60/340,901 |
| PRIOR PLICATION NUMBER: 60/340,901 |
| PRIOR PLICATION NUMBER: 60/340,901 |
| PRIOR PLICATION NUMBER: 60/340,901 |
| PRIOR PLICATION NUMBER: 60/340,901 |
| PRIOR PLICATION NUMBER: 60/340,901 |
| PRIOR PLICATION NUMBER: 60/340,901 |
| PRIOR PLICATION NUMBER: 60/340,901 |
| PRIOR PLICATION NUMBER: 60/340,901 |
| PRIOR PLICATION NUMBER: 60/340,901 |
| PRIOR PLICATION NUMBER: 60/340,901 |
| PRIOR PLICATION NUMBER: 60/340,901 |
| PRIOR PLICATION NUMBER: 60/340,901 |
| PRIOR PLICATION NUMBER: 60/340,901 |
| PRIOR PLICATION NUMBER: 60/340,901 |
| PRIOR PLICATION NUMBER: 60/340,901 |
| PRIOR PLICATION NUMBER: 60/340,901 |
| PRIOR PLICATION NUMBER: 60/340,901 |
| PRIOR PLICATION NUMBER: 60/340,901 |
| PRIOR PLICATION NUMBER: 60/340,901 |
| PRIOR PLICATION NUMBER: 60/340,901 |
| PRIOR PLICATION NUMBER: 60/340,901 |
| PRIOR PLICATION NUMBER: 60/340,901 |
| PRIOR PLICATION NUMBER: 60/340,901 |
| PRIOR PLICATION NUMBER: 60/340,901 |
| PRIOR PLICATION NUMBER: 60/340,901 |
| PRIOR PLICATION NUMBER: 60/340,901 |
| PRIOR PLICAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            emaining Prior Application data removed - See File Wrapper or PALM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 80.9%; Score 17.8; DB 6; Length 301; Best Local Similarity 90.5%; Pred. No. 3.2e+02; Matches 19; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature

LOCATION: (263)...(263)

CTHER INFORMATION: n is equal to a,t,g, or c

US-09-912-293-219774
OTHER INFORMATION: n is equal to a,t,g,
                                                                                                                                                                                                                                                                                                                                          LOCATION: (61)...(61)
OTHER INFORMATION: n is equal to a,t,g,
                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (59) ...(59)
OTHER INPORMATION: n is equal to a,t,g,
                                                          NAME/KEY: misc_feature
LOCATION: (42)...(42)
OTHER INFORMATION: n is equal to a,t,g,
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (126)..(126)
OTHER INFORMATION: n is equal to a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (104). (104)
OTHER INFORMATION: n is equal to a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc_feature
LOCATION: (91). (91)
OTHER INFORMATION: n is equal to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NOS: 53
CuraSegList version 0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 TCCTTGCGGCTGCGGCTCA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TCCTTGCGCGCTGCGCCTCA 21
                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

ö

8

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13059, Application US/10144771
GENERAL INFORMATION: Craig
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
FILE REFERENCE: CL001321
CURRENT APPLICATION NUMBER: US/10/144,771
CURRENT FILING DATE: 2002-05-15
NUMBER OF SEQ ID NOS: 47235
SEQ ID NO 13059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.2%; Score 17.2; DB 9; Length 1231; 86.4%; Pred. No. '5.8e+02; ive 0; Mismatches 3; Indels 0;
                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 78.2%; Score 17.2; DB 11; Length 423; Best Local Similarity 86.4%; Pred. No. 5.8e+02; Matches 19; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2261, Application US/60288292
; Sequence 2261, Application US/60288292
; GENERAL INFORMATION:
    APPLICANT: Glenn, Matthew
    APPLICANT: Norriss, Michael G
    TITLE OF INVENTION: Compounds isolated from forage plants;
    TITLE OF INVENTION: Compounds for their use.
    FILE REFERENCE: 1058P
    CURRENT APPLICATION NUMBER: US/60/288,292
    CURRENT FILING DATE: 2001-05-02
    NUMBER OF SEQ ID NOS: 49762
; SOFTWARE: FESTSEQ for Windows Version 4.0
; SEQ ID NO 2261
LENGTH: 423
                                                                                                Length 341;
                                                                                                                                                           3; Indels
                                                                                                      Score 17.2; DB 6;
Pred. No. 5.8e+02;
0; Mismatches 3;
; LOCATION: (333)...(333)
; OTHER INFORMATION: n is equal to a,t,g, or c
US-09-912-293-44484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 5799, Application US/10366683
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      357 tctridcdcdcrdcrdccccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 TCCTTGAGCTTTGCGGCCTCAG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 recridededergedecreag 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 recrirededecrededecreag 22
                                                                                                                                                                                                                                                                       200 rccrrccrccrccccccrcrc 179
                                                                                                                                                                                                                    1 TCCTTGCGCGCTGCGGCCTCAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Rubenfield, Marc J. APPLICANT: Nolling, Jork APPLICANT: Deloughery, Craig
                                                                                                           Query Match
Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 86.4
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
CORGANISM: Lolium perenne
US-60-288-292-2261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: HUMAN
US-10-144-771-13059
                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
US-60-288-292-2261/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
US-10-144-771-13059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
US-10-366-683-5799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INVENTION: et. al.

APPLICANT: Rosen, et. al.

TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 100
FILES REFERENCE: PO-100
CURRENT APPLICATION NUMBER: US/09/912,293
CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: 09/19,651
PRIOR PILING DATE: 1993-08-09
PRIOR FILING DATE: 1993-08-09
PRIOR PILING DATE: 1993-08-09
PRIOR PILING DATE: 1993-08-09
PRIOR PILING DATE: 1994-02-15
PRIOR APPLICATION NUMBER: 08/196,363
PRIOR PILING DATE: 1994-02-15
PRIOR PILING DATE: 1994-02-15
PRIOR PILING DATE: 1994-03-31
PRIOR PILING DATE: 1994-03-31
PRIOR PLING DATE: 1994-03-31
PRIOR PILING DATE: 1994-03-31
PRIOR PILING DATE: 1994-03-31
PRIOR PILING DATE: 1994-03-31
PRIOR PILING DATE: 1994-03-31
PRIOR PILING DATE: 1994-03-31
PRIOR PILING DATE: 1994-03-31
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-10-3-31
PRIOR PILING DATE: 2000-10-3-31
PRIOR PILING DATE: 2000-10-3-31
PRIOR PILING DATE: 2000-10-3-31
PRIOR PILING DATE: 2000-10-3-31
PRIOR PILING DATE: 2000-10-3-31
PRIOR PILING DATE: 2000-10-3-31
PRIOR PILING DATE: 2000-10-3-31
PRIOR PILING DATE: 2000-10-3-31
PRIOR PILING DATE: 2000-10-3-31
PRIOR PILING DATE: 2000-10-3-31
PRIOR PILING DATE: 2000-10-3-31
PRIOR PILING DATE: 2000-10-3-31
PRIOR PILING DATE: 2000-10-3-31
PRIOR PILING DATE: 2000-10-3-31
PRIOR PILING DATE: 2000-10-3-31
PRIOR PILING DATE: 2000-10-3-31
PRIOR PILING DATE: 2000-10-3-31
PRIOR PILING DATE: 2000-10-3-31
PRIOR PILING DATE: 2000-10-3-31
PRIOR PILING DATE: 2000-10-3-31
PRIOR PILING DATE: 2000-10-3-31
PRIOR PILING DATE: 2000-10-3-31
PRIOR PILING DATE: 2000-10-3-31
PRIOR PILING DATE: 2000-10-3-31
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                       Length 15251;
                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                       79.1%; Score 17.4; DB 7;
94.7%; Pred. No. 4.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (326)...(326)
OTHER INFORMATION: n is equal to a,t,g, or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (236)..(236)
OTHER INFORMATION: n is equal to a,t,g, or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (257)..(257)
OTHER INFORMATION: n is equal to a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KRST: misc_feature
LOCATION: (280).
OTGATION: (280).
OTHER INFORMATION: n is equal to a,t,9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (285)..(285)
OTHER INFORMATION: n is equal to a,t,g,
                               SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 14274 LENGTH: 15251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
US-09-912-293-44484/c
US-09-912-293-44464, Application US/09912293
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     116 CCTTGCGCGCTGCGGCTC 134
                                                                                                                                                                                                                                                                                                                                     2 cerracecerececer 20
                                                                                                                                                                                                                               Query Match
Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (326)..(326)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (236)..(236)
                                                                                                                            ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14274
```

ö

ö

```
Search completed: April 18, 2003, 10:50:26 Job time : 3044.17 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 1321142 TCCATGAGCTCTGCGGCCTCAG 1321121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: HUMAN
                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
APPLICANT: BUSH, David
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/10/366,683
CURRENT APPLICATION NUMBER: 09/252,991
PRIOR APPLICATION NUMBER: 09/252,991
PRIOR FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 5799
LENGTH: 1440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION

SEQUENCE 5851, Application US/10366683

GENERAL INFORMATION:

APPLICANT: Rubenfield, Marc J.

APPLICANT: Rubenfield, Marc J.

APPLICANT: Bush, David

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF ILLING DATE: 2003-02-13

CURRENT APPLICATION NUMBER: US/10/366,683

CURRENT APPLICATION NUMBER: 09/252,991

PRIOR FILING DATE: 1999-02-18

NUMBER OF SEQ ID NOS: 33142

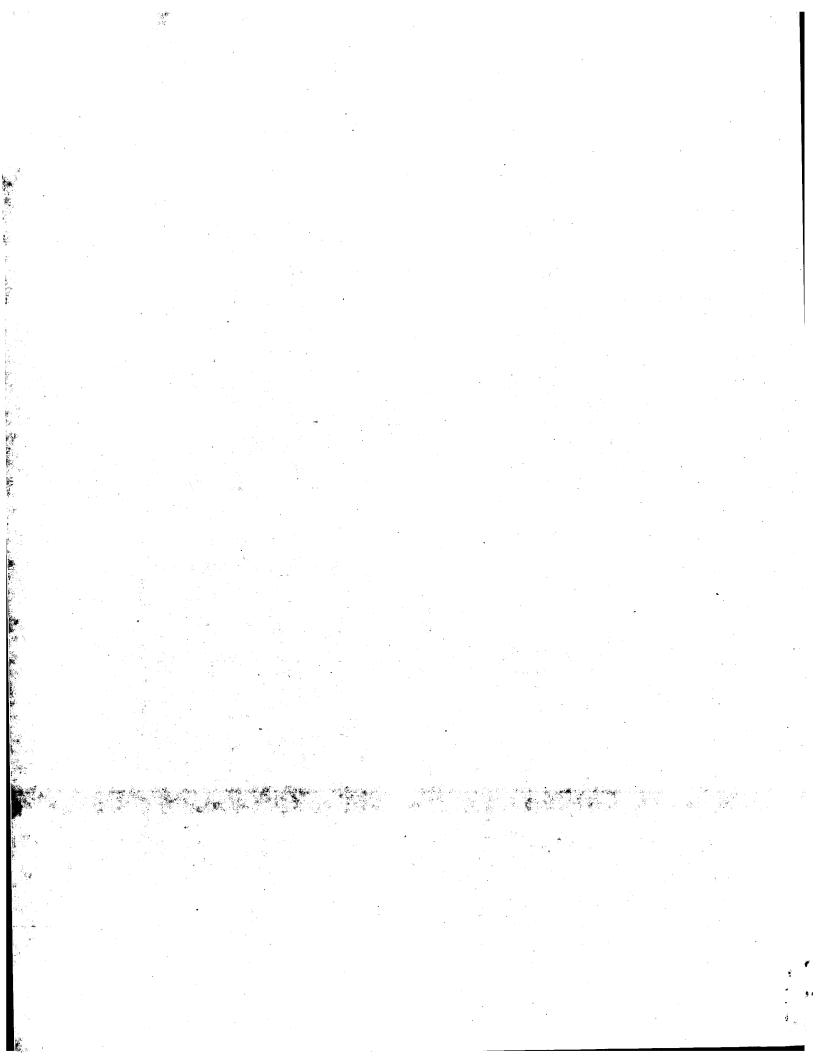
SEQ ID NO 5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5869, Application US/10366683
Gentence 5869, Application US/10366683
GENERAL INFORMATION:
APPLICANT: Nolling, Jork
APPLICANT: Nolling, Jork
APPLICANT: Bush, David
APPLICANT: Bush, David
APPLICANT: Bush, David
APPLICANT: Bush, David
APPLICANT: Bush, David
APPLICANTON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: WUMBER: US/10/366,683
CURRENT APPLICATION NUMBER: US/22,991
PRIOR APPLICATION NUMBER: 09/252,991
PRIOR PLING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 33142
LENGTH: 2226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                              Length 1440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 17.2; DB 9; Length 1920;
Pred. No. 5.9e+02;
0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                      Score 17.2; DB 9;
Pred. No. 5.8e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1301 TCCTTGCGCGCCGCGTCCTCGG 1322
                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-10-366-683-5799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-10-366-683-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TCCTTGCGCGCTGCGCCTCAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 récrirécécécécérecrices 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TCCTTGCGCGCTGCGGCCTCAG 22
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 86.4
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-10-366-683-5851/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-10-366-683-5869/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  쉽
```

```
US-09-948-128-252/c
; Sequence 252, Application US/09948128
; Sequence 252, Application US/09948128
; GENERAL INFORMATION:
; TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNPs) LOCATED ON CHITIES OF INVENTION: 17, METHODS OF DETECTION, AND USES THEREOF
; FILE REPERBENCE: CL001294
; CURRENT APPLICATION NUMBER: US/09/948,128
; CURRENT PILLING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 465
; SEQ ID NO 252
; SEQ ID NO 252
                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 78.2%; Score 17.2; DB 5; Length 1439395; Best Local Similarity 86.4%; Pred. No. 5.7e+02; Matches 19; Conservative 0; Mismatches 3; Indels 0;
                                                                                                            Query Match 78.2%; Score 17.2; DB 9; Length 2226; Best Local Similarity 86.4%; Pred. No. 5.9e+02; Matches 19; Conservative 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature

LOCATION: (1)...(1439395)

CTHER INFORMATION: n = A,T,C or G

US-09-948-128-252
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-10-366-683-5869
                                                                                                                                                                                                                                                                           1 TCCTTGCGCGCTGCGGCCTCAG 22
```



BC465076 EMI 33\_A1 AV433340 AV433340 BE254482 601111575 BC699633 602679365 AL528423 AL528423 AL229108 Tetracdon BC64757 ACENCOURT BC617183 602612018 BC617183 602612018 BC617183 602611041 AA120169 MIN33910.x B1818151 60303385 B1818151 60303385 BR843150 BB84150 BB842521 BB842521 BB843150 BB841100 BB842521 BB86287 BB843150 BB842621 BB843150 BB842621 BB843150 BB842621 BB854739 601075501 AW210189 U151109.y BC60688 BRY 2762 AZ879071 RPCI\_23-2 BF71052 BB6130902 BB630902 BB6130902 BB630902 BB613043 BB630902 BB61343 BB631343 BB81343 BB631343 BB81343 BB631343 BB61343 BB631343 BB61343 BB631343 BB61343 BB631343 BB61343 BB786598 602112155

Sequence:

Run on:

Searched:

Database

```
Anopheles gambiae GSS SP6 end of clone 03E18 of NotreDamel library from strain PEST of Anopheles gambiae (African malaria mosquito), Abilalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission

Direct Submission

Submitted (16-PEB-2000) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Web : www.genoscope.cns.fr)

Roth.C.W. Broy.P.T., Ke,Z., Collins,F.H. and Weissenbach,J.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (16-PEB-2000) BBMI, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                             BG699633
AL519496
AL519496
CNS035RV
BG614757
BG617103
BG77407
BG118151
BR120169
BR86876
BR845504
BR845504
BR845504
BR84150
BR84150
BR84150
BR84150
BR84106
AM210189
BR544739
AW210189
BG60686
AZ879071
BF719752
BG6908647
                                                                                                                                                                                                                                                                                            BH886739
AA797109
BI077950
BB613343
BE291303
BI659501
BE414309
BF786998
                                                                                                                                                                                                                                                                                                                                                                            BH577830
AQ745151
CNS06YM2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           African malaria mosquito.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL141159.1 GI:6999277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 1055)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anopheles gambiae
Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pasteur.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
CNSO1EYE/C
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL141159 Anopheles
BQ954241 AGENCOURT
BR312525 601897489
AA591524 vk23e01.r
AA433531 vf43a66.r
AW052407 rs35b02.y
                                                             April 18, 2003, 04:47:40; Search time 766 Seconds (without alignments) 465.145 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                       32308132
    GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                              16154066 seqs, 8097743376 residues
                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                         OM nucleic - nucleic search, using sw model
                                                                                                                               22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNS01EYE

-BQ954241

BF312525

AA591524

AA433531

AA052407
                                                                                                                             1 tccttgcgcgctgcggcctcag
                                                                                                                                               IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           em_gss_mam:*
em_gss_mus:*
em_gss_other:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H
                                                                                                      US-09-270-437D-11
22
                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hum: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   em_gas_inv:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gss_pln:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vrt:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            em_gss_pro:*
em_gss_rod:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     em_esthum:*
em_estin:*
em_estin:*
em_estin:*
em_estin:*
em_estin:*
gb_esti:*
gb_esti:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                           em_estfun:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    estom:*
gss:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                gb_htc: *
gb_est3: *
gb_est4: *
gb_est5: *
                                                                                                                                                                                                                                                                                                            em estba:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1055
1128
1696
250
448
461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        em_g88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       em gaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ē
                                                                                                                                                                                                                                                                                                EST: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83.6
83.6
80.9
80.9
                                                                                                                  Perfect score:
                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.4
18.4
17.8
17.8
```

Score

Result ě 4100

AQ745151 HS\_5502 A AL421200 T3\_end of

source

FEATURES

BASE COUNT ORIGIN

DEFINITION

RESULT 2 BQ954241

g 8

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

AUTHORS TITLE JOURNAL COMMENT

FEATURES

REFERENCE

```
/tissue_type="meuroblastoma" /tissue_type="meuroblastoma" /tab_host="meuroblastoma" /lab_host="meuroblastoma" /lab_host="meuroblastoma" /lab_host="meuroblastoma" /lab_host="meuroblastoma" /tab_host="meuroblastoma" /tab_host="meuroblastoma" /tab_host="mearoblastom" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="mearoblastoma" /tab_host="me
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS91524
vk23e01.r1 Knowles Solter mouse blastocyst B1 Mus musculus CDNA
clone_IMAGE:947448 5', mRNA sequence.
                                                                                                                                                                                                                               BF312525
601897489F1 NIH_MGC_19 Home. sapiens CDNA clone IMAGE:4126750 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
1 (bases 1 to 250)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria, Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 1696)
HIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-romail.nih.gov
Tissue Procurement: ATCC
CONA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
High quality sequence stop: 169.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83.6%; Score 18.4; DB 12;
95.0%; Pred. No. 1.3e+03;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |db_xref="taxon:9606"
|clone="IMAGE:4126750"
|clone_lib="NIH_MGC_19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1315 rctrdcdcdcrdaddcrt 1296
                                                                                                                                                                                                                                                                                                                                                                            BF312525.1 GI:11260337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA591524.1 GI:2404837
                                                   629 TCCTTGCGCGCTGCGGACTC 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 recrirecederecederere 20
                 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                 mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Local 19; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA591524
                                                                                                                                                                                                                                                                                                                                                    BF312525
                                                                                                                                                                                                                                                                                                                                                                                                                                                 human.
                                                                                                                                                                                                                                                                                                                                                                                                                     EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
AA591524/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                 BF312525/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                  RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGIN
                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.-GACTAGTTCTAGATCGCGAGCGGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.87 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor college of Medicine) and is available through Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DV954241 1128 bp mRNA linear EST 21-AUG-2002
AGENCOURT 8864349 Lupski sciatic_nerve Homo sapiens cDNA clone
IMAGE:6197933 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capabe: Temmilinih.gov
Email: capabe: Temmilinih.gov
Enail: capabe: Temmilinih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Prarayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LiNL at:
http://image.lln.gov
Plate: LLAM1608 row: m column: 06
High quality sequence stop: 338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 1128)
11H-MGC http://mgc.ndi.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="sciatic nerve"
/dev stage="adult, 70 yr"
/lab_host="adult, 70 yr"
/lab_host="adulto"
/note="vector: pCMV-SPORT6 (Life Technologies); Site_1:
Not1; Site_2: Sall; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TGAACCCAGGGTCGG-3' and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.6%; Score 18.4; DB 14; Length 1128; ilarity 95.0%; Pred. No. 1.2e+03; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                    ch 83.6%; Score 18.4; DB 17; Length 1055; 1 Similarity 95.0%; Pred. No. 1.2e+03; 19; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone_lib="Lupski_sciatic_nerve"
Location/Qualifiers
1. .1055
/organism="Anopheles gambiae"
                                                                                                                                                                                                                                                                 320 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
db_xref="taxon:9606"
clone="IMAGE:6197933"
                                                                                                                        /db.xref="texon:7165"
/clone="03E18"
/clone=11b="NotreDame1"
/note="end : SP6"
a 230 c 255 g 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BQ954241
BQ954241.1 GI:22369719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Technologies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262 ccrrdcccccrcrck 243
                                                                                                   /strain="PEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 CCTTGCGCGCTGCGGCCTCA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                            ಹ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   296
                                                                                                                                                                                                                                                                     244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human.
```

ö

Gaps ; 0

BASE COUNT ORIGIN

AUTHORS

```
100 t
                                                                                                                                                                                    organism="Mus musculus"
                                                                                                                                                                                                                                                                                                          /dev_stage="4 weeks"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                           tissue_type="heart"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 ccardccccrccccrcrcac 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pristionchus pacificus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTTGCGCGCTGCGGCCTCAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW052407
AW052407.1 GI:5914766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence.
                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
AW052407/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
COMMENT
                                                                                                                                              FEATURES
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            448 bp mRNA linear EST 29-MAY-1997 Vf43a06.rl Soares mouse NbMH Mus musculus cDNA clone IMAGE:846514 AA433531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla, Eutherla, Rodentia, Sciurognathi, Muridae, Murinae, Mus. I (dases I to 448) Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theisling, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Putative full length read vector to vector length is 251.
                                                                                                                           Contact: Marra M Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

80.9%; Score 17.8; DB 9; Length 250;
Best Local Similarity 90.5%; Pred. No. 1.66+03;
Matches 19; Conservative 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                 1. .250.
/organism="Mus musculus"
/strain="G57BL/6J x DBA/2J Fl"
/db_xref="teaxon:10090"
/clone="IMAGE:947448"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 t
                                                                        Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 CCCTGCGCGCTGCGTCTCAG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 CCTTGCGCGCTGCGGCCTCAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA433531.1 GI:2138449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
AA433531/c
LOCUS
DEFINITION
                                                                                   TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                           FEATURES
```

ò 셤

```
1 (bases 1 to 461)

McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T.,
Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.
Glbbons,M., Ritter,E., Bennett,J., Franklin,C., Tasgareishvilli,R.,
Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood, K., Steptoe,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:49866
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
The library was constructed by Dr. Ralf Sommer DNA Sequencing by:
Washington University Genome Sequencing Center
Contact Dr. Ralf Sommer (ralf.sommer@tuebingen.mpg.de) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW052407
r835b02.yl Sommer Pristionchus Pristionchus pacificus cDNA 5-
similar to SW:MYSA_CAEEL P12844 MYOSIN HEAVY CHAIN A ,, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pristionchus pacificus
Bukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80.9%; Score 17.8; DB 9; Length 448; 90.5%; Pred. No. 1.8e+03; 1.ve 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Washington Univ. Nematode EST Project, 1999
                                                                                                                                                                                                                                                                 /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:846514"
/clone_lib="Soares mouse NbMH"
```

ö

```
Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 CCTTGCGCGCTGCCTCCTCAG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE254482
BE254482.1 GI:9124910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="TU-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 cerracecerraces 22
                                                                                                                                              345 cerrececececececice 325
                                                                                                22
                                                                                                                                                                                                                                                                                                                                                                   AV433340.1 GI:8588565
  80.9%;
90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159 C
                                                                                             2 CCTTGCGCGCTGCGGCCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 512)
       0.09
Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20363100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
BE254482/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ROUTCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                               RESULT 8
AV433340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                      g
                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Eukaryota, Viridiplantae, Streptophyta, Eukaryota, Viridiplantae, Liliopsida, Poales, Poaceae, PACC clade, Panicoideae, Andropogoneae, Sorghum.

El (Dasses I to 490)

El (Dasses I to 40)

El (Dasses I to 40)

Ingublished (2000)

Unqublished (2000)

Lontact: Cordonnier-Pratt, MM

Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 583 0210
                                                                                                                                                 1..490
//crganism="Sorghum bicolor"
//db_xxef="taxon:4558"
//db_xxef="taxon:4558"
//clone lib="Embryo (EM1)"
//note="Organ: Embryos germinated for 24 hr; Vector:
//note="Organ: Embryos germinated for 24 hr; Vector:
//note="Organ: Embryos germinated for 24 hr; Vector:
//note="Organ: Embryos germinated for 24 hr; Vector:
//note="Organ: Embryos germinated for 24 hr; Vector:
//note="Organ: Embryos germinated for 24 hr; Vector:
//note="Organ: Embryos germinated for 24 hr; Vector:
//note="Organ: Embryos germinated for 24 hr; Vector:
//note="Organ: Embryos germinated for 24 hr; Vector:
//note="Organ: Embryos germinated for 24 hr; Vector:
//note="Organ: Embryos germinated for 24 hr; Vector:
//note="Organ: Embryos germinated for 24 hr; Vector:
//note="Organ: Embryos germinated for 24 hr; Vector:
//note="Organ: Embryos germinated for 24 hr; Vector:
//note="Organ: Embryos germinated for 24 hr; Vector:
//note="Organ: Embryos germinated for 24 hr; Vector:
//note="Organ: Embryos germinated for 24 hr; Vector:
//note="Organ: Embryos germinated for 24 hr; Vector:
//note="Organ: Embryos germinated for 24 hr; Vector:
//note="Organ: Embryos germinated for 24 hr; Vector:
//note="Organ: Embryos germinated for 24 hr; Vector:
//note="Organ: Embryos germinated for 24 hr; Vector:
//note="Organ: Embryos germinated for 24 hr; Vector:
//note="Organ: Embryos germinated for 24 hr; Vector:
//note="Organ: Embryos germinated for 24 hr; Vector: 24 hr; Vector:
//note="Organ: Embryos germinated for 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 hr; Vector: 24 h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ьваь 5076
EMI 33_A11.bl_A002 Embryo 1 (EM1) Sorghum bicolor cDNA, mRNA
sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyÄ, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11arity 90.5%; Score 17.8; DB 10; Length 461; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 others
                                                                                                                    /organism="Pristionchus pacificus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prepared by mass excision."
199 c 178 g 38 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seg primer: JEN REV
High quality sequence stop: 484
POLYA-No.
information about this clone.
Seg primer: -40RP from Gibco
High quality sequence stop: 414.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 CCTTGAGCGCTGCGGCCTCGG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG465076.1 GI:13393954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 ccrrecececrececrcae 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sorghum.
                                                                                                       1, .461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG465076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG465076/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
```

```
BE254482 708 bp mRNA linear BST 13-JUL-2000 601111575F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352314 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                   AV433340 AV43340 Porphyra yezoensis TU-1 Porphyra yezoensis cDNA clone PM027e05 r.5', mRNA sequence.
AV433340
                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Abases 1 to 708)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Porphyra yezoensis TU-1"
/note="vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-WGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 514)
Nikaido,I., Asamizu,B., Nakajima,M., Nakamura,Y., Saga,N. and
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          Porphyra yezoensis.
Porphyra yezoensis
Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Generation of 10,154 expressed sequence tags from a leafy gametophyte of a marine red alga, Porphyra yezoensis DNA Res. 7, 223-227 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 512;
Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80.9%; Score 17.8; DB 10;
ilarity 90.5%; Pred. No. 1.8e+03;
Conservative 0; Mismatches 2;
  Score 17.8; DB 12;
Pred. No. 1.8e+03;
): Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .512
/organism="Porphyra yezoensis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 t
                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:2788"
/clone="PM027e05_r"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 g
```

```
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 CCTTGCGCGCTGCAGCCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nemut.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                       AL519496/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
AL528423/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                             /organism="Homo sapiens"
/db_xxef="taxon:9606"
/clone="InAMOR:335214"
/clone="InAMOR:335214"
/clone="InAMOR:335214"
/clone="Della MCC 16"
/tissue type="retinoblastoma"
/lab.host="PH10B (phage-resistant)"
/note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2: EcoR1; cDNA made by oligo-dT priming. Directionally-cloned into EcoR1/XhoI sites using the following 5' in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superseript II RT (Life Technologies).
36 a 159 c 188 g 125 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   767 bp mRNA linear EST 07-MAY-2001
60267936SFI NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4811824 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 767)
NH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Thasue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
TOSHIYUKi and Piero Carminci (RIKEN)
TOSHIYUKi and Piero Carminci (RIKEN)
TOSHIYUKi and Piero Carminci (RIKEN)
TOSHIYUKi and Piero Garminci (RIKEN)
TOSHIYUKi and Piero Garminci (RIKEN)
TOSHIYUKi and Piero Carminci (RIKEN)
TOSHIYUKi and Piero Carminci (RIKEN)
TOSHIYUKi and Piero Garminci (TIML)
TOSHIYUKi and Piero Garminci (TIML)
Flate: LiAMI0703 row: b column: 17
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: McC.clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
High quality sequence stop: 588.
Location/Qualifiers
1. 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: brain; Vector: pBluescriptR (modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17.8; DB 10; Length 708;
Pred. No. 1.9e+03;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="NIH MGC_95"
/tissue_type="hippocampus"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .767
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 616.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
/clone="IMAGE:4811824"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 ccrrececerreces 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BG699633.1 GI:13968143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 90.5%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
BG699633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
BG699633/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
```

ઠે 윱

```
/tissue_type="neuroblastoma cells"
/lab host="DH108"
/note="Organ: brain, Vector: pCMVSPORT 6; lst strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco FW sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact: Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Ball filangelifetech.com URL:
http://f.ilangelifetech.com URL:
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         856 bp mRNA linear EST 13-FEB-2001
AL519496 LTI_NPL004_NBC2 Homo sapiens cDNA clone CSODB004YI22 S
Arteson.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 856)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Organization
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Emall: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                                                Length 767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.9%; Score 17.8; DB 9; Length 856; 90.5%; Pred. No. 2e+03; .ive 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 others
                                                                                                                                                                                                                                            Query Match

80.9%; Score 17.8; DB 12;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /fulllength.invitrogen.com"
9 c 257 g 139 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone="CS0DB004Y122"
/clone_lib="LTI_NFL004_NBC2"
/eex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL519496.1 GI:12782989
                                                                                                                                                                                                                                                                                                                                   2 CCTTGCGCGCTGCGGCCTCAG 22
                                                                                                                                                                                                                                                                                                                                                               53 CCTTGCGCGCTGCAGCCCCAG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 CCTTGCGCGCTGCGGCCTCAG 22
```

```
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 C
                                                                                                               3 (bases 1 to 936)
Genoscope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5', mRNA sequence.
                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
BQ684757/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                          REFERENCE
AUTHORS
                                                                                                                                                                    TITLE
JOURNAL
                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                         COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N AL229108

AL229108.1 GI:7888103

AL229108.1 GI:7888103

AL229108.2 GI:7888103

AL229108.1 GI:7888103

GSS; genome survey sequence.

Tetraodon nigroviridis.

SM Tetraodon nigroviridis.

Achinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei, Achinopterygii, Neopterygii, Percomorpha, Tetraodontiformes, Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes, Acanthomorpha, Tetraodontiformes, Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes, Bost-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Bernot, A., Barnot, A., Ressenbach, U., Brottier, P., Quetier, F., Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="neuroblastoma cells"
/tissue_type="neuroblastoma cells"
/lab host="DH10B"
/lab host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6, 1st strand cDNA
/note="Organ: brain; Vector: pCMVSPORT 6; list strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
enriched, double-stranded cDNA was digested with Not I and
enriched, into the Not I and Eco RV sites of the pCMVSPORT 6
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
by Life Technologies. Contact: Feng Liang Life
by Life Technologies. Contact: Feng Liang Life
Drive Rockville, Maryland 20850, USA Fax: (1) 301 610
Drive Rockville, Maryland 20850, USA Fax: (1) 301 610
Http://fullength.invitrogen.com"
http://fullength.invitrogen.com"
83 a 302 c 273 g 145 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gld by DNA linear GSS 15-WAY-2000 Tetracdon nigroviridis genome survey sequence PUC-Ori end of clone 214B09 of library G from Tetracdon nigroviridis, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                          AL528423 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC029YH22 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 936)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primatee; Catarrhini; Hominidae; Homo. Li, W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.9%; Score 17.8; DB 9;
90.5%; Pred. No. 2e+03;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODC029YH22"
/clone_lib="LTI_NFL003_NBC3"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTTGCGCGCTGCGGCCTCAG 22
                                                                                                                        AL528423.1 GI:12791916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTTGCGCGCTGCAGCCCCAG
                                                                                     prime, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Local 19; Conserve
                                                                                                           AL528423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
CNS035RV
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35
                                                    LOCUS
DEFINITION
                                                                                                                                                                           SOURCE
                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                             ACCESSION
                                                                                                                                     VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
/ordenism="Homo sapiens"
/by xref="taxon:9606"
/clone="InMAGE:6250250"
/clone="InMAGE:6250250"
/clone="InMAGE:6250250"
/clone="InMAGE:6250250"
/clone="InMAGE:6250250"
/clone="InMAGE:6250250"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone="InMAGE:62500"
/clone=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BQ684757
AGENCOURT_8343533 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6250259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: capabs-remail.nih.gov
Tissue Procurement: ArC.
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
tolumn: 12
High quality sequence stop: 710.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (12-APR-2000)
Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large rhis sequence is a single read project of the Terraodon nigroviridis scale clone-end sequencing project of the Terraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (Dases 1 to,938)
          of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="G"
/note="Genoscope sequence ID : C0AG214CA05SP1~end
Weissenbach, J.
Charaterization and repeat analysis of the compact genome
freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17.8; DB 1
pred. No. 2e+03;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              276 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BQ684757
BQ684757.1 GI:21810073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 rchcececereces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 80.9%;
Best Local Similarity 90.5%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 recrrecedencedecerca
```

```
BG617183 961 bp mRNA linear EST 18-APR-2001
G2015581F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4734237 5',
MRNA sequence.
BG617183
                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryoča, Metazoa; Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 961)
of California, Berkeley) using ZAP-cDNA synthesis Kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
http://image.llnl.gov
Round chrowel the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov a column: 22
High quality sequence stop: 211.
                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                             ô
                                                                                                       Query Match

80.9%; Score 17.8; DB 14; Length 938;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        °,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

80.9%; Score 17.8; DB 12; Length 961;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
/clone="IMAGE:4734237"
/clone llb="NIH MGC 76"
/lab_host="DH10B (TI phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .961
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                             BG617183.1 GI:13668554
                                                                                                                                                                                    2 CCTTGCGCGCTGCGGCCTCAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                704 rctrdcgcgccgccdctrck 684
                                                                                                                                                                                                                        26 ccrricciccicidadeccedas 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TCCTTGCGCGCTGCGGCCTCA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253
                                                                                                                                                                                                                                                                                                                                                                                                                                     human.
                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                            RESULT 15
BG617183/c
                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                  LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                    δ
                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
```

Search completed: April 18, 2003, 07:31:53 Job time : 770.167 secs

			I
		·	
			* · · · · · · · · · · · · · · · · · · ·
			9. 1.
	·		

```
April 18, 2003, 04:46:26; Search time 305.273 Seconds (without alignments) 2192.677 Million cell updates/sec
                                                                                                                                                                                                                                                                             4109280
GenCore version 5.1.4 p5_4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                             2054640 segs, 14551402878 residues
                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                       1 ccaactggtggccattcagcttc 23
                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                    OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                   IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                em_htgo_mus:*
em_htgo_other:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      em_htg_vrt:*
em_sy:*
em_htgo_hum:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    em_vi:*
em_htg_hum:*
em_htg_inv:*
em_htg_other:*
em_htg_other:*
                                                                                                                                         US-09-270-437D-12
23
                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                      9b htg: *
9b_om: *
9b_om: *
9b_om: *
9b_ox: *
9b_ox: *
9b_ph: *
9b_r: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fun:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hum:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        em om:
                                                                                                                                                                                                                                                                                                                                                                                                          GenEmbl: *
                                                                                                                                         Title:
Perfect score:
Sequence:
                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                              Searched:
                                                                                    Run on:
```

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		AR171864 Sequence	Sequen	Homo	Homo B	Homo	Homo	Ношо	AC025556 Homo 8ap1	ACOSILIS HOMO BADI	Iner	ACTOTOSS MUB MUBCU	Mus	Mus	ACISTUS MUB MUBCU	בלים שיים היים היים היים היים היים היים הי	SCOTOR DECLOSES	TINGO TO CIOSCOTA	Lidacana Ascalona	AL135901 Human DNA	AC009208 Drosophil	ALBORI14 Mus muscu		Drosc		Mous	Drosc	Homo	MUB	AJZ/7662 HOMO Bapi	ACOLSZUO HOMO	2007	Mer n	Human	APON4285 Homo Rapi	Rattu	AC073330 Homo sapi	Human	Ношо	Ното ва		Mus musc	Ното вар	AC118834 Rattus no			14nesr DAT 17-DEC-2001							Stockert, E., Jager, E., Alexander, K.	ling cancer associated antigen.	מונים מונים
OI B	1 :																								0	0																	9 AC079630		ALIGNMENTS			patent US 6297364.		7910814				Tsang, S.,	id molecule encoding	
% Query Match Length Di		.0 1708	00.0 1946	00.0 2130	00.0 2381	00.0 65435	00.0 147767	00.0 154604	00.0 159122	00.0 168613	.1 499350	.3 54441	.3 5444I	יייייייייייייייייייייייייייייייייייייי	260//2 5	0771	7 3536	3022	7 14668	7 149433	7 152443	.7 179191	.7 181542	.7 182494	.7 205336	.7 226950	7 257909	0 131145	.0 TP8037	.U 1/4986	0 2138/3	01001	1 10918	1 133451	1 145327	1 152760	.1 155704	.1 156461	.1 168140	.1 168949	.1 175882	.1 176128	79.1 178388 9	.1 178588			AD171864	5 from		1 GI:1	Unknown.	Unknown.	assitied. (bases 1 to 1708)		and Old,L.J. Isolated mucleic acid	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
Result No. Score		c 1 23	7	(7)	4	~	0	7	. 7	,	7 5	, c	12 19.	17	14	. 01	17	18	19	20 18.	1 18.	22 18.	23 18.	24 18.	25 18.	9 1	27 18.	28		30 18	D a	22 10.	0 4	35	18.	7 18.	38 18.	9 18.	0 18.	1 18.	42 18.	43 18.	c 44 18.2	18.		RESULT 1	,	z	ž	VERSION ARI7		ORGANISM Unkn		AUTHORS Chen	and TITLE IBOL	

```
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOURCE
                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
AF198254/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                               BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEYWORDS
 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                               ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               요
                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRI 26-JAN-1999
mRNA, complete
                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                PAT 17-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Z (Dases 1 to 2130)
Nielsen,J., Christiansen,J., Lykke-Andersen,J., Johnsen,A.H.,
Wewer,U.M. and Nielsen,F.C.
Direct Submission
Submitted (30-DEC-1998) Institute of Molecular Biology, University
of Copenhagen, Soelvgade 83H, Copenhagen DK-1307, Denmark
                                                                                                                                                                                                                                                                                                                                                                           Olionashine...

(Dases 1 to 1946)

Chen,Y.-T., Gure,A., Tsang,S., Stockert,E., Jager,E., Alexander,K. and Old,L.J.

Isolated nucleic acid molecule encoding cancer associated antigen, the antigen itself, and uses thereof

Patent: US 6297364-A 7 02-OCT-2001;

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (2013)
Nielsen; J., Christiansen, J., Lykke-Andersen, J., Johnsen, A.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wewer, U.M. and Nielsen, F.C.
A family of insulin-like growth factor II mRNA-binding proteins
represses translation in late development
Mol. Cell. Biol. 19 (2), 1262-1270 (1999)
                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                   ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1946;
                                                                                                   core 23; DB 6; Length 1708; red. No. 0.94; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF117106 2130 bp mRNA linear
Homo gapiens IGF-II mRNA-binding protein 1 (IMP-1)
                                                             5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 23; DB 6; 100.0%; Pred. No. 0.95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               u
                                                               ų
   Patent: US 6297364-A 5 02-OCT-2001;
Location/Qualifiers
1. .1708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                               314
                                                                                                                                                                                                                                                                AR171866 1946 bp
Sequence 7 from patent US 6297364.
AR171866
                                                                                                       Score ?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="unknown"
528 c 553 g
                                              /organism="unknown"
                                                               þ
                                                               473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 CCAACTGGTGGCCATTCAGCTTC 284
                                                                                                                                   .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23
                                                                                                                                                                                 68 CCAACTGGTGGCCATTCAGCTTC 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                               1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                           AR171866.1 GI:17910816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF117106
AF117106.1 GI:4191607
                                                                                                       Query Match
Best Local Similarity 100.0%;
Matches 23; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CCAACTGGTGGCCATTCAGCTTC
                                                             469 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .1946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                     Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                               447 a
                                                                                                                                                                                                                                                                                                                                      Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Simi
Matches 23;
                                                                                                                                                                                                                                      RESULT 2
AR171866/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS
DEFINITION
                                     source
                                                                                                                                                                                                                                                                                                                                        SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF117106/c
                                                               BASE COUNT
                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE
PUBMED
         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
                                                                              ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                            셤
                                                                                                                                                                  ઠ
```

```
/translation="MOKLYIGNLNESVTPADLEKVPAEHKISYSGQFLVKSGYAFVDC
PDEHWAMKAIETFSGKVELQGKRLEIEHSVPKKQRSRKIQIRNIPPQLRWEVLDSLLA
QYGTVENCEQVNTESETAVNAVTYSRREGTRQAIMKLNGHQLENHALKVSYIPDBQIA
QYGTVENCEQVNTESETAVNAVTYSRREGTRQAIMKLNGHQLENHALKVSYIPDBQIA
ROBENGRREGGEGSGRGQPRQGSPVAAGAPAKQQOVDIPLRLLVPTQYVGAIIGKEGATI
RNITKQTQSK LDVHRENAGAAEKAISVHSTPEGCSSACKMILBIMHGEAKDTYTADE
VPLKILAHNNFVGRLIGKEGRNIKKVVEQDTETKITISSLQDLTLYNPERTITVKGAIE
NCCRAEQEIMKKVREAYENDVAAMSLQSHLIPGLNIAAVGLFPASSSAVPPPPSSYTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF198254 2381 bp mRNA linear PRI 02-MAR-2000
Homo sapiens mRNA-binding protein CRDBP mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAPYSSFMQAPEQEMYQVFIPAQAVGAIIGKKGQHIKQLSRFASASIKIAPPETPDSK
VRMVIITGPPEAQFKAQGRIYGKLKEENFFGPKGEVKLETHIRVPASAAGRVIGKGGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 2381)
Ioannidis, P., Trangas, T., Dimitriadis, E. and Samiotaki, M.
Direct Submission
Submitted (25-0CT-1999) G. Papanikolaou Research Center, St Savvas Hospital, 171 Alexandras Avenue, Athens, Attica 11522, Greece Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVNELQNLTAAEVVVPRDQTPDENDQVIVKIIGHFYASQMAQRKIRDILAQVKQQHQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. I (bases I to 2381)
Ioannidis,P., Trangas,T., Dimitriadis,E., Samiotaki,M., Panoutsakopoulos,G., Kyriazoglou,I., Voutzoulias,S., Falapalis,C.M., Kittas,C., Agnantis,N. and Pandis,N. Ectopic expression of a KH-domain containing protein, highly homologous to both human IMP-1 and mouse CRD-BP, in benign and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /notes"KH-domain containing protein; similar to Mus musculus CRD-BP (C-myc mRNA coding region determinant-binding protein) and Homo sapiens IMP-1 (insulin growth factor II mRNA-binding protein)"
                                                                                                                                                                                                                       'note="binds multiple sites in IGF-II mRNA 5'UTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 23; DB 9; Length 2130; 100.0%; Pred. No. 0.95; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                       /product="IGF-II mRNA-binding protein 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            395 t
                                                                                                                                                                                                                                                                                                                        /protein_id="AAD09826.1"
/db_xref="GI:4191608"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .2381
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"

    .2130
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    .72130

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  malignant mesenchymal tumors
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /map="17q21.3-q22"
/cell_line="MCF-7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                584 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            442 CCAACTGGTGGCCATTCAGCTTC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                            codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF198254.1 GI:7141071
                                                                                                                            /gene="IMP-1"
                                                                                                                                                                                     gene="IMP-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GQSNQAQARRK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
```

BASE COUNT ORIGIN

```
): gap of
3058: con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : gap
5340:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4572:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3793:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3794 3893:
3894 457
4573 4672:
4673 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280 2379:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bitten, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Baatlan, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Baatlan, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campoplano, A., Chang, J., Chock, A., Cooke, P., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Colangelo, M., Collins, S., Collymore, A., Cook, S., Govette, M., Collins, S., Collymore, A., Cook, S., Glande, S., Goyette, M., Cage, D., Galagan, J., Gardyna, S., Gord, S., Goyette, M., Kells, C., LaRocque, K., Landers, T., Lehoczky, J., Levine, R., Liu, G., Macthews, C., Macchand, P., McKernan, K., Marguis, N., Matthews, C., Macchand, P., Major, J., Marguis, N., Matthews, C., Macchan, C., McEvan, P., McKernan, K., Morpheeters, R., Milova, T., Milonga, Y., Murphy, T., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Naylor, 
                                                                                                      / translation= www.yrgytold.
/ translation= www.yrgytoldexypadlexypadhkisysggplyksgyapydc
PDEHWAMKA IETFSGKVELGGRRLEIEHSVPKKORSRKIGIRNIPPOLRWEVLDSLLA
QYGTVENCEQUNTESETAVWNYYSRREQTROAIMKLANGHOENHALKYSYIPDBGIA
QYGTVENCEQUNTESETAVWNYYSRREQTROAIMKLANGHOENHALKYSYIPDBGIA
QOPBUNGRRGGRGSRGORGSPVAAGAPAKOQOYDIPLLLUYPTQYYGAIIGKEGATI
RNITKQTQSKLDVHRKENAGAAEKAISVHSTPEGCSSACKMILBIMHKEAKDTKTADE
PRYTLAHNIVYGRLIGKGRRAIMKKVEDDTFTKTTISSLQDITTYNPERTITYKGAIE
NCCRARGEIMKKVRASYENDVAAMSLQSHLFFGLNLAAVGLFPASSSAVPPPSSYY
AAPYSSFWQAPEQEWVQVFIPAQAVGAIIGKKGQHIKQLSRFASASIKTAPPETPDSK
TVNBLIGNLTAABVVVERDQTPDBENDQVIVKIIGHFYASQMAGRKIRDILAQVKQOHQK
GQSNQARRK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65435 bp DNA linear HTG 13-DEC-2001 SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 23; DB 9; Length 2381; 100.0%; Pred. No. 0.96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
/product="mRNA-binding protein CRDBP"
/protein_id="AAF37203.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone RP11-78C17 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        434 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    664 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       738 ccaacregregecarreagerre 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC104587.1 GI:17646987
HTG; HTGS_PHASE0.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 65435)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    687 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    596 a
```

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE JOURNAL REFERENCE

AUTHORS

REFERENCE

TITLE JOURNAL

COMMENT

DEFINITION

RESULT 5 AC104587 LOCUS

ò 셤

```
NOTE: This record contains 84 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. Will be sequenced to completion. In the event that the record is updated, the accession number will
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project_Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9474 9497 95 100 bb 5441 6128; contig of 688 bp in length 6129 628; gap of 100 bp 629 6309; contig of 681 bp in length 629 6309; contig of 611 bp in length 6910 7009; gap of 100 bp 7710 7010 7726; contig of 611 bp in length 7727 826; gap of 100 bp 8508 8607; gap of 100 bp 8608 9282; contig of 675 bp in length 8508 8607; gap of 100 bp 100 bp 10056 10155; gap of 100 bp 10056 10155; gap of 100 bp 10056 10155; gap of 100 bp 100 bp 10156 10165; gap of 100 bp 100 bp 10156 10165; gap of 100 bp 100 bp 10156 101616; contig of 670 bp in length 10156 10161; contig of 681 bp in length 11717 116; gap of 100 bp 100 bp 118178 11377; contig of 681 bp in length 11378 11377; contig of 681 bp in length 11378 11377; contig of 681 bp in length 11378 11377; contig of 681 bp in length 11378 11377; gap of 100 bp 1100 bp 11378 11377; contig of 681 bp in length 11378 11377; contig of 681 bp in length 11531 11534; contig of 705 bp in length 11531 11534; contig of 705 bp in length 11531 1534; contig of 703 bp in length 11531 1534; contig of 703 bp in length 11531 1543; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16338 16437; gap of 100 bp 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16438 17126: contig of 689 bp in length 17127 17266: gap of 100 bp 1727 17266: gap of 100 bp 1727 17266: gap of 100 bp 17298 17998 19654: contig of 657 bp in length 17998 19654: gap of 100 bp 18755 18754: gap of 100 bp 18755 18754: gap of 100 bp 18759 20216: contig of 684 bp in length 19539 20216: contig of 684 bp in length 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of 100 bp 20217 20316: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 bp
of 635 bp in length
100 bp
of 679 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                680 779: gap of 100 bp
780 1495: contig of 716 bp in length
1496 1595: gap of 100 bp
1596 2279: contig of 684 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 bp
E 679 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 bp
E 668 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          679: contig of 679 bp in length
                                                                                                                                                                                     Center project name: L22859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig of
                                                                                                                                                                                                                                               Center clone name: 78_C_17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig of
```

```
13494 347943; agap or 100 bp 31492; agap of 100 bp 31492; agap of 100 bp 31402; agap of 100 bp 31402; agap of 100 bp 31402; agap of 100 bp 31502; agap of 100 bp 31502; agap of 100 bp 31502; agap of 100 bp 31502; agap of 100 bp 31503; agap of 100 bp 31503; agap of 100 bp 31503; agap of 100 bp 31503; agap of 100 bp 31503; agap of 100 bp 31503; agap of 100 bp 31503; agap of 100 bp 31503; agap of 100 bp 31503; agap of 100 bp 31503; agap of 100 bp 31503; agap of 100 bp 31503; agap of 100 bp 31503; agap of 100 bp 31503; agap of 100 bp 31503; agap of 100 bp 31503; agap of 100 bp 31503; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 100 bp 40559; agap of 
18 22550: contig of 673 bp in length 22550: contig of 673 bp in length 151 22650: gap of 100 bp in length 23305: contig of 655 bp in length 162 23305: contig of 655 bp in length 162 23405: gap of 100 bp in length 162 25697: gap of 100 bp in length 162 25697: contig of 686 bp in length 162 25697: contig of 686 bp in length 162 25697: contig of 688 bp in length 162 2555: gap of 100 bp in length 162 2555: gap of 100 bp in length 162 2555: gap of 100 bp in length 163 2597: contig of 689 bp in length 163 28905: contig of 689 bp in length 163 28905: contig of 689 bp in length 163 28905: contig of 680 bp in length 163 28905: contig of 680 bp in length 163 28005: contig of 680 bp in length 163 28005: contig of 680 bp in length 163 28005: contig of 680 bp in length 163 28005: contig of 680 bp in length 163 28005: contig of 680 bp in length 163 28005: contig of 680 bp in length 163 28005: contig of 680 bp in length 163 28005: contig of 680 bp in length 163 28005: contig of 680 bp in length 163 28005: contig of 680 bp in length 163 28005: contig of 680 bp in length 183 28005: contig of 680 bp in length 183 28005: contig of 680 bp in length 183 28005: contig of 680 bp in length 183 28005: contig of 680 bp in length 183 28005: contig of 680 bp in length 183 28005: contig of 680 bp in length 183 28005: gap of 1800 bp in length 183 28005: gap of 1800 bp in length 183 28005: gap of 1800 bp in length 183 28005: gap of 1800 bp in length 183 28005: gap of 1800 bp in length 183 28005: gap of 1800 bp in length 183 28005: gap of 1800 bp in length 183 28005: gap of 1800 bp in length 183 28005: gap of 1800 bp in length 183 28005: gap of 1800 bp in length 183 28005: gap of 1800 bp in length 1800 bp in length 1800 bp in length 1800 bp in length 1800 bp in length 1800 bp in length 1800 bp in length 1800 bp in length 1800 bp in length 1800 bp in length 1800 bp in length 1800 bp in length 1800 bp in length 1800 bp in length 1800 bp in length 1800 bp in length 1800 bp in length 1800 bp in length 1800 bp in length 1800 bp in length 1800 bp i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46027; gap of 100 bp
46715; contig of 688 bp in length
46815; gap of 100 bp
47517; contig of 702 bp in length
47617; gap of 100 bp
48286; contig of 669 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ap of 100 bp contig of 676 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86: gap of 100 bp 49073: contig of 687 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73: gap of 100 bp
49848: contig of 675 bp
48: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49948: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45251: gap of
45927: con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0352 30451: gap of
10452 31136: cont
1137 31236: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2694 32793: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16456 26555: gap of 27238: con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48386:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49173:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1923 32022:
                                                                                                                                                                                                                                                                                                                          24109 24208:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19849
```

```
2. Chases 1 to 14776)

Birren, B. Linton, L. Nubbaum, C., Lander, B., Ali, A., Allen, N., Anderson, S., Barren, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B. Anderson, S., Barran, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B. Brown, A., Comarata, J., Campolano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Goyder, M., Gord, S., Goyder, M., Fallen, M., Farlen, R., Kalls, C., LaRoeque, K., Lamacares, R., Landers, T., Lehoczky, J., Levine, R., Inid, G., Macchan, P., Macchan, C., Macdonald, P., Mactona, K., Macheeters, R., Machan, P., McKernan, K., McPheeters, R., Meldrim, J., Morbuc, C., Norman, C.H., O'Connor, T., O'Domnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Palyara, V., Minhova, T., Raymond, C., Retta, R., Rieback, M., Riley, R., Rieb, C., Retta, R., Rieback, M., Riley, R., Rieb, C., Retta, R., Rieback, M., Riley, R., Schauer, S., Schuback, R., Severy, P., Spencer, B., Stange-Thomann, N., Subramanian, A., Talamaa, J., Tesfaye, S., Theodore, J., Travis, M., Subramanian, A., Taraia, B., Yew, W. J., Young, G., Zainoun, J., Raymond, C., Malson, B., Wu, X., Wyman, D., Yew, W. J., Young, G., Janette, Submission

AL Submission

AL Submission

AL Submission

AL Submission

AL Submission

AL Submission

AL Submission

AL Saratas, A., Kalls, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barren, B., Chanles Street, Cambridge, MA 02141, USA

Barren, B., Chang, J., Chang, Y., Boung, C., Yong, Cook, A., Bartie, P., Petreira, P., PetraGerald, M., Gage, D., Galagan, J., Garata, A., Kalls, C., Lander, E., Macchan, R., Mathews, C., Karatas, A., Kalls, C., Lander, T., Lohnson, R., Mathews, C., Macchan, J., Mathews, C., Macchan, J., Mathews, C., Macchan, J., Mathews, C., Macchan, J., Maylen, C., Nicol, R., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Nicol, R., Nicol, R., Nicol, R., Nicol, R., Nicol, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG 06-AUG-2002
                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                      Length 65435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens chromosome 17 clone CTD-2244F11 map 17, IN PROGRESS ***, 3 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                              Indels
                            50614 50713: gap of 100 bp 50714 51405: contig of 692 bp in length 51406 51505: gap of 100 bp 51506 52203: contig of 698 bp in length 52204 52303: gap of 100 bp 52304 52997: contig of 694 bp in length 52308 539779: contig of 682 bp in length
contig of 665 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC105030.4 GI:22123404
HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 17, clone CTD-2244F11
                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                  Score 23; DB 2;
Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        982 ccaacregreeccarreagerre 1004
                                                                                                                                                                                                                                                                                                                                                                                                                            CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 147767)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 147767)
                                                                                                                                                                                                                                                                                                         100.08;
                                                                                                                                                                                                                                                                                                                                     100.08;
                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                       23;
                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
AC105030
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

us-09-270-437d-12.rge

```
4662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5912
                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schubback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J. Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-FEB-2002 Local Local DNA Linear HTG 13-FEB-2002 SEQUENCE, 23 ordered pieces.
                                                                                                                                                                                                                                                                                        Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 6, 2002 this sequence version replaced gi:21426162.
All repeats were identified using RepeatMasKer:
Smit, A.F.A. & Green, [1956-1997)
http://ftp.genome.washington.edu/RM/RepeatMasKer.html
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 154604)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 17, clone RP11-145L16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. Gaps between the contigs are represented as runs of N. The order of the places is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 bp 64311 64410; gap of 100 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 23; DB 2; Length 147767; 100.0%; Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64411 86773: contig of 22363 bp in lengum
86774 86873: gap of 100 bp
86874 147767: contig of 60894 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      495 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACI04974.3 GI:18653683
HTG; HTGS PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="CITD1 Human BAC" 34009 c 33361 g 38110 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lone="CTD-2244F11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 106124 CCAACTGGTGGCCATTCAGCTTC 106146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100. Matches 23, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41792 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC104974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                         TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC104974/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                     COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

```
Salaren, B. Lincon, L., Musbaum, C., Lander, E., Ali, A., Allan, N., Anderson, S., Barren, B., Bastren, B., Bastren, B., Bastren, B., Bastren, B., Bastren, B., Bastren, B., Camazta, J., Camportan, Camazta, J., Camportan, Camparata, J., Camportan, Camparata, J., Camportan, Collins, S., Collymore, A., Cook, A., Cooke, P., Dakrellano, K., Dewar, J. S., Dodge, S., Faro, S., Farzellano, E., Chang, J., S., Dodge, S., Faro, S., Farzellano, E., Caham, L., Cardon, B., Cardon, J., S., Dodge, S., Govet, E., M., Catham, L., Cardon, S., Cardon, J., S., Dodge, S., Govet, E., M., Cardon, J., S., Dodge, S., Govet, E., M., Cardon, J., S., Dodge, S., Cardon, J., S., Lumazta, B., Ferreira, P., Fitzhugh, W., Gage, D., Kallago, B., Heaford, A., Horron, L., Hulme, Y., Ilang, B., Heaford, A., Horron, L., Hulme, Y., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis, M., Marquis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 bp of 1240 bp in length 100 bp in length 1010 bp in length 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of 100 bp contig of 1334 bp in length of 100 bp contig of 1150 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of 100 bp contig of 1028 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig of 190 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #261: contig of #8361: gap of 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1710 1809: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000 2099: gap of
2100 3127: co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7251: gap of
8261: cor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4562 4661: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5911: gap c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1999:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3128 3227: gap
3228 4561:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5811:
```

```
95001 99700: gap of 100 bp 99701 115353: contig of 15653 bp in length 115354 115453: gap of 100 bp 113254 131355: gap of 100 bp 113254 131355: gap of 100 bp 113356 gap of 100 bp 113356 gap of 100 bp 113356 gap of 100 bp 113356 gap of 100 bp 11356 gap of 100 bp 11356 gap of 100 bp 11356 gap of 1150 bp in length
                                                                                                                                                                                                                                                                                                                                                              72422 72521: gap of 100 bp
7252 84887: contig of 12366 bp in length
8488 84987: gap of 100 bp
84988 99600: contig of 14613 bp in length
                                                                                                                                                                                                                                                                                                                        60834 60933: gap of 100 bp 72421: contig of 11488 bp in length
                                                       12106 12205: gap of 100 bp
12206 35760: contig of 23555 bp in length
35761 35860: gap of 100 bp
158001 381000: contig of 2140 bp in length
38801 38100: gap of 100 bp
38101 41369: contig of 3269 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 154604: contig of 1999 bp in length. coation/Qualifiers
                                                                                                                                                                                                                                               47401 47500: gap of 100 bp
47501 53741: contig of 6241 bp in length
53742 53841: gap of 100 bp
53842 60833: contig of 6992 bp in length
9739: contig of 1378 bp in length 9839: gap of 100 bp 12105: contig of 2266 bp in length
                                                                                                                                                                                                           94: gap of 100 bp 47400: contig of 3206 bp in length
                                                                                                                                                                      69: gap of 100 bp 44094: contig of 2625 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="RP11-145L16"
/clone lib="RPCI-11 Human Male BAC"
.1709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 840, .12105
note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2206. .35760
note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1470. .44094
note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .810. .. 1999
note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           252. .8261
note="agsembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362. .9739
note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228. .4561
note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      662. .5811
note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    912. .7151
note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="assembly_fragment
lone_end:SP6
ector_side:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
db_xref="taxon:9606"
chromosome="17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131356 152505. US 152506 152605; gap of 154604; cont.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100. 3127
                                                                                                                                                                          41370 41469:
41470 4440
                                                                                                                                                                                                               44194:
                                                                                                                                                                                                                                                                                                                                                                                                 84888 84987:
84988 996
                                                                                                                                                                                                                 44095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
```

```
AC025556 159122 bp DNA linear HTG 01-SEP-2000
Homo sapiens chromosome 17 clone RP11-501C14, WORKING DRAFT
SEQUENCE, 17 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (10-MAR-2000) Genome Sequencing Center, Washington
Notarsisty School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Sep 1, 2000 this sequence version replaced gi:8570253.
                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 159122)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Score 23; DB 2; Length 154604;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert size: 181000; agarose-fp
Insert size: 157522; sum-of-contigs
Quality coverage: 3.86 in Q20 bases; agarose-fp
Quality coverage: 4.48 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                          2202 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site:http://genome.wustl.edu/gsc/index.shtml
Project Information
Center project name: H NH0501C14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: M13, 96% acquencing vector: M13, 96% of reads Chemistry: Dye-primer ET; 96% of reads Chemistry: Dye-terminator B19 Dye, 4% of read Assembly program: Phrap; version 0.990319 consensus quality: 148686 bases at least Q40 Consensus quality: 152251 bases at least Q30 Consensus quality: 154277 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---- Genome Center -----
                              The sequence of Homo sapiens clone
               note="assembly_fragment'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC025556.4 GI:9958273
HTG; HTGS PHASE1; HTGS_DRAFT.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 133577 CCAACTGGTGGCCATTCAGCTTC 133555
                                                                                                                                                                                                                                                                                                                                                                                                                        1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 159122)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC025556
                                                                                                                                                                                                                          misc_feature
misc_feature
                                                                                                            misc_feature
                                                                                                                                                                                       misc_feature
                                        misc_feature
                                                                           misc_feature
                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
AC025556
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                               à
```

```
Homo sapiens
                                                                                                                                                                                                                                                                                                                           RESULT 9
AC091133
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                               ઠે
consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                             is contig of 7635 bp in length
contig of 7745 bp in length
gap of unknown length
gap of unknown length
gap of unknown length
contig of 9509 bp in length
contig of 9317 bp in length
contig of 9312 bp in length
gap of unknown length
contig of 11992 bp in length
gap of unknown length
contig of 11992 bp in length
gap of unknown length
contig of 13305 bp in length
contig of 13305 bp in length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
contig of 15705 bp in length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contig of 3446 bp in length gap of unknown length gap of unknown length gap of unknown length contig of 7546 bp in length contig of 7106 bp in length contig of 7106 bp in length gap of unknown length gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159122: contig of 8256 bp in length tion/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 736. .15480
note="assembly_name:Contig11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . . .7635
note="assembly_name:Contig10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .5581. .25089
/note="assembly_name:Contig12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44610. .56601
/note="assembly_name:Contig15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              )6702. .64536 --
/note="assembly_name:Contig16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4637. .79941 --
note="assembly_name:Contig17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10042. .95746
note="assembly_name:Contig18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_name:Contig19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="assembly_name:Contig4"
29247. .132692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="assembly_name:Contig3"
26912. .129146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="assembly_name:Contig6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Organism="Homo sapiens"

db_xref="taxon:9606"

chromosome="17"

(clone="RP11-501C14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132793. . 135914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .15912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/
                                                                                                                                 7636
7736
                                                                                                                                                                                                                                                  35107
44510
44610
                                                                                                                                                                                                                                                                                                                                 64537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129147
                                                                                                                                                                                                                                                                                                                                                                                                                                                  25633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEATURES
```

```
misc_feature | 136012. 143550 | Jones* Semeshy Amen:Contigo* | Misc_feature | 136012. 143550 | Jones* Semeshy Amen:Contigo* | Misco_feature | 136012. 1435056 | Jones* Misco | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopolity | Miscopoli
```

```
fami]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
repeat_region
                                                                                                                                                                                                                                            unsure
                                                            unsure
                                                                                                                         unsure
                                                                                                                                                                               unsure
                                                                                                                                                                                                                                                                                            Direct Submission

Submitted (17-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases 1 to 168613)

8 interp. B. Musbaum, C. Lander, E., All, A., Allen, N., Anderson, S., Barra, N., Bastien, V., Blonder, E., Boquslavkiy, L., Boukhgalter, B., Barra, M., Calay, J., Charg, J., Charg, J., Charg, J., Charg, J., Charg, J., Charg, J., Charg, J., Charg, J., Charg, J., Charg, J., Charg, J., Chard, J., Cook, P., Dewar, K., Diaz, J.S., Dodge, S., Farreira, P., Partelano, K., Dewar, K., Diaz, J.S., Dodge, S., Farro, S., Ferreira, P., Pitzerald, M., Gage, D., Galagan, J., Farco, S., Ferreira, F., Tilev, J., Johnson, R., Indblad-Toh, K., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Karatas, A., Kells, C., Landers, T., Marthews, C., Mordan, C., Micol, R., Norbu, C., Norman, C., Machean, C., Macdonald, P., Malon, M., Mallen, J., Meneus, L., Mihova, T., Mlenga, V., Naylor, J., Olomell, P., O'Gunnor, T., O'Donnell, P., O'Nell, D., Oliver, M., Res, C., Rogov, P., Ruman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Roman, J., Roy, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Nicol, R., Vo, A., Wilson, B., Ww, Myman, D., Young, G., Zainoun, J., Liber, C., Limer, A., and Zody, M., A., Alles, C., A., Alles, C., A., Alles, C., A., Alles, C., A., Alles, C., A., Alles, C., A., Alles, C., A., Alles, C., A., Alles, C., A., Alles, C., A., Alles, C., A., Alles, C., A., Alles, C., A., Alles, C., A., Alles, C., A., Alles, C., A., Alles, C., A., Alles, C., Alles, C., Alles, C., Alles, C., A., Alles, C., Alles, C., A., Alles, C., Alles, C., Alles, C., Alles, C., Alles, C., Alles, C., Alles, C., Alles, C., Alles, C., Alles, C., Alles, C., Alles, C., Alles, C., Alles, C., Alles, C., Alles, C., Alles, C., Alles, C., Alles, C., Alles, C., Alles, C., Alles, C., Alles, C., Alles, C., Alles, C., Alles, C., Alles, C., Alles, C., Alles, C., Alles, C., Alles, C., Alles, C., Alles, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published (01-010-2002) Whitehead Institute/MIT Center for Genome Submitted (01-010-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 1, 2002 this sequence version replaced gi:21431160.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

thtp://ftp.genome.washington.edu/RM/RepeatMasker.html

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, R., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Schopback, R., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Triglilo, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zahnoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www-seg.wi.mit.edu
Contact: sequence_gubmissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="RP11-501C14"
/clone lib="RPCI-11 Human Male BAC"
19. .201
rpt family="(CA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quality SNGL region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="<30 quality SNGL region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                quality SNGL region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is5. ..s19
"rpt_family="AluJb"
156. 460
'note="<30 quality SNGL region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      394. .1503
note="single clone coverage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84. .488
note="<30 qual SNGL region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: L12028
Center clone name: 501_C_14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .041. .1349
rpt_family="AluSx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1293. .1296
/note="<30 qu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1271. .1278
/note="<30 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .168613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
```

```
complement (12586. .12878)
/rpt family="AluJb"
complement (12886. .13196)
/rpt family="AluY"
13727. .13995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y="AluJb"
\46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="AluJo".
complement (1302. .11433)
/rpt_family="FRAM"
complement (11503. .11662)
/rpt_family="L2"
/rpt_family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     family="AluSx"
ement(1507)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     omplement (11961, .12034)
cpt family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  omplement (15870. .16050)
                            1649. .1653

/note="30 quality SNGL re-

/note="30 quality SNGL re-

/note="30 quality SNGL re-

1933. .1937

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNGL re-

/note="450 quality SNG
                                                                                                                                                                                                                                                                                                                         /rpr_family="AluSp"
complement (4105. 4156)
/rpt_family="MER112"
4282. 4316
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="(T)n"
complement(4318, .4415)
/rpt_family="U6"
5302, .5438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="LiM4"
complement(6003. . 6200)
/rpt_family="LiM4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt family=" (GGAA) n"
14655. 14979
/rpt family="AluSq"
15410. 15453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="AluJb"
:349. .6651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rpt_family="AluSc" 4001. .14161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt family="(CA)n"
complement (15548...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                family="AluSg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       family="AluSx"
. .11138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rpt_family="AluSx"
454. .760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   454. .7628
rpt_family="AluSc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'rpt_family="AluSx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rpt_family="AluSq"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         656. .7945
'rpt_family="AluJb"
'965. .9277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rpt_family="AluSx"365. .9650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . .10143
_family="AluSx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ses. .6941
rpt_family="AluJo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rpt family="MIR" omplement (16367.
rpt_family="AluSg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="MIR"
complement(5443.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . .14161
```

셤 ð

```
NCYGELFDRLLPHLLSGQLPENAFGALPEILNOLGRRLLATGBHDTLOLLCOOGLAWF
YPPENDDAGAWMTLGFPLGATAYFEYCLELGRTNGYSKQMIFPLGYVREIAAEQL
GRAYEALGBRERAAFAQAAALRQGKAHFQ"

ÇOMPIement (1655. . 2056)
                                                                                                                                                                                                                                                                                                                                                             /procesi__de="BAC07867.1"
/procesi__de="BAC07867.1"
/banslation="MRVYULLYNPGTENBGIHSLQLGDRNLILMFESEDDANRYAMLL
RAQDFHAPSYVAIDAREVEDFCESSGYSCHLVPEGFVFTNBAERLFLAPPERNVEETD
WERENRVPPPAESEFSESEINTRIRQPFEKLL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Cransl_table=11
/ Cransl_table=11
/ produce="biopolymer transport ExbB like protein"
/ produce="biopolymer transport ExbB like protein"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="G1:22294037"
/ db_xref="db_xref="d1:22294037"
/ db_xref="d1:22294037"
/ d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="group3 RNA polymerase sigma factor"
/protein_id="BAC07869.1"
/brotein_id="BAC07869.1"
/branslation="MSVSISISAATASTAIVTQSPVNDPDRPLIEQCIAGHPKGFREL
YQRHQQYRSILFOCGAVALDDLYQEVFLAWKGLKGLKHEAKFSTWLYRIAWNAC
DYRRQLATRKSRHQQYLDQQQPFTTAPDLRQLHYEDLYQRGLATLPFYRSILVWHDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transl_table=11
/protein_id="BAC07870.1"
/db_xref="GI:22294039"
/tb_xref="GI:22294039"
/tb_xref="GI:Z22PPTEDTNLVKFLQTYAGTPPPPPDLQERIIKAAVQQHN
WHXRCWRLGYFLGVGAIATTAASVWFLKPTAQVAEQRPADGLETFIASNWQDLFESAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /trānslation="mikkoslatilicstisplavviptlagegoggmgmkvenini
TPEGRONLGAIRGRYQSGIEETRTGLRTAKDELRRIMASNASDEGIRAKHAGVQQLQO
KLATLRFESMLATRKILTPEGRQALAERMQNRQGGRRLER"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="tiloli6"

complement (2244, 3098)

/gene="tiloli6"

/note="ORF_ID:till0316"

/codon start="

/trans1_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Jenne-1367
/ Jenne-1819H
/ note="ONF ID: tro317"
/ transl rah.
                                                                                                                                                                                     complement (1655. .2056)
                                                                                                                                                                                                              /gene="tl10315"
/note="0RF_ID:tl10315
/nypothetical protein"
/codon start=1
/trans1_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transT_table=11
protein_id="BAC07871.1"
db_xref="GI:22294040"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (2244. .3098)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="ORF ID:tlr0318
unknown protein"
/codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID:tlr0319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ypothetical protein"
                                                                                                                                                           /gene="tll0315"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3664. .3987
/gene="tlr0318"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3664. .3987
/gene="tlr0318"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1071. .4499
/gene="tlr0319"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1071. .4499
/gene="tlr0319"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3062. .3667
/gene="sigh"
3062. .3667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon start=1
trans table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4652. .7339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GEAEKTLF
                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                             BCT 17-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sasamoto, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="BAC07865.1"
/db_xref="G1:22294034"
/tanslation="MQLIYRGAKXKTSEQHIPLVBSGAKGLYRGAPWYGHKPAETVPQ
PNHVLCWRGYTYQTYQPVATTAPRVSAAPSVVPQRKRDSWVEAHRRAILETLERRLQ
COMplement (557. .1654)
/gene="t110314"
/gene="t110314"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
/protein_id="BAC07866.1"
/db_xrefe="G1:22294035"
/translation="MVRVCACLIVKNEAAHLARCLGSVQPWVDDIVVVDTGSTDETPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAROFTERLFTFPWODDFAAARNYSLEQATGDWILVIDADEVLVTLGEPPVPLGGQLA
GSPFTAYQLLRREIGTGEGPSDFAIVRLFRNLPTLRYQGRFHEQLVSTAAAPLTIGTL
ETLRIDHYGYQPAQIQAKMRDRNIPILERIRASEGLPLHLLFALADMYQAVNNPVEAE
                                                                                                                                                                                                                                                                                                                                                                                                                          P005370 299350 bp DNA linear BCT 17-AUG-20
hermosynechococcus elongatus BP-1 DNA, complete genome, section
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nakamura,Y., Kaneko,T., Sato,S., Ikeuchi,M., Katoh,H., Sasamoto Watanabe,A., Iriguchi,M., Kawashima,K., Kimura,T., Kishida,Y., Kiyokawa,C., Kohara,M., Matsumoto,M., Matsumo,A., Nakazaki,N., Shimpo,S., Sugimoto,M., Takeuchi,C., Yamada,M. and Tabata,S. Complete genome structure of the thermophilic cyanobacterium DNA Res. (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Natheor, J.

Direct Submission
Submitted (05-JUN-2002) Takakazu Kaneko, Kazusa DNA Research
Institute, The First Laboratory for Plant Gene Research; 2-6-7
Kazusa kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail:kaneko@kazusa.or.jp,
URL:http://www.kazusa.or.jp,
URL:http://www.kazusa.or.jp,
Tel:81-438-52-3935(ex.2338), Fax:81-438-52-3934)
                                                                                                                                                                           Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermosynechococcus elongatus BP-1 (strain:BP-1) DNA.
Thermosynechococcus elongatus BP-1
Bactería; Cyanobactería; Chroococcales; Thermosynechococcus.
                                                                                                                                                                    ö
                                                                                Query Match 100.0%; Score 23; DB 9; Length 168613; Best Local Similarity 100.0%; Pred. No. 1.4; Matches 23; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .299350
/organism="Thermosynechococcus elongatus BP-1"
/fstrain="BP-1"
/db_xref="taxon:197221"
/note="BP-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="ORF_ID:tll0314
probable glycosyltransferase"
/codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="tlr0313"
/note="0RF_ID:tlr0313
hypothetical protein"
/codon gtart=1
/transT_table=11
/rpt_family="Alusx"
repeat_region 17040..17157
                                                                                                                                                                                                                                           2568 CCAACTGGTGGCCATTCAGCTTC 2590
                                                                                                                                                                                                        1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83. .457
/gene="tlr0313"
83. .457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AP005370 BA000039
AP005370.1 GI:22294033
                                                                                                                                                                                                                                                                                                                                                                                                             AP005370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kaneko, T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                             RESULT 10
AP005370/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
```

```
1 ccaacregresccarreagric 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                        LOCUS
DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                    RESULT 11
AC101033
                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /procued_airpu n unbaccusaide symbological id=mac07873.1"
/db_xref="101:22294042"
/db_xref="101:22294042"
/db_xref="101:22294042"
/translation="MAHLFISTGEVSGDLGGALJVKALYRLAAERGWPLEISALGGDR
/translation="MAHLFISTGEVSGDLGALPIKPTALQUZKRYLQOHPPDLVVLIDYIGGN
MAAAGAKVLIRNTGSTIGSVGLIBALPLIKPTALQUZKRYLLASPRILAIFPERASYYRHG
VAMGQPIRRHPAIPIVYYIAPQEWWMSHGLKTTQQIJVALSNRLAIFPERASYYRHG
ANVVWYGHPLLDRIAAAPGSERVARQSIGIAADBLAILDLSRKQBIQSLLPLIGAA
ANVVWYGHPLLDRIAAPGSERVARQSIGIAADBLAILDLSRKGGT
VNLETPALLNVPQVYITKVHPLSIMLYQRFLKFNLQFVSPPNLLVGRBIAARSGT
IDNITAAAFALLDHPEKRLAMQAGYAEMRAAMGTAGVVDRAATBILNIFQNG"
complement (9225. 10364)
                                                                                                                                                                                                                                                                                                                                                                              / LIANSIAGUESTE TO SUNGSTALINGS INTERNAL STREAM CONTROL INC.

FIDELE STREAM GOVERGE TO COCKADIA SLISSLE BLADALANGE IN STREAM CONTROL INC.

SGESTLYNEP CGAELLE PRAY TO FROE TO REPREME THAT FOR THE STREAM SGESTLYNEP CGAELLE POTTRONIS STREAM SGESTLYNEP CGAELLE POTTRONIS STREAM SGESTLYNEP COCKADIA STREAM SGESTLYNE STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM STREAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="BAACO7874.1"
/protein_id="BAACO7874.1"
/db_xref="G1:22294043"
/db_xref="G1:22294043"
/translation="MLSKGFEVELYTGKPTGEIVGLSDRIVKDLPGFVREPDSRNVEF
/translation="MLSKGFEVELYTGKPTGEIVGLSDRILSLGDTQRFYRSDPQNPYH
/TYPPYYLYDQALCDLIRPRFRIAAYLOSLGDLTLVPGSTLSLGDTQRFYRSDPQNPYH
TYTEQTYTGTRVTTASVHINIGLREPERALMRACRIVRLERAPIETALSASPFLDGQVTG
TYTEQTYTGTRVTASVHINIGLREPERALMRACRIVRLERAPIETALSASPFLDGQVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YHSTRWAI FPKT PPOVPLFTSHAHFTEWTEAQLOGGTWQNVTHLWSAVRPNGDRRPYD
LNRLELRICOLVTDPIALLAITALLEARLLOLLDTPDLDPLRWGDRETLAQLADENBQ
LLARKSLEAVLTHWRDRRQLTAAWIAELYEEVWPIAKAQGFSCFLVPIKKILRQGNT
AQQNLAQYAAGQTIPEIMAQAVQEMAANBGEFADQLCPPLAIVQG"
10533. . 11003
                                                                                                                                                                                                                                                                               /protein_id="BAC07872.1"
|db_xref="G1:22294041"
|translation="MSLNQSKKTAQGTWEAPNLVYRKFQAARDIAQGFKGQWQQFSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 299350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product="lipid A disaccharide synthase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 19.8; DE Pred. No. 64; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/transI_table=11
/protein_id="BAC07875.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (8059, .9222)
/gene="tll0321"
/note="vorser"
/codon start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (9225, .10364)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein" (codon start=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="ORF_ID:tlr0323
unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (8059. .9222)
                                                                                                                                                       /note="ORF_ID:tlr0320
unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="tlr0323"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10533. .11003
/gene="tlr0323"
                                                                                                                                                                                                                                                                table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="tll0321"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ilarity 91.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene •
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                     SGS
```

```
RESERVE 11
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTION 13
ACTIO
```

```
11154 11255; gap of 100 bp 11254 11255; gap of 100 bp 11965 12064; gap of 100 bp 12065 12717; contig of 53 bp in length 12718 12817; gap of 100 bp 12718 12817; gap of 100 bp 13535 13634; gap of 100 bp 13535 13634; gap of 100 bp 13535 13634; gap of 100 bp 13635 13634; gap of 100 bp 13635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15238 15549; contig of 712 bp in length 16050 16760; contig of 711 bp in length 16761; gap of 100 bp in length 16861 gap of 100 bp in length 17571 17670; gap of 100 bp in length 17571 17670; gap of 100 bp in length 1818 18480; gap of 100 bp in length 1818 18480; gap of 100 bp in length 1818 18480; gap of 100 bp in length 1937 20077 20078; gap of 100 bp in length 1937 20082 20881; gap of 100 bp in length 2088 21590; contig of 703 bp in length 2088 21590; contig of 703 bp in length 2088 21590; contig of 703 bp in length 22394 22494; contig of 703 bp in length 22394 22494; contig of 703 bp in length 22394 22494; contig of 711 bp in length 24925 24924; gap of 100 bp 23305 24924; contig of 712 bp in length 24925 24924; gap of 100 bp 24925 25534; contig of 710 bp in length 24925 25534; contig of 708 bp in length 24925 25534; contig of 708 bp in length 25335 25534; contig of 680 bp in length 25335 25534; contig of 680 bp in length 25335 25534; contig of 680 bp in length 25335 25534; contig of 680 bp in length 25335 25534; contig of 680 bp in length 25335 25534; contig of 680 bp in length 25335 25534; contig of 680 bp in length 25335 25534; contig of 680 bp in length 25335 25534; contig of 680 bp in length 25335 25534; contig of 680 bp in length 25335 25534; contig of 680 bp in length 25335 25534; contig of 680 bp in length 25335 25534; contig of 680 bp in length 25335 25534; contig of 680 bp in length 25335 25534; contig of 680 bp in length 25335 25534; contig of 680 bp in length 25335 25534; contig of 680 bp in length 25335 25534; contig of 680 bp in length 25335 25534; contig of 680 bp in length 25335 25534; contig of 680 bp in length 25335 25534; contig of 680 bp in length 25335 25534; contig of 680 bp in length 25335 25534; contig of 680 bp in length 25335 25534; contig of 680 bp in length 25335 25534; contig of 680 bp in length 25335 25534; contig of 680 bp in length 25335 25534; contig of 680 bp in length 25335 25534; contig of 680 bp in length 25335 25334; contig of 680 bp in length 25335 25534; contig of 680 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contry control of 703 bp in length p of 100 bp control of 700 bp in length control of 700 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0 bp
705 bp in length
                                                                                                                                                      contig of 699 bp in length of 100 bp
                                                                                                                                                                                                                                                                                                                                  100 bp
f 717 bp in length
                                                                                          of 100 bp contig of 668 bp in length
                                                                                                                                                                                                                                                                                                701 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig of 697 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 bp
f 706 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9666: gap of 100 bp 10361: contig of 695 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10461: gap of 100 bp
11153: contig of 692 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14433: gap of 100 bp
15137: contig of 704 bp in length
15237: gap of 100 bp
15949: contig of 712 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig of 701 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27315: gap of 100 bp 28025: contig of 710 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 bp
710 bp in length
100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51: gap of 100 bp 31252: contig of 701 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contig of 708 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43: gap of 100 bp
30451: contig of 708 bp in length
                                                                                                                                                                                                                                                                                                contig of
                                                   contig of
                                                                                                                                                                                                                                                                                                                                                                                  contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contig of 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11965 12064
12065 12717; conta-
12718 12817; gap of
13534; cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26514: gap of
27215: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28125: gap of 28835: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28935: gap of
29643: cont
                                                                    3176 3275: 3943: 3943: 3944 4043: 989 0 4742: 989 0 4742: 989 0 6843: 989 0 6843: 989 0 6861: 9843: 989 0 6861: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9850: 6850: 9857: 9857: 9857: 9850: 6850: 9857: 9857: 9850: 6850: 9857: 9850: 6850: 9857: 9850: 6850: 9857: 9850: 6850: 9857: 9850: 6850: 9857: 9850: 6850: 9857: 9850: 6850: 9857: 9850: 6850: 9857: 9850: 6850: 9857: 9850: 6850: 9857: 9850: 6850: 9857: 9850: 6850: 9857: 9850: 9857: 9850: 9857: 9850: 9857: 9850: 9857: 9850: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 9857: 98
2470: gap
3175:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 7257: gap c
7960: gap c
8060: gap c
8760: c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8860: gap o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30551
```

```
31353 31351, gap of 100 bp
31354 31355, gap of 100 bp
31355 31365, gap of 100 bp
31365 31365, gap of 100 bp in length
31367 31776, gap of 100 bp in length
31377 34455; contig of 179 bp in length
31377 34455; gap of 100 bp in length
31377 34455; gap of 100 bp in length
31377 34455; gap of 100 bp in length
31377 3456 31563; gap of 100 bp in length
31377 3456 31563; gap of 100 bp in length
31377 3456 31563; gap of 100 bp in length
31377 3456 31563; gap of 100 bp in length
3141 3158 3159; gap of 100 bp in length
3158 3159 3159; gap of 100 bp in length
3158 3159 3159; gap of 100 bp in length
3158 3159 3159; gap of 100 bp in length
3158 3159; gap of 100 bp in length
4004 4014; gap of 100 bp in length
4004 4014; gap of 100 bp in length
4158 4174; gap of 100 bp in length
4158 4174; gap of 100 bp in length
4158 4174; gap of 100 bp in length
4158 4174; gap of 100 bp in length
4158 4174; gap of 100 bp in length
4158 4174; gap of 100 bp in length
4158 4174; gap of 100 bp in length
4158 4174; gap of 100 bp in length
4158 4174; gap of 100 bp in length
4158 4174; gap of 100 bp in length
4158 4174; gap of 100 bp in length
4158 4174; gap of 100 bp in length
4158 4174; gap of 100 bp in length
4158 4174; gap of 100 bp in length
4158 4174; gap of 100 bp in length
4158 4174; gap of 100 bp in length
4158 4174; gap of 100 bp in length
4158 4174; gap of 100 bp in length
4158 4174; gap of 100 bp in length
4158 4174; gap of 100 bp in length
4158 4174; gap of 100 bp in length
4158 4174; gap of 100 bp in length
4158 4174; gap of 100 bp in length
4174 4174; gap of 100 bp in length
4174 4174; gap of 100 bp in length
4174 4174; gap of 100 bp in length
4174 4174; gap of 100 bp in length
4174 4174; gap of 100 bp in length
4174 4174; gap of 100 bp in length
4174 4174; gap of 100 bp in length
4174 4174; gap of 100 bp in length
4174 4174; gap of 100 bp
4174 4174; gap of 100 bp
4174 4174; gap of 100 bp in length
4174 4174; gap of 100 bp
4174 4174; gap of 100 bp
4174 4174; gap of 100 bp
4174 4174; gap of 100 bp
4174 4174; gap of 100 bp
4174 4174; g
```

Db 31076 AAATGGTGGCCATTCAGCTTC 31096

RESULT 12 AC101033/c

```
22 21590: contig of 709 bp in length 21690: gap of 100 bp 21690: gap of 100 bp 22393: contig of 703 bp in length 34 22493: gap of 100 bp 22304: gap of 100 bp 22304: gap of 100 bp 22304: gap of 100 bp 24016: contig of 712 bp in length 17 2416: gap of 100 bp 25 24924: gap of 100 bp 25 24924: gap of 100 bp 25 255934: contig of 708 bp in length 25 24924: gap of 100 bp 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 255934: contig of 708 bp in length 25 2559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 14331 contig of 100 bp in length 138 15237; gap of 100 bp in length 138 15237; gap of 100 bp in length 138 15237; gap of 100 bp in length 138 15237; gap of 100 bp in length 150 150 150 150 le049; gap of 100 bp in length 150 1570; contig of 711 bp in length 151 1570; contig of 710 bp in length 1570; gap of 100 bp in length 1571 1670; gap of 100 bp in length 18480; gap of 100 bp in length 18480; gap of 100 bp in length 1913; contig of 710 bp in length 1913; contig of 700 bp in length 19183; contig of 693 bp in length 1977 20076; gap of 100 bp in length 177 20076; gap of 100 bp in length 178 2081; contig of 705 bp in length 178 2081; contig of 705 bp in length 178 2081; contig of 705 bp in length 178 2081; gap of 100 bp in length 178 2081; contig of 705 bp in length 182 20881; gap of 100 bp in length 182 21590; contig of 709 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                            25734: gap of 100 bp
26414: contig of 680 bp in length
2514: gap of 100 bp
27215: contig of 701 bp in length
27315: gap of 100 bp
27315: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25: gap of 100 bp 28835: contig of 710 bp in length 28835: contig of 710 bp in length 25643: contig of 708 bp in length 43: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30551: gap of 100 bp
31252: contig of 701 bp in length
31352: gap of 100 bp
32065: contig of 713 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 p of 100 bp contig of 697 bp in length contig of 110 bp contig of 114 bp in length p of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13: gap of 100 bp
10451: contig of 708 bp in length
                                                                                                                                                                                                                            100 bp
f 700 bp in length
                                                                                                                                                                                                                                                                                                100 bp .
of 706 bp in length
                                                                                                                                                                                                                                                                                                                                                             9666: gap of 100 bp 10361: contig of 695 bp in length
                                                                                                         100 bp
of 697 bp
100 bp
of 703 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33677 33776: contig of 33677 33776: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16050 16700. ___ 10
16761 16860: gap of 16861 17570: contig of '
                                                                                                                                          늉
                                                                                                                                                                                                       contig of
                                                                                                                                                                                                                                                                                                                                     contig of
                                                                                                                                                                                                                                                                        contig of
             contig of
                                                                                                                                          contig
                                                                             contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15138 1523/; 2--
15238 15949; contri
15238 15949; do of
15950 16049; gap of
16760; contri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23205 23304: gap of 23305 24016: cont 24017 24116: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32165: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28125: gap of 28835: con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9184 19283: gap of 9284 19976: cont
                                                                                                                                                                                                                                         8060: gap of
8760: co
                                                                                                                                                                                                                                                                                                          8860: gap of
9566: co
                                                                                                            6460: gap c
7157: c
                                            5643: gap
6360:
                                                                                                                                                                            7257: gap
7960:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13535 13634: c
13635 1433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28935:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29743:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28026
28126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12818
                                                                                                                                                                                                                                                                                                                                                                                                                                       2E 2 (Dases I to 54441) Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N. Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Campopiano, A., Chang, J., Chazaro, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Dodge, S., Faro, S., Cooke, P., DeArellano, K., Daiz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ferreira, P., Fitzhugh, W., Gape, D., Galagan, J., Gardyna, S., Ferreira, P., Fitzhugh, W., Graham, L., Grand-Pierre, N., Gardyna, S., Gonds, C., Kamat, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Horton, L., Hulme, W., Illev, I., Johnson, R., MacLen, C., Macdonald, P., Major, J., Marquis, N., Mathews, C., Macdonald, P., Major, J., Marquis, N., Mathews, C., Mannan, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., O'Neil, D., O'Connor, T., O'Donnell, P., O'Neil, D., O'Connor, T., O'Donnell, P., O'Neil, D., O'Connor, T., O'Donnell, P., O'Neil, D., O'Connor, T., Seamon, S., Severy, P., Spencer, B., Santos, R., Schupback, R., Stage-Thomann, N., Subramanian, A., Tavis, N., Trayis, N., Ye, W.J., Young, G., Viel, R., Viel, R., Viel, R., Wilson, B., Wu, X., Waman, D., Ye, W.J., Young, G., Viel, R., Wilson, B., Wu, X., Waman, D., Ye, W.J., Young, G., Willeon, B., Wilson, B., Wu, X., Waman, D., Ye, W.J., Young, G., Willeon, B., Whittehea, Therrivit Anthre for Ganome Submitted B.
HTG 23-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (123-707-2001) Whitehead Institute/MIT Center for Genome Submitted (123-707-2001) Whitehead Institute/MIT Center for Genome All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * NOTE: This record contains 68 individual
* sequencing reads that have not been assembled into
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
      ACI01033 54441 bp DNA linear HTG :
Mus musculus clone RP23-8514, LOW-PASS SEQUENCE SAMPLING
ACI01033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: sequence submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 bp
of 705 bp in length
100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of 100 bp
contig of 699 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 689; contig of 689 bp in length
690 789; gap of 100 bp
790 1570; contig of 781 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of 100 bp contig of 700 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      668 bp in length
                                                                                                                                                                                                                                                                                                                                  Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-8514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: WIBR
Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2471 3175: contig of 70
3176 3275: gap of 100
3276 3943: contig of 66
344 4044 4742: contig of 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center clone name: 85_I_4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0: gap of
3175: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1571 1670: gap of
1671 2370: cor
                                                                                                               AC101033.1 GI:17059807
HTG; HTGS_PHASE0.
                                                                                                                                                                                                                                                                                                             (bases 1 to 54441)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2371 2470:
                                               DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
```

COMMENT

```
RS Birran, B. Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barran, V., Boguslavkiy, L., Boukhgalter, B. Anderson, S., Barran, J., Campoplano, A., Chang, J., Chazaro, B., Cohoepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cohoepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Ferreita, P., Fitzhugh, W., Calangan, J., Gardyna, S., Ferreita, P., Fitzhugh, W., Garde, D., Dodge, S., Farco, S., Goyette, M., Graham, L., Grand-Pierre, N., Jones, C., Kamet, A., Karatas, A., Kalls, C., LaRocque, K., Landers, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonalle, P., Major, J., Morpheters, R., Meltim, J., Meneus, L., Minova, T., Merkan, P., Morpheters, R., Meltim, J., Morphy, T., Naylor, J., Nguyen, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., O'Neil, D., O'Iver, J., Reetra, R., Rleback, M., Riley, R., Schauer, S., Schupback, R., Santos, R., Schauer, S., Schupback, R., Seanan, S., Severy, P., Spencer, B., Treiglito, J., Vassiliev, H., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 191918)

3 (bases 1 to 191918)

3 Sarren, B., Nusbaun, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barren, B., Chang, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galgan, J., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Lindblad-Toh, K., Liu, G., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Mendus, L., Micol, R., Morbu, C., Norman, C., McCarthy, M., Meldrim, J., Mayen, C., Nicol, R., Morbu, C., Norman, C., Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Funkphy, T., Naylor, J., Nguyen, C., Nicol, R., Stange, C., Rogov, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Schubea, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Vola, Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1. (bases 1 to 191918)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 21, 2002 this sequence version replaced gi:17060802. All repeats were identified using Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center clone name: 491 K 18

Sequencing vector: Plasmid; n/a; 100% of read Chemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phrap; version 0.960731

Consensus quality: 187629 bases at least 040

Consensus quality: 189823 bases at least 040
                                                                                                                                                                                         Birren, B., Nusbaum, C. and Lander, E. Mus musculus, clone RP24-491K18
                                                                                                                                                                                                                                                                                    Unpublished
ORGANISM
                                                                                                                                  REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC102692 191918 bp DNA linear HTG 21-AUG-2002
Mus musculus clone RP24-491K18, WORKING DRAFT SEQUENCE, 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 54441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50515 50514: 9ar contig or /2v r 50515 51234: contig or /2v r 51235 51334: gap of 100 bp 51335 52048 52147: gap of 100 bp in length 52048 52147: gap of 100 bp in length 52052: contig of 705 bp in length 52052: contig of 705 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ## 4407/9: contig of 708 bp in length 44088 contig of 708 bp in length 44088: contig of 709 bp in length 189 44888: contig of 709 bp in length 189 4569: contig of 718 bp in length 10 46609: gap of 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 1
14456 34555; gap of 100 bp 14556 35262; contig of 707 bp in length 5523 35622; gap of 100 bp 155363 36039; contig of 677 bp in length 56040 36139; gap of 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 10
                                                                                                                                                                                                                                                                          36942: gap of 100 bp 37638: contig of 696 bp in length 37738: gap of 100 bp 38430: contig of 692 bp in length 38530: gap of 100 bp 39243: contig of 713 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39343: gap of 100 bp

40042: contig of 699 bp in length

40841: contig of 699 bp in length

40841: contig of 699 bp in length

41641: contig of 706 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41747: gap of 100 bp 42457: contig of 710 bp in length 42557: gap of 100 bp 43271: contig of 714 bp in length 43371: gap of 100 bp 44799: contig of 708 bp in length 4479:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 54441: contig of 699 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC102692
AC102692.2 GI:22381681
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

84.3%; Score 19.4; DB 2;
Best Local Similarity 95.2%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /47: gap of
42457: con+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12458 42557: gap of 43271: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14989 44988: gap of 45691: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 38305 AAATGGTGCCATTCAGCTTC 38285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7321 47420: gap of
7421 48112: conf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9624 49723: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 AACTGGTGGCCATTCAGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41747:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .54441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5692 45791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8843 48942:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53643 53742:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
AC102692
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
```

```
misc_feature
                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
ORGANISM
                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                             LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                       RESULT 14
AC125105/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
  Consensus quality: 190404 bases at least Q20 Insert size: 193000; agarose-fp Insert size: 190618; sum-of-contigs Quality coverage: 6.7 in Q20 bases; agarose-fp Quality coverage: 6.8 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , 191918: contig of 62482 bp in length.
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33887 46341: contig of 100 bp
46342 46441: gap of 100 bp
46342 46441: gap of 100 bp
46442 84206: contig of 37765 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84207 84306; gap of 100 bp
84307 129336: contig of 45030 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19431 19530: gap of 100 bp
19531 23508: contig of 3978 bp in length
23509 23608: gap of 100 bp
23609 27494: contig of 3886 bp in length
                                                                                                                                                                                                                                                                                                                                                                          5353 5452: gap of 100 bp 5453 8172: contig of 2720 bp in length 8173 8272: gap of 100 bp 8273 11069: contig of 2797 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                           11070 11169: gap of 100 bp
11170 14718: contig of 3549 bp in length
14719 14818: gap of 100 bp
14819 19430: contig of 4612 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27495 27594: gap of 100 bp 27595 33786: contig of 6192 bp in length
                                                                                                                                                                                                                                                                              811 910: gap of 100 bp in length 11910: gap of 100 bp 911 1960: contig of 1050 bp in length 1961 2060: gap of 100 bp 1061 5352: contig of 3292 bp in length 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone lib="RPCI-24 Male Mouse BAC"
1. .810
'note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7595. .33786
note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16442. .84206
note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84307. .129336 /
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    453. .8172
note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273. .11069
note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111. .1960
note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1170. .14718
note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               061. .5352
note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
db_xref="taxon:10090"
clone="RP24-491K18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .19430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
```

```
Aus musculus chromosome UNK clone RP24-220B7, WORKING DRAFT SEQUENCE, 60 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (20-JUN-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 277892) MGPherson, J.D. and Waterston, R.H.
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 60 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                          ö
                                                                                                          Length 191918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert size: 170000, agarose-fp
Insert size: 272299; sum-of-contigs
Quality coverage: 0.00 in Q20 bases; agarose-fp
Quality coverage: 3.87 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig of 1253 bp in length
gap of unknown length
contig of 1232 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1214: contig of 1214 bp in length
1314: gap of unknown length
2486: contig of 1172 bp in length
2586: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing vector: plasmid; 100% changes vector: plasmid; 100% of reads chemistry: Dye-primer ET; 0% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 consensus quality: 248249 bases at least Q40 consensus quality: 257105 bases at least Q30 consensus quality: 264370 bases at least Q20
                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
                                                                                                                  DB
ture 129437. .191918
/note="assembly_fragment"
58327'a 40328 c 39648 g 52315 t
                                                                                                                    Score 19.4; DB
Pred. No. 99;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ...... Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence of Mus musculus clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----- Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC125105.1 GI:21490578
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: M13; 0%
                                                                                                                                                                                                                                              DD 111442 AAATGGTGGCCATTCAGCTTC 111462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (20-JUN-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 277892)
                                                                                                                                                                                                              3 AACTGGTGGCCATTCAGCTTC 23
                                                                                                                       84.3%;
95.2%;
                                                                                                                                                                 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                       Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               house mouse.
```

```
02: contig of 3041 bp in temporal contig of 2879 bp in length 281: gap of unknown length 281: gap of unknown length 281: gap of unknown length 147: contig of 2340 bp in length 147: contig of 2340 bp in length 147: gap of unknown length 147: gap of unknown length 147: gap of unknown length 147: gap of unknown length 147: gap of unknown length 147: gap of unknown length 147: gap of unknown length 147: gap of unknown length 147: gap of unknown length 147: gap of unknown length 147: gap of unknown length 147: gap of unknown length 16342: gap of unknown length 16342: gap of unknown length 1644: gap of unknown length 16556: gap of unknown length 16556: gap of unknown length 16556: gap of unknown length 16556: gap of unknown length 11882: contig of 5478 bp in length 16556: gap of unknown length 16556: gap of unknown length 16556: gap of unknown length 13322; contig of 1153 bp in length 12240: gap of unknown length 16566: gap of unknown length 16566: gap of unknown length 16756: gap of unknown length 16756: gap of unknown length 167591: gap of unknown length 167591: gap of unknown length 167591: gap of unknown length 167591: gap of unknown length 167591: gap of unknown length 167591: gap of unknown length 167591: gap of unknown length 167591: gap of unknown length 167591: gap of unknown length 177892: contig of 57805 bp in length 177892: contig of 57805 bp in length 177892: contig of 57805 bp in length 177892: contig of 57805 bp in length 177892: contig of 57805 bp in length 177892: contig of 57805 bp in length 177892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 277892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 19.4; DB 2;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . .1214
note="assembly_name:Contig14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :587. .3839
'note="assembly_name:Contig21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .0364. .11990 "
.note="assembly_name:Contig42"
.12091. .13171
.note="assembly_name:Contig45"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1315. .2486
/note="assembly_name:Contig18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .940. .5171 --
note="assembly_name:Contig28"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174. 10263
note="assembly_name:Contig41"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .277892
/organiem="Mus musculus"
/db_xref="taxon:10090"
/chromosome="UNK"
/clone="RP24-220B7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.3%;
95.2%;
                 71162
74203
74303
774303
77282
80522
80622
80528
80528
80528
80528
80528
80528
80528
80528
805459
805459
805459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276918
277018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                               9: gap of unknown length
2: contig of 1013 bp in length
3: contig of 1013 bp in length
3: contig of 1013 bp in length
3: gap of unknown length
0: contig of 1080 bp in length
1: contig of 1081 bp in length
1: gap of unknown length
1: gap of unknown length
1: gap of unknown length
2: gap of unknown length
3: gap of unknown length
4: gap of unknown length
4: gap of unknown length
5: gap of unknown length
6: gap of unknown length
7: gap of unknown length
7: gap of unknown length
8: gap of unknown length
8: gap of unknown length
8: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
9: gap of unknown length
length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gap of unknown length contig of 1719 bp in length gap of unknown length contig of 2143 bp in length gap of unknown length contig of 2258 bp in length contig of 2358 bp in length contig of 2355 bp in length gap of unknown length gap of unknown length gap of unknown length
                               6550
6650
7663
7763
9074
9074
10264
10364
10364
10391
113091
113172
113172
113172
113172
113172
113172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50953
51053
53196
53296
55554
55554
57989
71062
```

```
Email: cgapbs-rémail.nih.gov

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Lou Staudt

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing Dy: Baylor College of Medicine Human Genome

Sequencing Center

Center code: BCM-HGSC

Web site: http://www.hgsc.bcm.tmc.edu/cdna/

Conteact: villalon@bcm.tmc.edu.

Conteact: villalon@bcm.tmc.edu.

Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,

Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., M.,

A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,

Muzny, D.M., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="similar to hypothetical protein FLJ22595"
/product="similar to hypothetical protein fLJ22595"
/product="similar 10" hall 1150 11"
/db xref="d1:15341925"
/translation="MGSVNSRGHKABAQVVMMGLDSAGKTTLLYKLKGHQLVETLPTV
/translation="MGSVNSRGHKABAQVVMMGLDSAGKTTLLYKLKGHQLVETLPTV
/translation="MGSVNSRGHKABAQVVMMGLDSAGKTTLLYKLKGHQLVETLPTV
/translation="MGSVNSRGHKABAQVLABLIKTRNRLSLERFQDHCWELRGCSALTGE
GLPEALQSLWSLLKSRSCWCLQARAHGABERGDSKRS"
372 c 431 g 303 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov Series: IRAK Plate: 26 Row: i Column: 7.
                                                                                                                                                                                          BC013150
Homo sapiens, Similar to hypothetical protein FLJ22595, clone MRC:17429 IMAGE:4340470, mRNA, complete cds.
ö
                                                                                                                                                                                                                                                                                                                                                                       Direct Submission Submission National Institutes of Health, Mammalian Submitted (27-AUG-2001) National Institutes Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 81:7%; Score 18.8; DB 9; Length 1520; 1 Similarity 90.9%; Pred. No. 1.38+02; 20; Conservative 0; Mismatches 2; Indels 0.
  ö
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db xref="taxon:9606"
/clone="MGC:17429 IMACB:4340470"
/clone="Yppe="Lymph, lymphoma"
/clone lib="NJH MGC_85"
/lab_host="DH108"
/note="Vector: pGMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
       ä
         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ccaccidereccericacit 205
                                                                               1 CCAACTGGTGGCCATTCAGCTT 22
                                                                                                                                                                                                                                                                                     BC013150
BC013150.1 GI:15341924
                                                           23
                                                       3 AACTGGTGGCCATTCAGCTTC
                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                        sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg, R
                                                                                                                                                                                                                                                                                                                                                             Homo
                   20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226
                                                                                                                                                                                                                         LOCUS
                                                                                                                                                                              RESULT 15
BC013150/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REMARK
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                     ò
```

```
Search completed: April 18, 2003, 06:25:35
Job time : 582.273 secs
```

```
Nucleotides representing cancer-associated genes, used to develop products for the diagnosis, monitoring and treatment of cancers \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ36158 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-013284/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ36158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ36158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR primer for DNA DNA encoding cance An alternative for Human immune/haema CDNA encoding huma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanog
Drosophila melanog
Human immune/haema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanog
                                                                                                         (without alignments)
505.551 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                    April 18, 2003, 04:12:35 ; Search time 102.455 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
/SIDS2/gcgdata/geneseqn-emb1/NA2001B.DAT:*
/SIDS2/gcgdata/geneseqn-emb1/NA2002.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*/SIDS2/gcgdata/geneseqn-embl/NA1998.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*/SIDS2/gcgdata/geneseqn-emb1/NA1985.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*/SIDS2/gcqdata/geneseq/geneseqn-emb1/NA1988.DAT:*/SIDS2/gcqdata/geneseq/geneseqn-emb1/NA1988.DAT:*/SIDS2/gcqdata/geneseqn-emb1/NA1988.DAT:*/
                                                                                                                                                                                                                                                                                                  4370478
                                                                                                                                                                                                                                                                                                                                                                                                                                                         gcgdata/geneseq/genesegn-embl/NA1980.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.
GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                            2185239 seqs, 1125999159 residues
                                                                                                                                                                                 1 ccaactggtggccattcagcttc 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                      - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS2/gcgdata/geneseg/
                                                                                                                                                                                                                                                                                                                                                                                                                                     N_Geneseq_101002;*
:: /SIDS2/gcgdata/geneseq/
:: /SIDS2/gcgdata/geneseq/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /SIDS2/gcgdata/geneseg/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ36158
AAZ36151
AAZ36153
AAK58003
AAA49190
ABL28587
ABL28587
                                                                                                                                                                                                              IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                  US-09-270-437D-12
23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415
1109
2568
2834
3722
4870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115:
116:
119:
120:
23:
24:
                                                                                                                                                                   Perfect score:
                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.8
18.8
18.8
18.8
                                                        OM nucleic
                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
                                                                                       Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š.
```

Rat sequence diffe Mouse ischaemic co Region 3' of human Staphylococcus aur Mutant human D3 do Human D2 receptor	Human D3 dopaminer Procease from S. A Brayme Q36 coding Enzyme Q36 coding Drosophila melanog Drosophila melanog Drosophila melanog Human immune/haema	X 4 0 0 0 0 X	human procein enco Drosophila melanog Drosophila melanog CDNA encoding a mu Human prostate exp Human prostate exp Human prostate exp Drosophila melanog	Listeria innocua D Listeria innocue D Listeria monocytog Drosophila melanog Drosophila melanog Drosophila melanog
	13 AAQ24803 13 AAQ27988 16 AAT04156 16 AAT04158 23 ABL12003 23 AAK17080	2 AAK.7881 ABL30024 ABS20709 3 ABV61599 4 ABS08292 2 AAK11576 2 AAK11576		1 ABQ67860 1 ABQ69432 1 ABQ69432 1 ABL17257 1 ABL13725 1 ABL1775 1 ABL12981
	1272 1558 1558 1 2325 1 4172 6781 17170 22	7 M M M # 10 C M 10	0000000	2496 24 2496 24 2575 24 2830 23 2971 23 4212 23
774444		44.64.64.64.64.64.64.64.64.64.64.64.64.6		44.24.24.24.24.24.24.24.24.24.24.24.24.2
17.8 17.2 17.2 17.2 17.2	200000000000000000000000000000000000000	10.00 10.00 10.00 10.00 10.00	، وَ وَ وَ وَ وَ وَ وَ وَ وَ وَ وَ وَ وَ	16.6 16.6 16.6 16.6
0 10 110 110 110 110 110 110 110 110 11	C 220		. O O O O O O O O O O O O O O O O O O O	~ 444444

## ALIGNMENTS

Cancer associated antigen; KOC-1; cancer; vaccine; CT7; PCR primer; ss. old LJ; PCR primer for DNA encoding cancer associated antigen KOC-2. Knuth A, ы Jager Stockert E, (LUDW-) LUDWIG INST CANCER RES BP. 99WO-US05766 98US-0061709 Gure A, Tsang S, (first entry) Homo sapiens. 16-MAR-1999; 17-APR-1998; WO9954738-A1 11-FEB-2000 28-OCT-1999.

```
The present sequence represents a cancer associated antigen gene designated KOC-2. The specification also describes a cancer associated antigen designated cT7. The CT7 polymucleotide was isolated from SK-MEL-37 melanoma cells. The polympeticide has some homology with MAGE-10, limited to about 210 carboxy terminal amino acids. The amino terminal of the protein has a repetitive pattern, with repeats rich in the proline, glutamine and leucine, and an almost invariable core of the peptide given in AAX43877. The CT7 polypeptide can be processed to peptides which provoke lysis by cytolytic T cells. The polymucleotides and polypeptides can be used for treating a cancerous condition and acreening for or diagnosing annexous conditions. The cancer associated antigens can be used as an immunogenic or vaccine composition with an
                            per primers AAZ36157-58 were used to amplify a cancer associated antigen gene designated KOC-2. The specification also describes a cancer associated antigen designated CT7. The CT7 polynuclectide was isolated from SK-MEL-37 melanoma cells. The polypeptide has some homology with MAGE-10, limited to about 210 carboxy terminal amino acids. The amino terminal of the protein has a repetitive pattern, with repeats rich in the peptide given in AAY4877. The CT7 polypeptide can be processed to peptides which provoke lysis by cytolytic T cells. The polynuclectides and polypeptides can be used for treating a cancerous condition and acreening for or disagnosing cancerous conditions. The cancer associated antigens can be used as an immunogenic or vaccine composition with an antigens can be used as an immunogenic or vaccine composition with an
                                                                                                                                                                                                                                                                            adjuvant, e.g. a cytokine, a saponin, or granulocyte macrophage-colony stimulating factor (GM-CSF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotides representing cancer-associated genes, used to develop products for the diagnosis, monitoring and treatment of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cancer associated antigen; KOC-2; cancer; vaccine; CT7; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding cancer associated antigen KOC-2.
                                                                                                                                                                                                                                                                                                                                             Sequence 23 BP; 4 A; 8 C; 5 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gure A, Tsang S, Stockert E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 55; Page 40; 44pp; English.
Claim 108; Page 13; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ36151 standard; DNA; 1708 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CCAACTGGTGGCCATTCAGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US05766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0061709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-013284/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9954738-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ното варіеля
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ36151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ36151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
```

ö

0; Indels

100.0%; Score 23; DB 21; Length 23; 100.0%; Pred. No. 0.18;

Mismatches

.; 0

23

```
The present sequence represents an alternative form of a cancer associated antigen gene designated KOC-2. The specification also describes a cancer associated antigen designated CT7. The CT7 polymucleotide was isolated from SK-WEL-37 melanoma cells. The polympetide has some homology with MaCB-10, limited to about 210 carboxy terminal amino acids. The amino terminal of the protein has a repetitive pattern, with repeats rich in serine, proline, glutamine and leucine, and an almost invariable core of the peptide given in AAV43877. The CT7 polypeptide can be processed to peptides which provoke lysis by cytolytic T cells. The polymucleotides and polypeptides can be used for treating a cancerous condition and screening for or disposing treating.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conditions. The cancer associated antigens can be used as an immunogenic or vaccine composition with an adjuvant, e.g. a cytokine, a saponin, or granulocyte macrophage-colony stimulating factor (GM-CSF).
adjuvant, e.g. a cytokine, a saponin, or granulocyte macrophage-colony stimulating factor (GM-CSF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ξ;
                                                                                                                                                                                                                                                                                                                                       An alternative form of DNA encoding cancer associated antigen KOC-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotides representing cancer-associated genes, used to develop products for the diagnosis, monitoring and treatment of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 23; DB 21; Length 1946;
Pred. No. 0.36;
); Mismatches 0; Indels 0;
                                                                                                          ö
                                                                             Length 1708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Knuth A,
                                                                                                                                                                                                                                                                                                                                                                    Cancer associated antigen; KOC-2; cancer; vaccine; CT7; ss.
                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1946 BP; 502 A; 528 C; 553 G; 358 T; 5 other;
                                              Sequence 1708 BP; 447 A; 469 C; 473 G; 314 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jager E,
                                                                             Score 23; DB 21;
Pred. No. 0.35;
                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gure A, Tsang S, Stockert E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 55; Page 42; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 CCAACTGGTGGCCATTCAGCTTC 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23
                                                                                                                                                                                                                                                     BP
                                                                                                                                          1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                         68 cchacrecreccarreactric 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CCAACTGGTGGCCATTCAGCTTC
                                                                                  100.08;
                                                                                                                                                                                                                         RESULT 3
AAZ36153/c
ID AAZ36153 standard; DNA; 1946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0061709.
                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US05766
                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                     Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-013284/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                           W09954738-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23;
                                                                                                                                                                                                                                                                                                                    11-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-OCT-1999.
                                                                                                                                                                                                                                                                                       AAZ36153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
            ខ្លង់ខ្ល
                                                                                                                                                                           요
                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3
                                                                                                                                                                                                                                                                                                                                         Gaps
```

Knuth A,

Jager E,

```
29-SEP-2000; 2000US-0236369; 29-SEP-2000; 2000US-0236369; 29-SEP-2000; 2000US-0236369; 29-SEP-2000; 2000US-0236369; 20-CCT-2000; 2000US-02370370; 20-CCT-2000; 2000US-0237039; 20-CCT-2000; 2000US-0237039; 20-CCT-2000; 2000US-0237040; 213-CCT-2000; 2000US-023937; 20-CCT-2000; 2000US-0241786; 20-CCT-2000; 2000US-0241786; 20-CCT-2000; 2000US-0241786; 20-CCT-2000; 2000US-024186; 20-CCT-2000; 2000US-024186; 20-CCT-2000; 2000US-024186; 20-CCT-2000; 2000US-024186; 20-CCT-2000; 2000US-024186; 20-CCT-2000; 2000US-024186; 20-CCT-2000; 2000US-024186; 20-CCT-2000; 2000US-0246476; 08-NOV-2000; 2000US-0246476; 08-NOV-2000; 2000US-0246524; 08-NOV-2000; 2000US-0246524; 08-NOV-2000; 2000US-0246524; 08-NOV-2000; 2000US-0246526; 08-NOV-2000; 2000US-0246526; 08-NOV-2000; 2000US-0246526; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246526; 08-NOV-2000; 2000US-0246526; 08-NOV-2000; 2000US-0246526; 08-NOV-2000; 2000US-0246526; 08-NOV-2000; 2000US-0246526; 08-NOV-2000; 2000US-0246526; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-0246610; 08-NOV-2000; 2000US-02
                                                                                                      2000US-0233064
2000US-0233065
2000US-0234274
2000US-0234897
2000US-0234898
2000US-0235884
2000US-0235884
2000US-0235884
2000US-0236368
2000US-0236368
2000US-0236368
2000US-0236368
2000US-0236368
2000US-023688
2000US-023688
2000US-023688
2000US-023688
2000US-023688
2000US-023688
2000US-0237038
2000US-0237038
2000US-0237038
2000US-0237038
2000US-0237038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0249208.
2000US-0249209.
2000US-0249210.
                                                                                                                               21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
27-SEP-2000;
29-SEP-2000;
29-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2000;
01-DEC-2000;
                  Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ss.
                                                                                                                 Human 1mmune/haematopoietic antigen encoding cDNA SEQ ID NO:3063,
RESULT 4
AAKS8003/c
ID AAKS8003 standard; cDNA; 415 BP.
                                                                                                                                                                                                                                                                                                    31-JAN-2000; 2000US-0179065.
24-FEB-2000; 2000US-0180628.
26-FEB-2000; 2000US-0180654.
02-MAR-2000; 2000US-0189874.
17-MAR-2000; 2000US-0189874.
19-MAY-2000; 2000US-0190076.
19-MAY-2000; 2000US-020915.
26-JUN-2000; 2000US-0215135.
07-JUL-2000; 2000US-0215136.
07-JUL-2000; 2000US-0215136.
07-JUL-2000; 2000US-0215136.
07-JUL-2000; 2000US-0216880.
11-JUL-2000; 2000US-0216880.
11-JUL-2000; 2000US-0216880.
11-JUL-2000; 2000US-0216819.
11-JUL-2000; 2000US-0216819.
11-JUL-2000; 2000US-0216819.
11-JUL-2000; 2000US-0216819.
11-JUL-2000; 2000US-0216819.
11-JUL-2000; 2000US-0216819.
11-JUL-2000; 2000US-0225266.
11-JUL-2000; 2000US-0225266.
11-JUL-2000; 2000US-0225266.
11-JUL-2000; 2000US-0225266.
11-JUL-2000; 2000US-0225266.
11-JUL-2000; 2000US-0225266.
11-JUL-2000; 2000US-0225266.
11-JUL-2000; 2000US-0225266.
11-JUL-2000; 2000US-0225269.
11-JUL-2000; 2000US-0225689.
22-JUC-2000; 2000US-0225689.
22-JUC-2000; 2000US-022589.
22-JUC-2000; 2000US-022989.
21-SEP-2000; 2000US-022994.
                                                                                                                                                                                                                                                                          17-JAN-2001, 2001WO-US01354
                                                                                  06-NOV-2001 (first entry)
                                                                                                                                                                                                                    WO200157182-A2
                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                09-AUG-2001
                                                           AAK58003;
```

2000US-025039

Baughn MR;

Lu DAM,

Yue H,

Rosen CA,

SC

```
Human cDNA libraries from various tissues were screened for GTPase associated proteins (GTPAP). The present sequence is cDNA encoding human GTPAP-20. This sequence was derived from a cDNA library of the wrist synovial membrane tissue from a female with rheumatoid arthritis. This protein is expressed in reproductive, nervous and gastrointestinal tissue. The GTPAP proteins may be used to define agonists and antagonists of GTPAP proteins may be used to define to GTPAP. This means the GTPAP proteins may be useful for treatment or prevention of diseases associated with GTPAP such as cell proliferation disorders, autoimmune disorders, inflammatory disorders, immune system disorders, cancer, ADS, asthma, atherosclerosis, arthritis, systemic
                                                                                                                                                                                                                                                                                                                                                                                                                                         useful for diagnosing, preventing and treating various diseases such atherosclerosis, cancer, acquired immune deficiency syndrome (AIDS), asthma, and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1109 BP; 264 A; 297 C; 334 G; 214 T; 0 other;
                                                                                                                                                                                                                                                                                                                                           Bandman O, Lal P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lupus erythematosus and psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 9; Page 136; 144pp; English.
127..717
/*tag= a
/product= GTPAP20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL28587/c
ID ABL28587 standard; DNA; 2568
                                                                                                                                                                                                                  98US-0109592.
99US-0118610.
99US-0127990.
                                                                                                                                                                            99WO-US28013.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 90.9
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                       (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                             YT,
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-400073/34.
P-PSDB; AAY99669.
                                                                                                                                                                                                                                                                                                                                                 JL, Tang Y
Azimzai Y;
                                                                                           WO200031263-A2
                                                                                                                                                                                                                                                               06-APR-1999;
                                                                                                                                                                              23-NOV-1999;
                                                                                                                                                                                                                      23-NOV-1998;
                                                                                                                                      02-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                 Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL28587;
                                                                                                                                                                                                                                                                                                                                                                          ≀ang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) canino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) cativity, and can be used in gene therapy and vaccine production. (I) cativity, and polymucleotides may be used in the prevention, diagnosis and proteins and polymucleotides associated with inappropriate (I) expression. For expression by nectifying mutations or deletions in a patient's genome contact affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) cupplement the patients own production of (I). Additionally, (I) colymuclectides may be used to produce the secreted (I), by inserting proteins and polymuclectides may be used to produce the call to express the cancers and cancer metastases of haematopoietic-derived cells. AAK64703 cancers and cancer metastases of haematopoietic-derived cells. AAK64703 cancers and cancer metastases of haematopoietic antigen genomic concerns and cancer metastases of haematopoietic antigen genomic concerns and cancer metastases of haematopoietic antigen genomic represent human immune/haematopoietic antigen genomic represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Guanine nucleotide binding protein, GTP-binding protein, G-protein, GTPase, GTPase associated protein, GTPAP, cell proliferation, autoimmune, inflammatory, immune system disorder, cancer, AIDS, acquired immune deficiency syndrome, asthma, atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22; Length 415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 3063; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 415 BP; 92 A; 114 C; 130 G; 76 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA encoding human GTPase associated protein-20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.7%; Score 18.8; D
90.9%; Pred. No. 28;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 CCAGCTGGTGCCTTCAGCTT 205
                                                                                                                                                                                                                                                                                                                                Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA49190 standard; cDNA; 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 90.9%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CCAACTGGTGGCCATTCAGCTT
                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                    2000US-0251868.
2000US-0251869.
                                                                                                                                                                          08-DEC-2000; 2000US-0251989.
                                                                                                                                                                                                08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254097.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                               2000US-0251856
                                                                                                                                                                                                                                           05-JAN-2001; 2001US-0259678
                                                                                                                                                                                                                                                                                                                             Barash SC,
                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-483426/52.
P-PSDB; AAM85222.
                                                                                                06-DEC-2000; 2
08-DEC-2000; 2
08-DEC-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA49190;
```

```
ö
                                 Gaps
                                                                                                                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ds.
                                                                                                                                                                                                                                                                       Drosophila melanogaster genomic polynucleotide SEQ ID NO 37234.
                                 ö
Score 18.8; DB 21; Length 1109; Pred. No. 32;
                                 Indels
                                   0; Mismatches
                                                                                       238 CCAGCTGGTGGCCCTTCAGCTT 217
                                                                     CCAACTGGTGGCCATTCAGCTT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2001; 2001WO-US09231
      81.7%;
90.9%;
                                                                                                                                                                                                                                                 26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                              WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-2001.
```

arthritis; systemic lupus erythematosus; psoriasis; human; ss

Location/Qualifiers

Homo sapiens

Key

RESULT 5 AAA49190/c

셤 ò

```
New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                     The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

81.7%; Score 18.8; DB 23; Length 2568;
Best Local Similarity 90.9%; Pred. No. 37;
Matches 20; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster genomic polynucleotide SEQ ID NO 15985.
                                                                                                                                                                                                       Claim 1; SEQ ID NO 37234; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2568 BP; 686 A; 575 C; 664 G; 643 T; 0 other;
                                                                                            Myers EW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1965 CAACTGGTGCCACTCAGCTTC 1944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABL21504 standard; DNA; 2834 BP
                                                                                         PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PWD,
               23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 CAACTGGTGGCCATTCAGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                         감
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ፤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster.
                                                                                       Adams M,
                                                                                                                  WPI; 2001-656860/75.
                                                          (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adams M,
                                                                                                                                                                                                                                                                                                                                              ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200171042-A2.
                                                                                       Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL21504
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

Gaps

ö

18

```
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and inseful interactions in higher ewkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL9737-ABR2072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                      Human immune/haematopoietic antigén genomic sequence SEQ ID NO:26549.
                                                                                                                                                                                             81.7%; Score 18.8; DB 23; Length 2834; 90.9%; Pred. No. 37; 2.1 Indels 0;
Claim 1; SEQ ID NO 15985; 21pp + Sequence Listing; English.
                                                                                                                                                                     Sequence 2834 BP; 747 A; 689 C; 625 G; 773 T; 0 other;
                                                                                                                                                                                                                                                                    2773 chacrecrecacreactric 2794
                                                                                                                                                                                                                                                                                                                               AAK71737 standard; DNA; 3722 BP
                                                                                                                                                                                                                                               23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0215135.
2000US-0216647.
2000US-0216880.
2000US-0217487.
2000US-0217496.
                                                                                                                                                                                                                                              CAACTGGTGGCCATTCAGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0189874.
2000US-0190076.
2000US-0198123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JAN-2001; 2001WO-US01354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0186350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0205515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0225447
                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                          Query Match
Best Local Similarity 90.9
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                               06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                        AAK71737;
                                                                                                                                                                                                                                                                                                     7
 유
                                                                                                                                                                                                                                             ઠ
```

```
100US-0231968
                                    08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
                                          08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
                                                                                                                                  08-NOV-2000;
                                                                                                                               08-NOV-2000
                                                                                                                         01-NOV-2000
08-NOV-2000
                                                                                                                      20-OCT-2000
                30-AUG-2000;
                                  08-SEP-2000;
```

```
AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

canino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic

activity, and can be used in gene therapy and vaccine production. (I)

creatment of diseases associated with inappropriate (I) expression. For

treatment of diseases associated with inappropriate (I) expression. For

creatment of diseases associated with decreased

expression by rectifying mutations or deletions in a patient's genome

creatment the patients own production of (I). Additionally, (I)

cupplement the patients own production of (I). Additionally, (I)

creatment cids into a host cell and culturing the cell to express the

protein. (I) proteins and polynucleotides may be used to prevent,

cancers and cancer metastases of haematopoietic related diseases, especially

diagnose and treat immune/haematopoietic-derived cells. AAK64703

cc cancers and cancer metastases of haematopoietic antigen genomic

to AAX87694 represent human immune/haematopoietic antigen genomic

crepresent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 26549; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruben SM
                                                                                                                                                                                                                                                                                                                                                                                    2000US-0251479.
2000US-0251856.
2000US-0251868.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                               1000US-0251030
                                                                                                                                                                                                                                                                                           2000US-0249299
                                                                                                                                                                                                                                                                                                                     000US-0250160
                                                                                                                                                                                                                                                                                                                                                                           000US-0256719
                                                                                                                                                                                                                                                                                                                                                                                                                                                 000US-0251989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001US-0259678
                                                                                                                                                                                                                                                                                                                                   000US-0250391
                                     2000US-0246613
2000US-0249207
                                                                                                                                                                                                                                                                                                                                                                                                                                                            000US-025199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosen CA, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-483426/52.
                                      08-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                       08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                           06-DEC-2000;
                                                                                                                                                                                                                                                      .7-NOV-2000;
                                                                                                                                                                                                                                                                   7-NOV-2000;
                                                                                                                                                                                                                                                                                              17-NOV-2000;
                                                                                                                           17-NOV-2000;
                                                                                                                                         17-NOV-2000;
                                                                                                                                                     17-NOV-2000;
                                                                                                                                                                   17-NOV-2000;
                                                                                                                                                                                 17-NOV-2000;
                                                                                                                                                                                                            17-NOV-2000;
                                                                                                                                                                                             17-NOV-2
```

Gaps

ö

DB 22; Length 3722; Indels

Score 18.8; DE Pred. No. 39; 0; Mismatches

81.7%;

Query Match 81.7 Best Local Similarity 90.9 Matches 20; Conservative

Sequence 3722 BP; 990 A; 887 C; 926 G; 919 T; 0 other;

1 CCAACTGGTGGCCATTCAGCTT 22

ઠે

```
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and insecticides, theractions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                             Drosophila melanogaster genomic polynucleotide SEQ ID NO 37231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 37231; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4870 BP; 1239 A; 1201 C; 1083 G; 1347 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Myere EW;
2041 CCAGCTGGTGGCCCTTCAGCTT 2020
                                                                                    ABL28586 standard; DNA; 4870 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li PWD,
                                                                                                                                                                                                                                                                                                                                                  23-MAR-2001, 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                             26-MAR-2002 (first entry)
                                                                                                                                                                                                                              pharmaceutical; gene; ds
                                                                                                                                                                                                                                                        Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                            (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                     WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interactions
                                                                                                                                                                                                                                                                                                                    27-SEP-2001
                                                                                                                   ABL28586;
                                                       RESULT 9
           윱
```

ö Gaps ö Query Match
81.7%; Score 18.8; DB 23; Length 4870;
Best Local Similarity 90.9%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 2; Indels 0. Indels 7 0; Mismatches

```
ABK63547 standard; cDNA; 3628 BP.
                                                         (first entry)
                                                       18-JUN-2002
                                     ABK63547;
RESULT 10
ABK63547/
ID ABK6
XX
AC ABK6
XX
DT 18-JI
XX
DE RAL
```

Rat, 88; hepatotoxin; expressed sequence tag; EST; drug screening; differential expression; centrilobular necrosis; steatosis. Elashoff MR Castle AL, Johnson KR, 2000US-244880P. 2001US-290645P. 2001US-290645P. 2001US-292336P. 2001US-297457P. 2001US-298484P. 30-JUL-2001; 2001WO-US23872. Mendrick D, Porter MW, (GENE-) GENE LOGIC INC. WPI; 2002-241625/29. Rattus norvegicus WO200210453-A2. 06-JUN-2001; 2 13-JUN-2001; 19-JUN-2001; 31-JUL-2000; LS-MAY-2001; 22-MAY-2001, 09-JUL-2001; 11-MAY-2001; 07-FEB-2002 02-NOV-2000

these toxic Predicting toxic effects of compounds or the progression of these tox effects by determining the changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or cells -

Claim 1; Seq ID No 1454; 239pp; English.

The invention relates to methods for predicting toxic effects of compounds or the progression of these toxic effects by determining the compounds or the progression of these toxic effect by determining the toxin and comparing these to gene expression in unexposed tissues or cells. Also included are methods of predicting at least one toxic effect of a compound or progression of a toxic effect, preferably the expression in a tissue or cell sample exposed to the compound of two or more genes listed in the specification, where differential expression of the genes is indicative of at least one toxic effect or progression of the method can also be used to identify an agent which modulates the coxic response and predict cellular pathways that a compound modulates to in a cell. The methods utilise a set of at least two probes (on a solid support in kit form), where each of the probes comprises a sequence that support in kit form), where each of the probes comprises a sequence that support in kit form), where each of the probes comprises a sequence that support in kit form), where each of the probes comprises a sequence that support in kit form), where each of the probes comprises a sequence that specifically hybridises to a gene listed in the specification, a computer captession level in a tissue or cell sample expression level in a tissue or cell sample expression and tox identifying the expression and for identifying toxicity markers in dentification of the physiological state of the phase of the contract of the physiological state of the phase of cell exposed to a known toxin. The genes and toxicity markers for the seminal proportion or identification of the physiological state of the phase of cell capted to a known toxin. The genes and toxicity markers in dentification or identification of the physiological state of the phase of cell capted to a parameter of the phase of cell capted to a cell of a cell of the phase of the phase of the phase of the phase of the phase of the phase of the phase of the phase of the pha from a gene sample that has been exposed to a compound or agent. Hepatotoxicity is characterised by centrilobular necrosis and steatosis. The present sequence is an expressed sequence tag (EST) or cDNA derived from a genwhich is differentially expressed in response to a hepatotoxic agent. 

Sequence 3628 BP; 1035 A; 698 C; 838 G; 1057 T; 0 other;

Gape Score 17.8; DB 24; Length 3628; Pred. No. 1.2e+02; 0; Mismatches 2; Indels 0; ö 77.4%; 19; Conservative Best Local Similarity Query Match Matches

3 AACTGGTGGCCATTCAGCTTC 23

ઠ

Rat sequence differentially expressed in response to a hepatotoxin #1454.

ô

ö

G-protein-coupled receptors; tumour; psychosis; Parkinson's disease; arterial hypertension; hypothalamo-hypophyseal axis; open reading frame; ss.

/note= "corresponds to nucleot 1013-1206 of AAQ24803"

Location/Qualifiers 47. 240 /\*tag= a

misc\_feature

Homo sapiens

Region 3' of human D3 dopaminergic receptor ORF.

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (1) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (1). The method is useful for examining the ischaemia condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB199912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. AB199913 and AB199914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                     Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.4%; Score 17.8; DB 24; Length 8212; 90.5%; Pred. No. 1.3e+02; indels 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                    Mouse ischaemic condition related cDNA sequence SEQ ID NO:1027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 8212 BP; 1663 A; 2301 C; 2300 G; 1948 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ishii Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nagata T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 2592-2596; 2690pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Takahashi Y,
                                                                                                      AB199884 standard; cDNA; 8212 BP.
1355 AGCTGGAGGCCATTCAGCTTC 1335
                                                                                                                                                                                                                                                                                                                                                                                                      18-MAY-2001; 2001WO-JP04192.
                                                                                                                                                                                                                                                                                                                                                                                                                                       18-MAY-2000; 2000JP-0145977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 90.5'
                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Asai S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-034733/04
                                                                                                                                                                                                                                                                                                                                      WO200188188-A2.
                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ishikawa K,
                                                                                                                                                                                07-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                         22-NOV-2001
                                                                                                                                                AB199884;
```

Human D3 dopaminergic receptor polypeptide(s) - for in-vitro screening of new dopaminergic drugs and diagnosis and treatment of various psychiatric, cardiovascular, neurological and neuro-endocrinological disorders

ņ,

Schwartz JC, Sokoloff

Giros B, Martres MP, WPI; 1992-183673/22.

(INRM ) INSERM INST NAT SANTE RECH MEDICALE.

91WO-FR00810 90FR-0013731

16-OCT-1991; 06-NOV-1990;

WO9207937-A.

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                              A Sau3A human genomic DNA bank was screened with two rat D3 receptor probes to identify open reading frames. The rat D3 probe #2 containing the coding sequence for the C-terminal part and transmembrane domains VI and VII of rat D3 identified 1 positive clone. The sequence given here corresponds to part of the 3 region of the human D3 gene. This sequence is one of the preferred fragments able to code for a polypeptide with the properties of the human D3 receptor. The sequence is also useful as a probe to diagnose e.g. pathological expression of the D3 receptor, polymorphism of the D3 receptor gene or point mutations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 17.2; DB 13; Length 306; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 306 BP; 63 A; 92 C; 69 G; 82 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus contig SEQ ID #752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV75063 standard; DNA; 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y Match
Local Similarity 86.4%;
les 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Fig 4; 51pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CCAACTGGTGGCCATTCAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ccaaarddregccarrererr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV75063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV75063
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠ
```

1006 AACTGGTGGCCACTGAGCTTC 1026

g

à

23

3 AACTGGTGGCCATTCAGCTTC

AAQ24805 standard; DNA; 306 BP

RESULT 12 AAQ24805 (first entry)

19-NOV-1992

AAQ24805;

88

```
Matches 19; Conservative
                                                             WPI; 1997-374922/35.
                                                                                                                                          Local Similarity
                                           05-JAN-1996;
          misc_feature
                                      07-JAN-1997;
                            EP786519-A2
                                 30-JUL-1997
                                                                                                                                                                              19-NOV-1992
                                                     Barash SC,
                                                        Rosen CA;
                                                                                                                                                                         AAQ24809;
                                                                                                                                        Query Match
                                                                                                                                                                 AAQ24809
ò
                                                                                                                                                      g
                                                                                                                                                                       $$$$$$$$
```

```
This ORF codes for a mutant D3 receptor with four amino acid substitutions relative to the wild-type receptor sequence (two of the nucleotide substitutions are silent). The mutant receptor retains its dopaminergic receptor properties. The mutant containing all the mutations in the Features Table is preferred but mutants which contain at least one of the mutations are also covered by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human D3 dopaminergic receptor polypeptide(s) - for in-vitro screening of new dopaminergic drugs and diagnosis and treatment of various psychiatric, cardiovascular, neurological and neuro-endocrinological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 17.2; DB 13; Length 1203;
Pred. No. 1.9e+02;
0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1203 BP; 252 A; 351 C; 311 G; 289 T; 0 other;
  arterial hypertension; hypothalamo-hypophyseal axis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sokoloff
                                                                                                                                                                                                 ē
                                                                                                                                                                                                                                                                      "A is replaced by G"
                                                                                                                                                                                                                                                                                                                        /*tag= c
/note= "C is replaced by T"
                                                                                                                                                                                                                                                                                                                                                                                                                                    Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ້ວ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ວ້
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INRM ) INSERM INST NAT SANTE RECH MEDICALE.
                                                                                                                                                                      '*tag= a
'note= "A is replaced by
                                                                                                                                                                                                                                                                                                                                                                                                   d
"G is replaced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e
"T is replaced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= f
/note= "T is replaced by
                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schwartz JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA99614 standard; cDNA; 1261 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 37; 51pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91WO-FR00810,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90FR-0013731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch
l Similarity 86.4%;
19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CCAACTGGTGGCCATTCAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      984 CCAAATGGTGGCCATTGTGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .nvention. See AAQ24803-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-FEB-2001 (first entry)
                                                                                                                                                                                                                                             /*tag=
/note= '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                   *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                        *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Martres MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1992-183673/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAR24247.
                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9207937-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Giros B,
                                                                                                                                  mutation
                                                                                                                                                                                                                  mutation
                                                                                                                                                                                                                                                                                             mutation
                                                                                                                                                                                                                                                                                                                                                                       nutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA99614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local
Matches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA99614
ID AAA9
XX
AC AAA9
XX
DT 02-F
of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access medium, preferably selected from a floppy or hard disk, random access the S.aureus DNA sequences allows puterive functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic that protein-encoding or regulatory regions of commercial, therapeutic industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can also be used in a kit for the immunodetection of sources in a sample. S.aureus is a implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, surfacement and surgical wound infections, scalded skin syndrome, toxic shock for recombinant production of the polypeptides. The new DNA sequences can be used (and their fragments) are useful as primers or probes for isolating computer readable medium.
                                                                                                      /*tag= a //*tag=                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence represents one of 5191 Staphylococcus aureus DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G-protein-coupled receptors; tumour; psychosis; Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of anti-S.aureus vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 17.2; DB 18; Length 1019;
Pred. No. 1.8e+02;
0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dillon PJ, Fannon MR, Kunsch CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1019 BP; 364 A; 194 C; 159 G; 240 T; 62 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 1646-1647; 3271pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mutant human D3 dopaminergic receptor.
                                                          Location/Qualifiers
901..960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                640 CAACTGGTGGTAATTCAGGTTC 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ24809 standard; DNA; 1203 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                          97EP-0100117.
                                                                                                                                                                                                                                                                                                                                                                                                                            96US-0009861,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.8%;
86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 CAACTGGTGGCCATTCAGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
     Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Choi GH,
```

ö

Gaps

ö

```
The present sequence is the human D2 receptor CDNA. The sequence was expressed in the same cell line as the putative rat D4 receptor gene in a method to confirm that the putative D4 receptor does code for a deparative receptor does code for a second companied by the part of the putative D4 receptor. The rat D4 receptor was shown to preferentially bind dopamine antagonists such as clozapine. The D4 receptor CDNA is useful for screening drugs which specifically bind to the receptor and have selective effects on the cardiovasculature and retinal tissues through interactions with the receptor. Such compounds may act as vasoregulators or may have ionotropic effects. The D4 receptor protein may be used for the production of polyclonal or monoclonal antibodies which receptors the dependence but do not recognise other dopamenergic receptors. The antibodies may be used in immunocytochemical studies and for identification and isolation via flow
                                                                                                                                                                                                                                                                                                                                                                                              screening for compounds that selectively bind to a rat D4 dopamine receptor (DDR), useful for identifying dopamine (ant)agonists, comprises exposing cells transfected with a nucleic acid encoding the DDR to candidate compounds
                         Human; D4 dopamine receptor; cardiovascular system; retinal tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1261 BP; 265 A; 363 C; 328 G; 305 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Column 35-38; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sorting of D4 expressing cell types.
                                                   vasoregulator; D2 receptor; ss.
                                                                                                                                                                                                                                       94US-0261293.
93US-0014013.
                                                                                                                                                                                                      95US-0475742.
                                                                                                                                                                                                                                                                                              (UNIW ) UNIV WASHINGTON.
Human D2 receptor cDNA.
                                                                                                                                                                                                                                                                                                                                   Todd RD, O'Malley KL;
                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-655527/63
                                                                                                                                                                                                        07-JUN-1995;
                                                                                                                                                                                                                                         16-JUN-1994;
28-JAN-1993;
                                                                                              Homo sapiens
                                                                                                                                                                  19-SEP-2000.
                                                                                                                                 US6121015-A.
```

ö Query Match 74.8%; Score 17.2; DB 21; Length 1261; Best Local Similarity 86.4%; Pred. No. 1.9e+02; Matches 19; Conservative 0; Mismatches 3; Indels 0; ð

Gaps

1 CCAACTGGTGGCCATTCAGCTT 22

990 CCAAATGGTGGCCATTGTGCTT 1011

q

Search completed: April 18, 2003, 05:45:26 Job time : 105.455 secs

```
GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
```

OM nucleic - nucleic search, using sw model

Run on:

April 18, 2003, 04:53:41; Search time 22.4773 Seconds (without alignments) 313.809 Million cell updates/sec US-09-270-437D-12 Title: Perfect score:

1 ccaactggtggccattcagcttc 23 Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

Searched:

Total number of hits satisfying chosen parameters: 441362 seqs, 153338381 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

/cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\* /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\* /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\* /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\* /cgn2\_6/ptodata/1/ina/PcTUS\_COMB.seq:\* /cgn2\_6/ptodata/1/ina/pcTUS\_COMB.seq:\* Issued\_Patents\_NA:\* 4.0.0

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ò	Sequence /, Appli	à,	Sequence 3, Appli	'n	ĵ.	1:	1 -	Ϊ.	<b>⊣</b> (	, נ ע כ	200	2 0	m (	5	30,	0 0	30	29	9	5	30,	~	-	ì =	٠.	12,
SUMMARIES	ΙD	US-09-061-709-5	US-09-061-709-7	US-08-475-742-16	US-08-714-677-3	US-08-393-540-3	US-08-714-537-3	US-08-714-677-11	US-08-393-540-11	US-08-714-537-11	US-09-261-855-1	US-08-518-878B-29	US-08-518-878B-30	US-08-24-522B-29	US-08-294-522B-20	US-08-24-322B-30	115-06-807-05-18-20	118-08-807-801A-30	US-08-4/0-868A-29	05-4000-074-00-00	67-189-017-60-51	05-189-017-60-01	05-08-946-719A-29	US-08-946-719A-30	9	US-08-324-533-1	US-09-313-300-10	US-09-129-112-18	US-09-323-873A-12
	DB	4	4	m	~	~	~	~	7	N	4	-	ч	-	-	ı N	~	۰,	1 (	• ~	י נ	י ר	3 (	η.	₩.		4	4	4
	Query Match Length	1708	1946	1261	2325	2325	2325	3073	3073	3073	2224	112	112	112	112	112	112	112	112	112	113	110	4 -	777	3941	1445	1238	1434	401
de	Query	100.0	100.0	74.8	74.8	74.8	74.8	74.8	74.8	74.8	72.2	70.4	70.4	70.4	70.4	70.4	70.4	70.4	70.4	70.4	70.4	70.4			4.00	9.6	68.7		67.8
	Score	23	23	17.2	•	17.2	17.2	17.2	17.2	17.2	16.6	16.2	16.2	16.2	16.2	16.2	16.2	16.2	16.2	16.2		16.2	16.3		٠,	4		•	15.6
	ult No.	н.	~	ო	4	S)	9	7	8	ο .	9	11	12	13	14	15	91	17	18	19	20	21	2		2 5	* L	n,	١٥	<u>.</u>
	Result No.	O	U								υ	o	υ	υ	υ	υ	υ	υ	υ	o	U	U	0	) (	,	1	0	U.	. •

Sequence 5, Appli Sequence 128, App Sequence 7, Appli Sequence 15, Appli Sequence 15, Appli Sequence 5, Appli Sequence 13, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli	Sequence 10, Appl Sequence 10, Appl
US-08-419-075-5 US-09-004-638-128 US-08-611-587-7 US-08-611-587-1 US-09-149-476-152 US-08-676-974-5 US-09-098-487-5 US-09-098-487-5 US-09-293-549-13 US-08-714-577-1 US-08-714-537-1 US-08-714-537-1 US-08-714-537-1 US-08-714-537-1 US-08-714-537-1 US-08-714-537-1 US-08-714-537-1 US-08-714-577-10 US-09-30-69-17 US-08-714-70-17 US-08-714-70-17	US-08-714-537-10
こようこよこここそこここことももここ	0
453 1038 1117 1117 1227 2277 2277 2277 2216 2216	2936
677.8 677.8 677.8 677.8 677.8 677.8 677.8 677.8	67.8
115.66 115.66 115.66 115.66 115.66 115.66 115.66 115.66	15.6
2266666666666444444 860126466666444444	22
0 000000 000	

## ALIGNMENTS

```
Facelia No. 2597364
Facelia No. 2597364
Facelia No. 2597364
Facelia No. 2597364
Facelia No. 2597364
Facelia No. 2607647
Facelia No. 2607647
Facelia No. 2607647
Facelia No. 2607647
Facelia No. 2607647
Facelia Rapelia No. 2607647
Facelia Rapelia No. 260767
Facelia Rapelia No. 260767
Facelia Rapelia No. 260767
Facelia Rapelia No. 260767
Facelia Rapelia No. 260767
Facelia Rapelia No. 260767
Facelia Rapelia No. 260767
Facelia Rapelia No. 260767
Facelia Rapelia No. 260767
Facelia Rapelia No. 260767
Facelia Rapelia No. 260767
Facelia Rapelia No. 260767
Facelia Rapelia No. 260767
Facelia Rapelia No. 260767
Facelia Rapelia No. 260767
Facelia Rapelia No. 260767
Facelia Rapelia No. 260767
Facelia Rapelia Rapelia No. 260767
Facelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rapelia Rape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 23; DB 4; Length 1708; 100.0%; Pred. No. 0.043; ive 0; Mismatches 0; Indels (
                                                        Sequence 5, Application US/09061709B Patent No. 6297364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAACTGGTGGCCATTCAGCTTC 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 23, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
US-09-061-709-5/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-061-709-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

Sequence 7, Application US/09061709B
Patent No. 6297364
GENERAL INFORMATION:
APPLICANT: Gure, Ali
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Knuth, Alexander
APPLICANT: Much, Alexander
APPLICANT: Much, Alexander
APPLICANT: Office of the foliated of the fol RESULT 2 US-09-061-709-7/c

```
APPLICANT: KUBOTA, Michio
APPLICANT: TSUSAKI, Kenji
APPLICANT: TSUSAKI, Kenji
APPLICANT: TSUSAKI, Kazuhiko
APPLICANT: BUGIMOTO, TOSHIYAKI
APPLICANT: BUGIMOTO, TOSHIYAKI
APPLICANT: BUGIMOTO, TOSHIYAKI
APPLICANT: DINVENTION: DINZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USES
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USES
NUMBER OF SEQUENCES: 17
CORRESPONDESS: ADDRESS: ADDRESS: ADDRESSE: BROWDY AND NEIMARK, P.L.L.C.
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 17.2; DB 2; Length 2325; Pred. No. 26;
                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 3;
419 Seventh Street, N.W., Suite 400
                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION OBTA:
APPLICATION NUMBER: US/08/393,540
FILING DATE: 23-FEB-1995
APPLICATION NUMBER: UP 090728
FILING DATE: 06-APR-1994
FILING DATE: 06-APR-1994
FILING DATE: 23-FEB-1994
FILING DATE: 23-FEB-1994
FILING DATE: 23-FEB-1994
FILING DATE: 23-FEB-1994
FILING DATE: 23-FEB-1994
FILING DATE: 26-FEB-1994
FILING DATE: 18-FEB-1994
FILING DATE: 18-FEB-1994
FILING DATE: 06-APR-1994
APPLICATION NUMBER: HP 090705
APPLICATION NUMBER: HP 090705
APPLICATION NUMBER: HP 090705
APPLICATION NUMBER: HP 090705
APPLICATION NUMBER: HP 090705
APPLICATION NUMBER: HP 090705
APPLICATION NUMBER: HP 090705
APPLICATION NUMBER: HP 090705
APPLICATION NUMBER: HP 090705
APPLICATION NUMBER: HP 090705
APPLICATION NUMBER: HP 090705
APPLICATION NUMBER: HP 090705
APPLICATION NUMBER: HP 090705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 3, Application US/08393540 ; Patent No. 5871993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 1896 CAACCGGCGGCGTTCAGCTTC 1917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: BROWDY, Roger L. REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: KI
TELECOMMUNICATION INFORMATION
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGIH: 2325 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1..2325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linea
                                   Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , NAME/KEY:
, LOCATION:
US-08-714-677-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-393-540-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KUBOTA, Michio
APPLICANT: TSUSAKI, Kenji
APPLICANT: MARUTA, Kazuhiko
APPLICANT: SUGIMOTO, TOSHIYUKi
TITLE OF INVENTION: DNA BNCOLING ENZYME, RECOMBINANT DNA AND
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: O'MAlley, Karen L
APPLICANT: O'MAlley, Karen L
APPLICANT: O'MAlley, Karen L
APPLICANT: O'MAlley, Karen L
APPLICANT: Todd, Richard D
TILE OFFI INVENTION: Gene Encoding the Rat Dopamine D4 Receptor
FILE REFERENCE: WU 102 CON DIV
FILE REFERENCE: WU 102 CON DIV
CURRENT FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: US 08/21,293
EARLIER PILING DATE: 1995-06-16
EARLIER FILING DATE: 1993-01-28
NUMBER OF SEQ ID NOS: 16
SOFTWARE PATENTIN OFFI ION
SEQ ID NO 16
LENGTH: 1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 17.2; DB 3; Length 1261;
Pred. No. 24;
                                                                                                                                                                                                                                                     100.0%; Score 23; DB 4; Length 1946; 100.0%; Pred. No. 0.044; 1.1ve 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUBLICATION INFORMATION:
JOURNAL: C. R. Acad. Sci., D, Sci. Nat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-475-742-16
; Sequence 16, Application US/08475742
; Patent No. 6121015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08714677
Patent No. 5871977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    990 ccaaarecreeccarrererr 1011
                                                                                                                                                                                                                                                                                                                                                                                                                    306 cchácregredechricherre 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (1). . . (1261)
OTHER INFORMATION: Human d3 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CCAACTGGTGGCCATTCAGCTT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74.8%;
86.4%;
                           CURRENT FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 86.4 Matches 19; Conservative
                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                              TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VOLUME: 311
PAGES: 501-508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-475-742-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
US-08-714-677-3
                                                                                                                                                                                            FEATURE:
US-09-061-709-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                               셤
```

Gaps

ö

```
Sequence 11, Application US/08714677

Sequence 11, Application US/08714677

Fatent No. 5871977

Fatent No. 5871977

Fatent No. 5871977

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No. 587197

Fatent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 2325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 17.2; DE Fred. No. 26; O; Mismatches
                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATE:
APPLICATION NUMBER: US/08/393,540
FILING DATE: 06-ARR-1994
FILING DATE: 06-ARR-1994
APPLICATION NUMBER: JP 047956
FILING DATE: 23-FEB-1994
APPLICATION NUMBER: JP 047940
FILING DATE: 23-FEB-1994
APPLICATION NUMBER: JP 047940
FILING DATE: 23-FEB-1994
APPLICATION NUMBER: JP 09705
FILING DATE: 06-ARR-1994
APPLICATION NUMBER: JP 090705
FILING DATE: CG-ARR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: Z5,618
REFERENCE/DOCKET NUMBER: Z5,618
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-628-197
TELEPHONE: 202-628-197
TELEPHONE: 202-737-3528
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2325 base paire
                                            OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 1896 CAACCGCCGCCGTTCAGCTTC 1917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 CAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 74.8%;
Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
1..2325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-714-537-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-714-677-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08714537
Factor to 187194
FAREATE INFORMATION:
FAREATE INFORMATION:
FAREATE INFORMATION:
FAREATE INFORMATION:
FAREATE INFORMATION:
FAREATE INFORMATION:
FAREATE OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 2325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                    MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/39,540
FILING DATE: 23-FEB-1995
PILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 090728
PILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 047966
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 047940
FILING DATE: 23-FEB-1994
PRIOR APPLICATION NUMBER: UP 090705
FILING DATE: 23-FEB-1994
ATORNEY/AGENT INPORMATION:
APPLICATION NUMBER: UP 090705
ATORNEY/AGENT INPORMATION:
AREITANTON NUMBER: Z5,618
ATORNEY/AGENT INPORMATION:
NAME: BROWDY, ROGER L.
RESISTRATION NUMBER: Z5,618
TELEPHONE: 202-628-5197
TELEPRAX: 202-737-3528
INPORMATION FOR SEC ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENTTH: 2325 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 74.8%; Score 17.2; E
Best Local Similarity 86.4%; Pred. No. 26;
Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 1896 CAACCGGCGCGCTTCAGCTTC 1917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 2325 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 CAACTGGTGGCCATTCAGCTTC
                                        ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1..2325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) NAME/KEY:
) LOCATION:
US-08-393-540-3
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-714-537-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
APPLICANT: KUBOTA, Michio
APPLICANT: TSUSAKI, Kenji
APPLICANT: MAKUTA, Kazuhiko
APPLICANT: SUGIMOTO, TOSHIYUKI
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USES
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 3073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUDRESSEE: BROWDY AND NEIMARK, P.L.L.C. STREET: 419 Seventh Street, N.W., Suite 400 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 17.2; Di
Pred. No. 27;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DALL.
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/393,540
APPLICATION NUMBER: 1995
TO NATE: 23-FEB-1995
TO NATE: 23-FEB-1995
PAPLICATION NUMBER: JP 090728
FILING DATE: 06-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 047956
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 047940
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 090705
FILING DATE: 06-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
NAME: BROWDY, ROGET L.
NAME: BROWDY, ROGET L.
TELEPHONE: 202-628-5197
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UMBER: JP 090728
06-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08714537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2573 CAACCGGCGGCCGTTCAGCTTC 2594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 3073 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.8%;
86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 CAACTGGTGGCCATTCAGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 86.4
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 23-FER APPLICATION NUMBER: FILING DATE: 06-APF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , NAME/KEY:
; LOCATION:
US-08-393-540-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: KUBCHA, Michio
APPLICANT: TSUSAKI, Kenji
APPLICANT: TSUSAKI, Kenji
APPLICANT: SUGIMOTO, TOSHIYUKI
TITLE OF INVENTION: DINA ENCODING ENZYME, RECOMBINANT DNA AND
TITLE OF INVENTION: BINXTME, TRANSFORMANT, AND THEIR PREPARATIONS AND USES
TITLE OF SEQUENCES: 17
NUMBER OF SEQUENCES: 17
NUMBER OF SEQUENCES: 17
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 3073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND 1

CALLESSEE: ALL NETWARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIF: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRANT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17.2;
Pred. No. 27
                                                  FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/393,540
FILING DATE: 23-FEB-1995
FILING DATE: 06-APR-1994
PRIOR APPLICATION NUMBER: UP 090728
FILING DATE: 23-FEB-1994
PRIOR APPLICATION NUMBER: UP 047956
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 047940
FILING DATE: 06-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 090705
FILING DATE: 06-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25.618
REPERENCE/DOCKET NUMBER: L5.618
REPERENCE/DOCKET NUMBER: L5.618
REPERENCE/DOCKET NUMBER: L5.618
REPERENCE/DOCKET NUMBER: L5.618
REPERENCE/DOCKET NUMBER: L5.618
REPERENCE/DOCKET NUMBER: L5.618
REPERENCE/DOCKET NUMBER: L5.618
REPERENCE/DOCKET NUMBER: L5.618
REPERENCE/DOCKET NUMBER: L5.618
REPERENCE/DOCKET NUMBER: L5.618
REPERENCE/DOCKET NUMBER: L5.618
REPERENCE/DOCKET NUMBER: L5.618
REPERENCE/DOCKET NUMBER: L5.618
REPERENCE/DOCKET NUMBER: L5.618
REPERENCE/DOCKET NUMBER: L5.618
REPERENCE/DOCKET NUMBER: L5.618
REPERENCE/DOCKET NUMBER: L5.618
REPERENCE/DOCKET NUMBER: L5.618
REPERENCE/DOCKET NUMBER: L5.618
REPERENCE/DOCKET NUMBER: L5.618
REPERENCE/DOCKET NUMBER: L5.618
REPERENCE/DOCKET NUMBER: L5.618
REPERENCE/DOCKET NUMBER: L5.618
REPERENCE/DOCKET NUMBER: L5.618
REGURANICATION NUMBER: L5.618
REGURANICATION NUMBER: L5.618
REGURANICATION NUMBER: L5.618
REGURANICATION NUMBER: L5.618
REGURANICATION NUMBER: L5.618
REGURANICATION NUMBER: L5.618
REGURANICATION NUMBER: L5.618
REGURANICATION NUMBER: L5.618
REGURANICATION NUMBER: L5.618
REGURANICATION NUMBER: L5.618
REGURANICATION NUMBER: L5.618
REGURANICATION NUMBER: L5.618
REGURANICATION NUMBER: L5.618
REGURANICATION NUMBER: L5.618
REGURANICATION NUMBER: L5.618
REGURANICATION NUMBER: L5.618
REGURANICATION NUMBER: L5.618
REGURANICATION NUMBER: L5.618
REGURANICATION NUMBER: L5.618
REGURANICATION NUMBER: L5.618
REGURANICATION NUMBER: L5.618
REGURANICATION NUMBER: L5.618
REGURANICATION NUMBER: L5.618
REGURANICATION NUMBER: L5.618
REGURANICATION NUMBER: L5.618
REGURANICATION NUMBER: L5.618
RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/393,540 FILING DATE: 23-FEB-1995 CLASSIFICATION: 435
      APPLICATION NUMBER: US/08/714,677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/08393540 Patent No. 5871993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2573 CAACCGGCGGCGTTCAGCTTC 2594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 74.8%;
Best Local Similarity 86.4%;
Matches 19; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
678..3002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , NAME/KEY:
; LOCATION:
US-08-714-677-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
US-08-393-540-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
```

```
; TOPOLOGY:
US-08-518-878B-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 29, Application US/08518878B
Retent No. 5702902
GENERAL INFORMATION:
APPLICANT: Tarteglia, Louis A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: ROSS, Jeffrey

TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN

TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE

FILE REFERENCE: 960296.95131

CURRENT APPLICATION NUMBER: US/09/261,855A

CURRENT FILLING DATE: 1999-03-03

NUMBER OF SEQ ID NOS: 46

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 1

LENGTH: 2224
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 3073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 2224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 74.8%; Score 17.2; I Best Local Similarity 86.4%; Pred. No. 27; Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 72.2%; Score 16.6; D
Best Local Similarity 82.6%; Pred. No. 50;
Matches 19; Conservative 0; Mismatches
      ; Sequence 1, Application US/09261855A ; Patent No. 6255055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2573 CAACCGGCGGCGTTCAGCTTC 2594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 563 CCAGTTGATGGCCATTTAGCTTC 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 CAACTGGTGGCCATTCAGCTTC 23
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        CDS
678..3002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Mus musculus
US-09-261-855-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
US-08-518-878B-29/c
                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                       , LOCATION:
US-08-714-537-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-261-855-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
MUNDER OF SEQUENCES 17

ADDRESSOR SEQUENCES 17

ADDRESSOR SEQUENCES ADDRESS 17

ADDRESSOR PROBLEM OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF THE AGENCY OF
```

```
US-08-294-522B-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-294-522B-29/c
US-08-294-522B-29/c
Sequence 29, Application US/08294522B
9 Sequence 29, Application US/08294522B
9 Sequence 29, Application US/08294522B
1 Sequence 29, Application US/08294522B
1 TATLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION:

                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 112;
                                                                                                                                                                                                                                                                                                                                                                Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBLE FORM:
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Pc-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294,522B
FILING DATE: 23-AUG-1994
CLASSIPFCATION: 514
ATTORNEY/AGENT INPERMATION:
                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 16.2; DE
Pred. No. 50;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                            Score 16.2;
Pred. No. 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7653-015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
INFORMATION FOR SEQ ID NO: 29: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
US-08-294-522B-30/c
; Sequence 30, Application US/08294522B
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
JOPOLOGY: linear
US-08-518-878B-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 AGCTGGAGGCATTCAGCTTC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 AACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                    Query Match 70.4%;
Best Local Similarity 85.7%;
Matches 18; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 AACTGGTGGCCATTCAGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 AGCTGGAGGGCATTCAGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 112 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: PANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-294-522B-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
```

```
Sequence 29 Application US/08807861A
Fatent No. 5853975
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: METHOD IN METHOD IN THE
TITLE OF INVENTION: METHOD IN THE
TITLE OF INVENTION: METHOD IN THE
TITLE OF INVENTION: METHOD IN THE
TITLE OF INVENTION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP. METHOD IN THE
STARP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Treatment of Body Weight Disorders, Including Obesity
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Emmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION WHERE. US/08/807,861A FILING DATE: 26-FEB-1997 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294,522B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
70.4%; Score 16.2; 1
Best Local Similarity 85.7%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                              CITY: New York
STATE: New York
ZIP: 10036-2711
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 23-AUG-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA 30,742
REGISTRATION NUMBER: 30,742
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPAX: (212) 869-8864/9741
INFORMATION FOR ESQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 AACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 AGCTGGAGGGCATTCAGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 112 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
```

```
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 33-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
FERENCE/DOCKET NUMBER: 30,42
REFERENCE/DOCKET NUMBER: 30,42
FILECHOWINICATION INFORMATION:
TELECHOWINICATION INFORMATION:
TELECHONICATION INFORMATION:
TELECHONICATION INFORMATION:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 29:
TELECHONICATION NO: 20: 20: 20
```

Query Match
Best Local Similarity 85.7%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 3; Indels C
Qy 3 AACTGGTGGCCATTCAGCTTC 23
Db 62 AGCTGGAGGCATTCAGCTTC 42

ô

0; Gaps

Search completed: April 18, 2003, 07:34:30 Job time: 23.4773 secs

				e de la companya de l
		·		
E				
<b>/</b> -				
	8.13 TO ST			
, ,				
	A STATE OF THE STA			
×				
<b>)</b>				
		garania e kuji Kalendari da Arabi da Arabi da Arabi da Arabi da Arabi da Arabi da Arabi da Arabi da Arabi da Arabi da Arabi da		
		•		
r A				\$
				4
<b>N</b> ,				
			•	· · · · · · · · · · · · · · · · · · ·

```
GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
```

OM nucleic -	OM nucleic - nucleic search, using sw model	
Run on:	April 18, 2003, 06:35:31; Search time 95.4848 Seconds (without alignments) 241.975 Million cell updates/sec	/8ec

1 ccaactggtggccattcagcttc 23 US-09-270-437D-12 23 Title: Perfect score: Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

639749 segs, 502280978 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications NA:\*

1: /cgn2\_6/ptodata/1/pubpna/USO7\_PUBCOMB.seq:\*
2: /cgn2\_6/ptodata/1/pubpna/NSO7\_NEW\_PUB.seq:\*
2: /cgn2\_6/ptodata/1/pubpna/USO6\_NEW\_PUB.seq:\*
4: /cgn2\_6/ptodata/1/pubpna/USO6\_NEW\_PUB.seq:\*
5: /cgn2\_6/ptodata/1/pubpna/USO6\_NEW\_PUB.seq:\*
6: /cgn2\_6/ptodata/1/pubpna/USO8\_NEW\_PUB.seq:\*
7: /cgn2\_6/ptodata/1/pubpna/USO8\_PUBCOMB.seq:\*
6: /cgn2\_6/ptodata/1/pubpna/USO8\_PUBCOMB.seq:\*
9: /cgn2\_6/ptodata/1/pubpna/USO8\_PUBCOMB.seq:\*
10: /cgn2\_6/ptodata/1/pubpna/USO8\_PUBCOMB.seq:\*
11: /cgn2\_6/ptodata/1/pubpna/USO9\_PUBCOMB.seq:\*
12: /cgn2\_6/ptodata/1/pubpna/USO9\_PUBCOMB.seq:\*
13: /cgn2\_6/ptodata/1/pubpna/USO9\_PUBCOMB.seq:\*
13: /cgn2\_6/ptodata/1/pubpna/USO0PUBCOMB.seq:\*
14: /cgn2\_6/ptodata/1/pubpna/USO0PUBCOMB.seq:\*
14: /cgn2\_6/ptodata/1/pubpna/USO0PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 5, Appli Sequence 7, Appli Sequence 152, App Sequence 152, App Sequence 3226, A Sequence 11802, A Sequence 11802, A Sequence 11802, A Sequence 1, Appli Sequence 1201, Ap Sequence 121, Appli Sequence 1414, Appli Sequence 1478, Appli Sequence 1778, Appli Sequence 1, Appli Sequence 233, Appli Sequence 233, Appli Sequence 233, Appli Sequence 233, Appli Sequence 233, Appli Sequence 233, Appli Sequence 233, Appli Sequence 233, Appli Sequence 233, Appli Sequence 233, Appli Sequence 623, Appli Sequence 623, Appli Sequence 623, Appli Sequence 624, Appli
SUMMARIES	US-09-899-651-5 US-09-899-651-7 US-08-781-986A-1454 US-08-781-986A-1522 US-09-864-761-13758 US-09-864-761-15758 US-09-864-761-13758 US-09-864-761-131802 US-09-864-761-1313 US-09-813-6131 US-09-938-842A-1201 US-09-938-842A-1201 US-09-938-842A-1201 US-09-938-842A-1201 US-09-938-842A-1201 US-09-938-842A-1201 US-09-938-842A-1201 US-09-938-842A-1301 US-09-938-842A-1301 US-09-938-842A-1301 US-09-938-842A-1301 US-09-938-842A-1301 US-09-893-737-233 US-09-893-737-233
	100 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
% Query Match Length DB	1708 1946 1946 1019 258 454 454 454 709 1632 11932 11932 1294 2214 2218 2218 1532 1532 1532 1532 1532 1532 1532 1532
& Query Match	1000.0 10000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1
Score	23 17.28 17.28 17.28 16.88 16.86 16.20 16.
Result No.	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

Sequence 18, Appl Sequence 126, App Sequence 226, App Sequence 226, App Sequence 222, App Sequence 2471, A Sequence 2471, A Sequence 2132, A Sequence 2132, A Sequence 2132, A Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 6525, A Sequence 218, Appl Sequence 6525, A Sequence 618, Appl Sequence 618, Appl Sequence 611, Appl Sequence 611, Appl Sequence 611, Appl Sequence 611, Appl Sequence 611, Appl Sequence 611, Appl Sequence 611, Appl Sequence 611, Appl Sequence 611, Appl Sequence 611, Appl Sequence 611, Appl Sequence 611, Appl Sequence 611, Appl Sequence 611, Appl	
US-09-129-112-18 US-09-822-830A-124 US-10-006-816A-226 US-10-006-816A-226 US-10-006-816A-226 US-09-864-761-25555 US-09-864-761-21312 US-09-864-761-21312 US-09-864-761-21312 US-09-864-761-21312 US-09-864-761-484 US-09-864-761-484 US-09-864-761-6525 US-09-864-761-6525 US-09-864-761-6525 US-09-864-761-6525 US-09-864-761-6525 US-09-864-761-6525 US-09-864-761-6525 US-09-864-761-6525 US-09-864-761-6525 US-09-864-761-6525 US-09-864-761-12193 US-09-864-761-12193 US-09-964-761-12193 US-09-964-761-12193 US-09-964-761-12193 US-09-964-761-12193 US-09-964-761-12193 US-09-964-761-186	
100 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
1434 1506 3939 3939 11507 11507 151 151 151 441 441 441 441 441 441 441	
688.7.7 688.7.7.8 668.7.7.8 677.8 677.8 677.8 677.8 677.8 677.8 677.8 677.8 677.8 677.8 677.8 677.8 677.8	
15.88 15.88	
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	
0 0 0 0 0	

## ALIGNMENTS

```
Sequence 5, Application US/09899651

Sequence 7, Application US/09899651

Sequence 8, Application US/09899651

SEREMAL INFORMATION:
SEQUENCE 1, Ali
APPLICANT: Chen, Ali
APPLICANT: Tang, Solam
APPLICANT: Tang, Solam
APPLICANT: Stocker, Elsabeth
APPLICANT: Stocker, Elsabeth
APPLICANT: Stocker, Elsabeth
APPLICANT: Stocker, Elsabeth
APPLICANT: Stocker, Elsabeth
APPLICANT: Stocker, Elsabeth
APPLICANT: Orgen, Ali
APPLICANT: Orgen, Ali
APPLICANT: Orgen, Ali
APPLICANT: Orgen, Ali
APPLICANT: Orgen, Ali
APPLICANT: Orgen, Ali
APPLICANT: Orgen, Ali
APPLICANT: Orgen, Ali
APPLICANT: Orgen, Ali
APPLICANT: Orgen, Ali
APPLICANT: Orgen, Ali
APPLICANT: Orgen, Ali
APPLICANT: Orgen, Ali
APPLICANT: Orgen, Ali
APPLICANT: Orgen, Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICANT: Ali
APPLICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 23; DB 10; Length 1708; Best Local Similarity 100.0%; Pred. No. 0.065; Matches 23; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
RESULT 1
US-09-899-651-5/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-899-651-5
```

RESULT 2
US-09-899-651-7/c
Squence 7, Application US/09899651
Patent No. US20020111470a1
GENERAL INFORMATION: 68 CCAACTGGTGGCCATTCAGCTTC 46 g

1 CCAACTGGTGGCCATTCAGCTTC 23

ઠે

ô

```
Query Match
Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches .19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-781-986A-752
US-09-917-800A-1454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                           δ
                                                                                                                                                         TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer TITLE OF INVENTION: Associated TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof FILE REFERENCE: LUD 5538
CURRENT APPLICATION NUMBER: US/09/061,709
PRIOR PILING DATE: 2001-07-06
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANIZM: Rattus norvegicus
PEATURE:
OTHER INFORMATION: Genbank Accession No. US20020119462A1 U20796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 23; DB 10; Length 1946; Pred. No. 0.065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Blashoff, Michael
APPLICANT: Gene Logic, Inc.
IIILE OF INVENTION: Molecular Toxicology Modeling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DAFE: 2001-07-31
PRIOR PLLIAGION NUMBER: US 60/222,040
PRIOR PLING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR PILING DATE: 2001-05-15
PRIOR PILING DATE: 2001-05-20
PRIOR FILING DATE: 2001-05-20
PRIOR PILING DATE: 2001-05-05
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR PILING DATE: 2001-06-13
PRIOR PILING DATE: 2001-06-13
PRIOR PILING DATE: 2001-06-13
PRIOR PILING DATE: 2001-06-13
PRIOR PILING DATE: 2001-06-13
PRIOR PILING DATE: 2001-06-19
PRIOR PILING DATE: 2001-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-09-917-800A-1454/c
; Sequence 1454, Application US/09917800A
; parent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               306 CCAACTGGTGGCCATTCAGCTTC 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CCAACTGGTGGCCATTCAGCTTC 23
                                                              Tsang, Solam
Stockert, Elisabeth
Jager, Elke
Knuth, Alexander
Old, Lloyd J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                        Chen, Yao-Tseng
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 23; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FEATURE:
US-09-899-651-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
```

```
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                         ö
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 7; Length 1019;
                                                                         ö
Length 3628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20850
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
COMPOTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
FILING DATE:
APPLICATION NUMBER: ASCII TEXSISTEDATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAMME: BEHEADOM, BOD
NAMME: BEHEADOM, BOD
NAMME: BEHEADOM, BOD
NAMME: BELCOMMUNICATION NUMBER: OF STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLING STELLIN
           DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: Us*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 17.2; 1
Pred. No. 43;
           77.4%; Score 17.8; 90.5%; Pred. No. 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-864-761-32265/c
US-09-864-761-32265, Application US/09864761
Sequence 32265, Application US/09864761
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          640 CAACTGGTGGTAATTCAGGTTC 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53
                                                                                                                                                                                                                            Db 1355 AGCTGGAGGCCATTCAGCTTC 1335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.8%;
milarity 86.4%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 755
SEQUENCE CHARACTERISTICS:
                                                                                                                                                              3 AACTGGTGGCCATTCAGCTTC
```

```
APPLICANT: Warren, Wealey C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indele
                                                                                                     PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-08-08
PRIOR FILING DATE: 2000-08-08
PRIOR PILING DATE: 2000-08-08
PRIOR PILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: US 60/23,366
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-13
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: MAP TO ACOO2093.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73.0%; Score 16.8; 190.0%; Pred. No. 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11802, Application US/09960352; Patent No. US20020137139A1; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             376 ccacideaeeccaricaecr 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 CAACTGGTGGCCATTCAGCT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-960-352-11802/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-864-761-15758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: MAP TO ACO02093.1

OTHER INFORMATION: EXPRESED IN LUNG, SIGNAL = 0.5

OTHER INFORMATION: EST HUMAN HIT: BE798126.1, EVALUE 1.000

OTHER INFORMATION: SWISSPROT HIT: P34369, EVALUE 8.006-14

OTHER INFORMATION: NT HIT: 9111426714, EVALUE 1.006-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PELICATION NUMBER: US 60/180,312
PRIOR PELICATION NUMBER: US 60/180,312
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-02-06
PRIOR PELING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 99/632,366
PRIOR PELING DATE: 2000-00-04
PRIOR PELING DATE: 2000-00-04
PRIOR PELING DATE: 2000-00-04
PRIOR PELING DATE: 2000-00-04
PRIOR PELING DATE: 2000-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-20
PRIOR PELING DATE: 2001-01-20
PRIOR PELING DATE: 2001-01-20
PRIOR PELING DATE: 2001-01-20
PRIOR PELING DATE: 2001-01-20
PRIOR PELING DATE: 2001-01-20
PRIOR PELING DATE: 2001-01-20
PRIOR PELING DATE: 2001-01-20
PRIOR PELING DATE: 2001-01-20
PRIOR PELING DATE: 2001-01-20
PRIOR PELING DATE: 2001-01-20
PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 16.8;
Pred. No. 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15758, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CAACTGGTGGCCATTCAGCT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 ccacregaeccarrcaecr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
US-09-864-761-15758/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-864-761-32265
```

ô

셤 ઠ

```
US-U9-B64-761-21356

Sequence 21356, Application US/09864761

Sequence 21356, Application US/09864761

Sequence 21356, Application US/09864761

Sequence 21356, Application US/09864761

Sequence 21356, Application G.

APPLICANT: Rank, David K.

APPLICANT: Hanzel, David K.

APPLICANT: Hanzel, David K.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wenbleng

TITLE OF INVENTION: GENOWEDERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL CURRENT PELLOR UNMER: US 09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PILING DATE: 2000-08-03

PRIOR PLING DATE: 2000-08-03

PRIOR PLING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR PILING DATE: 2001-13-0

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IS-09-873-637-1/c
Sequence 1, Application US/09873637
Sequence 1, Application US/09873637
Sequence 1, Application US/09873637
Sequence 1, Application US/09873637
GENERAL INFORMATION:
APPLICANT: Ross, Jeffrey
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
FILE REFERENCE: 960296.95131
CURRENT APPLICATION NUMBER: US/09/873,637
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2224;
                                                                                                                                                                         Length 510;
                                                                                                                                                                                                                                       Indels
                                       FEATURE:
OTHER INFORMATION: MAP TO AC023314.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
US-09-864-761-13431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10;
                                                                                                                                                                            Score 16.6; DB 10;
Pred. No. 78;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 16.6;
Pred. No. 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            563 CCAGTIGATGGCCATTTAGCTTC 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                      351 ccaactrereactartcaecare 329
                                                                                                                                                                                                                                                                                                           1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.2%;
82.6%;
                                                                                                                                                                                   Query Match 72.2%;
Best Local Similarity 82.6%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
CORGANISM: Mus musculus
US-09-873-637-1
         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13411, Application US/09864761

Betent No. US20020048763A1

Betent No. US20020048763A1

Betent No. US20020048763A1

APPLICANT: Rank, David R.

APPLICANT: Rank, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                        Length 453;
                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                     TYPE: DNA ORGANISM: Bos taurus CTHER INFORMATION: Clone ID: 50-LIB34-078-Q1-E1-E10 US-09-960-352-11802
                                                                                                                                                                                                                                                                                                     Score 16.6; DB 10;
Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: GENE EXPRESSION ANALISIS
FILE REFERENCE: Accomica-X-1
CURRENT PELLING DATE: 2001-05-23
PRIOR PELLCATION NUMBER: US 60/180,312
PRIOR PELLING DATE: 2000-02-04
PRIOR PILLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-06-26
PRIOR PELLING DATE: 2000-06-36
PRIOR PELLING DATE: 2000-06-36
PRIOR PELLING DATE: 2000-06-36
PRIOR PELLING DATE: 2000-06-32
PRIOR PELLING DATE: 2000-00-37
PRIOR PELLING DATE: 2000-10-04
PRIOR FILLING DATE: 2000-10-04
PRIOR FILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-30
PRIOR PILLING DATE: 2000-09-21
PRIOR PILLING DATE: 2000-09-21
PRIOR PILLING DATE: 2000-09-21
PRIOR PILLING DATE: 2000-09-21
PRIOR PILLING DATE: 2000-00-31
PRIOR PILLING DATE: 2000-00-31
PRIOR PILLING DATE: 2000-00-31
PRIOR PILLING DATE: 2000-01-29
PRIOR PILLING DATE: 2000-01-29
PRIOR PILLING DATE: 2000-01-29
PRIOR PILLING DATE: 2000-01-29
PRIOR PILLING DATE: 2000-01-29
                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 11802
LENGTH: 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     331 ccaacregreecagrecaecrec 309
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                               Query Match 72.2%;
Best Local Similarity 82.6%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
```

```
### APPLICANT: Renat, Sharton G.
### APPLICANT: Renat, Sharton G.
### APPLICANT: Renat, Sharton G.
#### APPLICANT: Renat, Sharton G.
#### APPLICANT: Renat, Barid R.
#### APPLICANT: Renat, Barid R.
#### APPLICANT: Renat, Barid R.
#### APPLICANT: Renat, Barid R.
#### APPLICANT: Renat, Barid R.
#### APPLICANT: Renat, Barid R.
#### APPLICANT: Gran, Wensheng
#### APPLICANT: Chan, Wensheng
#### APPLICANT: Renat, Grant RENATESION ANALYSIS BY MICROARRAY
#### APPLICANT: Renation RENATE: About Co.2-23
#### RENATE: About Co.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENATE: ABOUT CO.2-23
#### RENAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 70.4%; Score 16.2; DB 9; Length 1632; Best Local Similarity 85.7%; Pred. No. 1.4e+02; Matches 18; Conservative 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4614, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             375 AGCTCTTGGCCATTCAGCTTC 355
                                                                            ; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1201
i LENGTH: 1632
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 AACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1201, Application US/09938842A

Patent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Jeff
APPLICANT: Wang, Xun

TILLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: SAME, AND METHODS OF USE

CURRENT APPLICATION NUMBER: US/09/938,842A

FILE OF INVENTION: SAME, AND 60/227,866

FRIOR APPLICATION NUMBER: US 60/227,866

FRIOR PRILING DATE: 2000-08-24

FRIOR FILING DATE: 2001-08-24

FRIOR FILING DATE: 2001-01-16

FRIOR FILING DATE: 2001-01-16

FRIOR FILING DATE: 2001-01-01-16

FRIOR FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N: EXPRESSED IN FETAL LIVER, SIGNAL = 5.3

N: EXPRESSED IN LUNG, SIGNAL = 68

N: EXPRESSED IN BRAIN, SIGNAL = 5.9

N: EXPRESSED IN HBLAD, SIGNAL = 5.9

N: EXPRESSED IN HELA, SIGNAL = 1.2

N: EXPRESSED IN PLACENTA, SIGNAL = 45

N: EXPRESSED IN PLACENTA, SIGNAL = 45

N: EXPRESSED IN ADULT LIVER, SIGNAL = 9.2

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEART, SIGNAL = 3.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 70.4%; Score 16.2; DB 10; Length 709; Best Local Similarity 85.7%; Pred. No. 1.38+02; Matches 18; Conservative 0; Mismatches 3; Indels 0
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APLICATION NUMBER: PCT/USO1/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-30
PRIOR PRIOR PILING DATE: 2000-09-30
PRIOR PILING DATE: 2000-09-30
PRIOR PILING DATE: 2000-09-30
PRIOR PILING DATE: 2000-09-30
PRIOR PILING DATE: 2000-09-30
PRIOR PILING DATE: 2000-09-30
PRIOR PILING DATE: 2000-09-30
PRIOR PILING DATE: 2000-09-30
PRIOR PILING DATE: 2000-09-30
PRIOR PILING DATE: 2001-01-39
PRIOR PILING DATE: 2001-01-39
PRIOR PILING DATE: 2001-01-39
PRIOR PILING DATE: 2001-01-39
PRIOR PILING DATE: 2001-01-39
PRIOR PILING DATE: 2001-01-39
PRIOR PILING DATE: 2001-01-39
PRIOR PILING DATE: 2001-01-39
PRIOR PILING DATE: 2001-01-39
PRIOR PILING DATE: 2001-01-39
PRIOR PILING DATE: 2001-01-39
PRIOR PILING DATE: 2001-01-39
PRIOR PILING DATE: 2001-01-39
PRIOR PILING DATE: 2001-01-39
PRIOR PILING DATE: 2001-01-39
PRIOR PILING DATE: 2001-01-39
PRIOR PILING DATE: 2001-01-39
PRIOR PILING DATE: 2001-01-39
PRIOR PILING DATE: 2001-01-39
PRIOR PILING DATE: 2001-01-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 AACTTGGGGCCCTTCAGCTTC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: BY OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN OTHER INFORMATION: EN 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
```

```
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05
PRIOR FILING DATE: 2001-06-22
NUMBER OF EQ ID NOS: 5379
LENGTH: 2418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: April 18, 2003, 10:14:07 Job time : 97.6515 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1181 AACTGGGGGGCACTCAGCTTC 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 AACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1478, Application US/09938842A
Sequence 1478, Application US/09938842A
Sequence 1478, Application US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zuu, 1009
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFRENCE: SCRIP1300-3
FILE REPRENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/227,866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hedrick, Joseph A.
APPLICANT: Wang, Ludyan
APPLICANT: Wang, Ludyan
APPLICANT: Wang, Ludyan
APPLICANT: Wang, Ludyan
APPLICANT: Murgolo, Micholas J.
APPLICANT: Greene, Jonathan R.
APPLICANT: Greene, Jonathan R.
APPLICANT: Johnston, James A.
APPLICANT: Bazan, J. Fernando
TILLE REFERENCE: DX0884K(2d)
CURRENT APPLICATION NUMBER: US/09/372,348A
CURRENT FILING DATE: 1999-08-11
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                     Query Match 70.4%; Score 16.2; DB 10; Length 1994; Best Local Similarity 85.7%; Pred. No. 1.4e+02; Matches 18; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70.4%; Score 16.2; DB 9; Length 2244; B5.7%; Pred. No. 1.4e+02; Indels 0 tive 0; Mismatches 3; Indels 0
                                                    OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 68
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.9
OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 5.9
OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 45
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 9.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 9.5
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.6
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.6
US-09-864-761-4614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/09372348A Publication No. US20030028005A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2047 ccaccieciecieccaricacci 2027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 AACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CCAACTGGTGGCCATTCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: (1)..(2244)
US-09-372-348-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEO ID NO 14
LENGTH: 2244
TYPE: DNA
ORGANISM: primate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-09-938-842A-1478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
Sequence 3, Application US/10261482

| Sequence 3, Application US/20203036089A1
| Publication No. US20030036089A1
| GENERAL INFORMATION: US20030036089A1
| APPLICANT: WEI, Ming-Hui et al | APPLICANT: WEI, Ming-Hui et al | ITILE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED | ITILE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR | ITILE OF INVENTION: PROTEINS, AND USES THEREOF | ITILE OF INVENTION: PROTEINS, AND USES THEREOF | ITILE OF INVENTION: PROTEINS, AND USES THEREOF | ITILE OF INVENTION NUMBER: 09/684,393 | PRIOR FILING DATE: 2000-10-10 | PRIOR APPLICATION NUMBER: 60/172,600 | PRIOR APPLICATION NUMBER: 60/172,600 | PRIOR FILING DATE: 1999-12-20 | PRIOR FILING DATE: 1999-12-20 | PRIOR FILING DATE: 1999-12-20 | SOFTWARE: FastSEQ for Windows Version 4.0 | SEQ ID NO 3 | LENGTH: 8001 | PRIOR FILING DATE: 1900-14 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILING DATE: 1900-15 | PRIOR FILIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 8001;
       Length 2418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.4%; Score 16.2; DB 9;
.85.7%; Pred. No. 1.6e+02;
tive 0; Mismatches 3;
Query Match 70.4%; Score 16.2; DB 9; Best Local Similarity 85.7%; Pred. No. 1.4e+02; Matches 18; Conservative 0; Mismatches 3;
```

Title:

```
81.7
  18.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                 April 18, 2003, 05:48:17 ; Search time 1266.05 Seconds (without alignments) 456.759 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pending Patente NA Main:*

(ggn2 6/ptodata/1/pna/US06 COMB.seq:*
Ggn2 6/ptodata/1/pna/US06 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna/US08 COMB.seq:*
Ggn2 6/ptodata/1/pna
GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cgn2_6/ptodata/1/pna/US102A_COMB.seq:
/cgn2_6/ptodata/1/pna/US102B_COMB.seq:
                                                                                                                                                                                                                                                                                                                                                                                           24791104 segs, 12571243825 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                            1 ccaactggtggccattcagcttc 23
                                                                                    - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                      IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                               US-09-270-437D-12
23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0 ...
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                     Perfect score:
                                                                                      OM nucleic
                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database
                                                                                                                                   Run on:
```

```
| cgm2 6/ptodata/1/pna/US6000 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6001 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6002 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6004 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6004 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6005 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6005 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6005 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6001 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6010 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6011 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6011 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6011 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6012 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6012 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6012 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6012 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6012 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6012 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6012 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6012 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6012 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6012 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6012 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6012 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6012 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6012 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6012 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6012 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6012 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6013 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6013 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6013 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6013 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6013 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6013 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6013 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6013 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6013 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6013 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6013 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6013 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6013 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6013 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6013 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6013 COMB. seq: *
| cgm2 6/ptodata/1/pna/US6013 COMB. seq: *
| cgm2 6/ptodata/1/pna/US
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		seguence 152, App	Sequence 5, Appli	Sequence 5, Appli	Sequence 2082 An	,			de '0477 appende 7740, Ap	Sequence 4721, Ap	Seguence 4721. An	Segmence 517 App		2000	Sednence 338, App	998	Seguence 731, App	0518	Semion of a constant	•	sednence 3346, Ap	Seguence 1742. An			sequence 12212, A	Sequence 3063, Ap
ID	TS-60-126-246-4	11S-09-230-232	110 00 00 11	05-09-889-651-5	US-09-625-102-2082	US-09-270-437-7	US-09-899-651-7	US-09-617-182-2240	110-00-407-00-4104	TZ/ #=000-/05-60-80	US-U9-487-566A-4721	US-08-792-586-517	US-09-534-843-43302	US-09-107-426-998	110-60-001-000	110 00 101 00 111	15/-/08-97/-60-91	US-08-401-791A-10518	US-08-401-791B-10518	118-09-652-121-3346	DECC-131-300 CO CO	US-US-Z70-767-1742	US-09-270-767-17024	715-09-270-646B	21221-05-012-C0 C0	PCT-US01-01354-3063
80		2	9 6	9	24	16	33	23	α	9 6	9	11	20	15	4	0	,	80	œ	25		9	16	4		4
* Query Match Length DB	482	1708	100	0071	1738	1946	1946	2512	412		71	235	235	246	246.	300	9 0	338	338	348		000	367	367		4.10
& Query Match	100.0	100.0	100	9 6	0.001	100.0	100.0	100.0	86.1	1 20		84.3	84.3	81.7	81.7	7	1 .	7.19	81.7	81.7	7		81.7	81.7		7.70
Score	23	23	6	9 6	7 (	53	23	23	19.8	0.0		L 9 . 4	19.4	18.8	18.8	18.8	0 0	0.0	18.8	18.8	1 a	9 0	. B.	18.8	9	0
Result No.	o u	0	۳ ن	,	,	ი <sup>,</sup>	o U	o 2	ω υ	0		2 :	T U	c 15	c 13	C 14	ָר ה	,	9 ! U	c 17	α C		7	20 0		f i

```
APPLICANT: Chen, Yao-Tseng
APPLICANT: Gree, Ali
APPLICANT: Gree, Ali
APPLICANT: Gree, Ali
APPLICANT: Greet, Elisabeth
APPLICANT: Josev. Blee
APPLICANT: Josev. Blee
APPLICANT: Josev. Blee
APPLICANT: Josev. Blee
APPLICANT: Old, Lloyd J.
APPLICANT: Old, Lloyd J.
APPLICANT: Old, Lloyd J.
APPLICANT: Old, Lloyd J.
APPLICANT: Old, Lloyd J.
APPLICANT: Old, Lloyd J.
APPLICANT: Old, Lloyd J.
APPLICANT: Old, Lloyd J.
APPLICANT: Old, Lloyd J.
APPLICANT: Old, Lloyd J.
APPLICANT: Old, Lloyd J.
APPLICANT: Old, Lloyd J.
APPLICANT: Old, Lloyd J.
APPLICANT: Old, Lloyd J.
APPLICANT: Old, Lloyd J.
APPLICANT: Old, Lloyd J.
APPLICANT: APPLICANTON UNMBER: US/09/270,437A
CURRENT FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 8
APPLICANT: AND S.
APPLICANT: AND S.
APPLICANT: AND S.
APPLICANT: AND S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 23; DB 16
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 23; Conservative 0; Mismatches
                                 Sequence 5, Application US/09270437A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens FEATURE:
RESULT 2
US-09-270-437-5/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-270-437-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                   Sequence 14442, A
Sequence 261, App
Sequence 2712, App
Sequence 2712, App
Sequence 205, App
Sequence 1129, App
Sequence 1129, App
Sequence 348, App
Sequence 282, App
Sequence 284, App
Sequence 288, App
Sequence 298, App
Sequence 298, App
Sequence 298, App
Sequence 298, App
Sequence 298, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11836, A
Sequence 40121, A
Sequence 39753, A
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 28, App.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Yu, Jimmy Y.
APPLICANT: Yu, Jimmy Y.
APPLICANT: Greenawalt, Lila B.
APPLICANT: Greenawalt, Lila B.
APPLICANT: Greenawalt, Lila B.
APPLICANT: Roseberry, Ana M.
APPLICANT: Roseberry, Ana M.
APPLICANT: Wright, Rachel J.
TITLE OF INVENTION: WOLECULES ASSOCIATED WITH GROWTH AND DEVELOPMENT
FILE REFERENCE: PT-0002 P
CURRENT APPLICATION NUMBER: US/60/126,246
CURRENT APPLICATION NUMBER: 1999-03-24
SUUMBER OF SEG ID NOS: 413
SOFTWARE: PERL PROGram
                                 Sequence 1
Sequence 2
Sequence 1
Sequence 2
Sequence 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 23; DB 56; Length 482; 100.0%; Pred. No. 2; 0; Mismatches 0; Indels '
                            US-09-277-227-14442
US-09-277-227-14442
US-09-597-214442
US-09-9109-627-14442
US-09-652-121-5712
US-09-916-628-261
US-09-940-6858-205
US-09-940-6858-205
US-09-940-6858-205
US-09-344-649-1129
US-09-344-649-1129
US-09-726-807-3047
US-09-587-218-288-348
US-09-587-218-288-348
US-09-587-218-288-348
US-60-137-258-348
US-60-195-053-1243
PCT-USO1-27760-298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-60-173-464-11836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/60126246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: RUSSO, Frank D.
APPLICANT: Spiro, Peter A.
APPLICANT: Banville, Steve C.
APPLICANT: Banville, Steve C.
APPLICANT: Bratcher, Shawn R.
APPLICANT: Oben, Howard J.
APPLICANT: Cohen, Howard J.
APPLICANT: Shah, Purce
APPLICANT: Shah, Purce
APPLICANT: Chalup, Michael S.
APPLICANT: Chalup, Michael S.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Jones, Anissa L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENERAL INFORMATION:
APPLICANT: Hodgson, David M.
APPLICANT: Lincoln, Stephen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; FEATURE: -
; OTHER INFORMATION: 39667.1
US-60-126-246-152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PEI
SEO ID NO 152
    18.8
118.8
118.8
118.8
118.8
118.8
118.8
118.8
118.8
118.8
118.8
118.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠ
```

Gaps

DB 16; Length 1708; 0; Indels

1708

```
ö
                                                                                                                                                                                                                                                  APPLICANT: Tsang, Solam
APPLICANT: Tsang, Solam
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Gager, Elisabeth
APPLICANT: CAURT, Alexander
APPLICANT: CAURT, Alexander
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: Associated
TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
TITLE OF INVENTION NUMBER: US/09/899,651
CURRENT FILING DATE: 2001-07-06
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 8
SEQ ID NO S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 100.0%; Score 23; DB 33; Length 1708; Best Local Similarity 100.0%; Pred. No. 2.5; Onservative 0; Mismatches 0; Indels 0; Mamatches 23; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
US-09-625-102-2082
; Sequence 2082, Application US/09625102
                                                                                                                                                            Sequence 5, Application US/09899651
GENERAL INFORMATION:
APPLICANT: Chen, Yao-Tseng
APPLICANT: Gure, Ali
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 ccaacrdereecarrcaecrrc 46
68 ccaacregreecearreactric 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
                                                                                                              RESULT 3
US-09-899-651-5/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; FEATURE:
US-09-899-651-5
```

CCAACTGGTGGCCATTCAGCTTC 20

42

g

ô

```
Antigen, The Antigens Per Se, And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4721, Application US/09487566
GENERAL INFORMATION:
APPLICANT ROSEN. et. al.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products; FILE REFERENCE: PO44
CURRENT PAPLICATION NUMBER: US/09/487,566
NUMBER OF SEQ ID NOS: 5506
SEQUENCE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 23; DB 33; Length 1946; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 23; DB 23; Length 2512; 100.0%; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2240, Application US/09617182
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Gearing, David P.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A.
TITLE OF INVENTION: HUMAN FETAL THYMUS LIBRARY
FILE REFERENCE: 1600.1145-001;
CURRENT FILING DATE: 2000-07-14
PRIOR FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 2410
SOFTWARE: FaetSEQ for Windows Version 3.0
SEQ ID NO 2240
LENGTH: 2512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                      TITLE OF INVENTION: Antigen, The Antigens P.
FILE REFERENCE: LUD 5538
CURRENT APPLICATION NUMBER: US/09/899,651
CURRENT FILING DATE: 2001-07-06
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 7
SED IN NO 7
CURRENT: 11946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (163)
OTHER INFORMATION: n equals a,t,g, or
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               306 CCAACTGGTGGCCATTCAGCTTC 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      747 CCAACTGGTGGCCATTCAGCTTC 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
CORGANISM: HOMO Bapiens
US-09-617-182-2240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-617-182-2240/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
US-09-487-566-4721/c
                                                                                                                                                                                                                                                                                                                                                                                              US-09-899-651-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 4721
LENGTH: 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              les Encoding Cancer Associated Antige
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANTON NUMBER:
CURRENT FILING DATE:
CURRENT FILING DATE:
CURRENT FILING DATE:
CURRENT FILING DATE:
CURRENT FILING DATE:
CURRENT FILING DATE:
CURRENT FILING DATE:
CURRENT FILING DATE:
CURRENT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING DATE:
APPLICANT FILING 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer TITLE OF INVENTION: Associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
100.0%; Score 23; DB 24; Length 1738;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 23; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 23; DB 16; Length 1946; 100.0%; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: CHEAL Yao-Tseng
APPLICANT: Gure, Ali
APPLICANT: Tasng, Solam
APPLICANT: Tasng, Solam
APPLICANT: Tasng, Solam
APPLICANT: Jager, Elsebeth
APPLICANT: Jager, Elke
APPLICANT: Much, Alexander
APPLICANT: Much, Alexander
APPLICANT: Much, Alexander
APPLICANT: Lub 51381 PCT
CURRENT APPLICATION NUMBER: US/09/270,437A
CURRENT FILING DATE: 1999-03-16
KILB REFERENCE: Lub 55381 PCT
CURRENT FILING DATE: 1999-03-16
KUMBER OF SEQ ID NOS: 8
SEQ ID NO
LENGTH: 1946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAMB/KKY: misc feature
OTHE INFORMATION: Incyte ID No: 457674.1
US-09-625-102-2082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
US-09-270-437-7/c
i Sequence 7, Application US/09270437A;
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1697 ccaacredreccarreactre 1719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       306 CCAACTGGTGGCCATTCAGCTTC 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/09899651 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tsang, Solam
Stockert, Elisabeth
Jager, Elke
Knuth, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Chen, Yao-Tseng
APPLICANT: Gure, Ali
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
US-09-899-651-7/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-270-437-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
```

ô

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gooding, Douglas H.
APPLICANT: Lane, John C.
APPLICANT: Lane, John C.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Shable, James L.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM TITLE OF INVENTION: COLON WITH CROHN'S DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 235;
                                                                                                 ö
                                    Length 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FOUR:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Filed Herewith
CLASSIFICATION NUMBER: 60/010,832
APPLICATION NUMBER: 60/010,812
APPLICATION NUMBER: 60/010,812
APPLICATION NUMBER: 60/010,812
APPLICATION NUMBER: 99.139
RETERRONG PROCKET NUMBER: 99.139
RETERRONG MOTHORIANION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMMUNICATION INF
                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 19.4; DB 11;
Pred. No. 99;
0; Mismatches 1;
                                                DB 18;
                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2231
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
                                             86.1%; Score 19.8;
91.3%; Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                   Sequence 517, Application US/08792586 GENERAL INFORMATION:
                                                                                                                                                                                                                   253 ¢¢ca¢règrègecarrèactre 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gooding, Douglas H.
Lane, John C.
Delegeane, Angelo M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204
                                                                                                                                                                  1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 84.3%;
Best Local Similarity 95.2%;
Matches 20; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Stuart, Susan G.
                                                    Query Match
Best Local Similarity 91.3
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 3174 PORTE CITY: PALO ALTO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
IMMEDIATE SOURCE:
CLONE: 775742
                                                                                                                                                                                                                                                                                                                           RESULT 10
US-08-792-586-517/c
US-09-487-566A-4721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rosen, et. al.

APPLICANT: Rosen, et. al.

TILLE OF INVENTION: Human Genes, Sequences, and Expression Products 44

FILE REFERENCE: PO-44

CURRENT APPLICATION NUMBER: US/09/487,566A

CURRENT APPLICATION NUMBER: 60/116,668

PRIOR APPLICATION NUMBER: 60/116,668

PRIOR PILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 5508

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 4721

LENGTH: 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 18; Length 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 91.3%; Pred. No. 70;
Matches 21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (313)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (387)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (395)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (412)
OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (163)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (282)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: misc feature
; LOCATION: (412)
; OTHER INFORMATION: n equals a,t,g, or
US-09-487-566-4721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (402)
OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9.
1.09-487-566A-4721/c
1.Sequence 4721, Application US/09487566A
2.GENERAL INFORMATION:
                                                                      OCATION: (282)
THER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                          ö
                                                                                                                                                                                 LOCATION: (313)
OTHER INFORMATION: n equals a,t,9,
                                                                                                                                                                                                                                                                                                                        DIHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 CCCACTGGTGGGCATTCAGCTTC 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AME/KEY: misc feature
                                                                                                                                            NAME/KEY: misc feature GOCATION: (313)
                                                                                                                                                                                                                                                          NAME/KEY: misc feature LOCATION: (387)
                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (395)
                                 NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                CCATION
                                                                                                                                                                                                                                              EATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gooding, Douglas H.

APPLICANT: Gooding, Douglas H.

APPLICANT: Stuart, Susan G.

APPLICANT: Stuart, Susan G.

APPLICANT: Naughton, Rebecca B.

ITILE OF INVENTION: HUMAN UMBILICAL CORD MONONUCLEAR CELLS

INTILE OF INCTEP PHARMACEUTICAL CORD MONONUCLEAR CELLS

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA
                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                      Length 246;
                                                                                                                                                                                                                                                               Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/051,750
                                                                                                                                                                                                            Score 18.8; DB 15;
Pred. No. 1.9e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 81.7%; Score 18.8; DB 49;
Best Local Similarity 90.9%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLAASSIFICATION:
NAME: CERRONE MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PD-07
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 855-0555
INFORMATION FOR SEQ ID NO: 998:
SEQUENCE CHARACTERISTICS:
LENGTH: 246 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                       204 ccacciderecccricaccii 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 ccAgcredrecccrrcAgcrr 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CCAACTGGTGGCCATTCAGCTT 22
                                                                                                                                                                                                            81.7%;
    246 base pairs
                                                                                                                                                                                                Query Match
Best Local Similarity 90.9:
Matches 20; Conservative
                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: HEREWITH CLASSIFICATION:
                                                                                                            ; IMMEDIATE SOURCE;
; CLONE: 3421335H1
US-09-107-426-998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
CLONE: 3421335H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-60-051-750-998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
                                                                                                                                                                                                                                                                                              ઠ
                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
         GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Delegeaner, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNOCLEOTIDES ENCODING OR REGULATING SIGNAL TRANSDUCTION MOLEC CURRENT APPLICATION WUMBER: 105/95/34,843
CURRENT APPLICATION WUMBER: 2000-03-24
Prior application data removed - refer to PALM or file wrapper SOFTWARE: PERL Program
SOFTWARE: PERL Program
LENGTH: 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 998, Application US/09107426
GENERAL INFORMATION:
APPLICANT: Gooding, Douglas H.
APPLICANT: Stuart, Susan G.
APPLICANT: Ito, Laura Y.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM NUMBER OF SEQUENCES: 1626
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

84.3%; Score 19.4; DB 20; Length 235;
Best Local Similarity 95.2%; Pred. No. 99;
Matches 20; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: INCTTE PHARMACEUTICALS, INC.
STREET: 3114.PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,426
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) NAME/KEY: misc_feature
) OTHER INFORMATION: Incyte ID No: hu00282360
) NAME/KEY: unsure
) CCCATION: 178, 197, 226
) OTHER INFORMATION: a, t, c, g, or other
US-09-534-843-43302
Application US/09534843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: HEREWITH
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PD-0
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 CAACIGGIGGCCCTICAGCIT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (415) 855-0555
                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
```

```
;
TOPOLOGY: lis
US-08-401-791A-10518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart, & Olstein. ADDRESSE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart, & Olstein. STREET: 6 Becker Farm Road CITY: Roseland STATE: New Jersey COUNTRY: USA ZIP: 07068 COMPUTER EADABLE PORM: MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Dillon, Patrick
APPLICANT: Li, Haodong
APPLICANT: Li, Haodong
APPLICANT: Earle-Hughes, Julie
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products
NUMBER OF SEQUENCES: 17621
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81.7%; Score 18.8; DB 29; Length 328; 90.9%; Pred. No. 2e+02; tive 0; Mismatches 2; Indels 0
                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gearing David P.
APPLICANT: Holtman, Douglas A.
APPLICANT: Kingsbury Gillian A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION NUMBER: US/09/726,807
CURRENT APPLICATION NUMBER: US/09/726,807
CURRENT PILING DATE: 2000-11-30
PRIOR PAPLICATION NUMBER: 60/168,040
PRIOR PAPLICATION NUMBER: 1999-11-30
NUMBER OF SEQ ID NOS: 4076
SOUTHARE: FASELSEQ FOR WINGOWS VERSION 4.0
SEQ ID NO 731
LENGTH: 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10518, Application US/08401791A GENERAL INFORMATION:
APPLICANT: Haseltine, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Blilot
REGISTRATION NUMBER: 3258
REFERENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION:
                        Sequence 731, Application US/09726807
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) NAME/KEY: misc_feature

) LCCATION: (1)...(328)

; OTHER INFORMATION: n = A,T,C or G

US-09-726-807-731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 cchacradradcccrrchacrr 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haseltine, William
Rosen, Craig
Ruben, Steve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CCAACTGGTGGCCATTCAGCTT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.9
Matches 20, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-08-401-791A-10518/c
US-09-726-807-731/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
Sequence 12, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 5, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 10107, A
Sequence 11894, Sequence 11894, Sequence 11894,
                                                                                                    April 18, 2003, 06:35:28; Search time 256:311 Seconds (without alignments) 400.770 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2590, Ap
Sequence 4108, Ap
Sequence 2117, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pending_Patents_NA_New:*

1: /cgn2_6/ptodata71/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata71/pna/NS06_NEW_COMB.seq:*

3: /cgn2_6/ptodata71/pna/US08_NEW_COMB.seq:*

4: /cgn2_6/ptodata71/pna/US08_NEW_COMB.seq:*

5: /cgn2_6/ptodata71/pna/US09_NEW_COMB.seq:*

6: /cgn2_6/ptodata71/pna/US09_NEW_COMB.seq:*

7: /cgn2_6/ptodata71/pna/US09_NEW_COMB.seq:*

8: /cgn2_6/ptodata71/pna/US09_NEW_COMB.seq:*

9: /cgn2_6/ptodata71/pna/US10_NEW_COMB.seq:*

9: /cgn2_6/ptodata71/pna/US10_NEW_COMB.seq:*

10: /cgn2_6/ptodata71/pna/US10_NEW_COMB.seq:*

11: /cgn2_6/ptodata71/pna/US10_NEW_COMB.seq:*
GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-270-437D-12
US-09-270-437D-5
US-09-270-437D-7
US-09-724-676-7
US-09-724-676-6
US-09-724-676-6
US-09-724-676-10
US-09-724-676-10
US-09-724-676-10
US-09-724-676-9
US-09-724-676-9
US-09-724-676-9
US-09-724-676-9
US-09-724-676-9
US-09-724-676-9
US-09-724-676-9
US-09-724-676-9
US-09-99-912-239-212894
US-10-170-235-10107
US-10-170-235-10107
US-10-170-235-39653
US-10-170-238-39653
117
                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                         5897297 seqs, 2233080881 residues
                                                                                                                                                                          US-09-270-437D-12
23
1 ccaactggtggccattcagcttc 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               · SUMMARIES
                                                               OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0*
Maximum Match 100*
Listing first 45 summaries
                                                                                                                                                                                                                                                   IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2040
2040
2069
2019
2119
2158
2158
2208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0
100.0
100.0
100.0
                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                    Run on:
```

C 24 17.2 74.8 201 11 US-60-4 C 25 17.2 74.8 201 11 US-60-4 C 25 17.2 74.8 359 8 US-10-10-10 C 28 17.2 74.8 359 8 US-10-10-10 C 29 17.2 74.8 359 8 US-10-10-10 C 31 17.2 74.8 359 8 US-10-10-10 C 31 17.2 74.8 601 7 US-09-94 C 33 17.2 74.8 601 7 US-09-94 C 34 17.2 74.8 601 7 US-09-94 C 35 17.2 74.8 601 7 US-09-94 C 35 17.2 74.8 601 7 US-09-94 C 35 17.2 74.8 601 7 US-09-94 C 38 17.2 74.8 601 7 US-09-94 C 38 17.2 74.8 601 7 US-09-94 C 38 17.2 74.8 601 7 US-09-94 C 39 17.2 74.8 601 7 US-09-94 C 39 17.2 74.8 601 7 US-09-94 C 39 17.2 74.8 601 7 US-09-94 C 39 17.2 74.8 601 7 US-09-94 C 39 17.2 74.8 601 7 US-09-94 C 39 17.2 74.8 601 7 US-09-94 C 39 17.2 74.8 601 7 US-09-94 C 39 17.2 74.8 601 7 US-09-94 C 39 17.2 74.8 601 7 US-09-94 C 39 17.2 74.8 1100 8 US-10-10-10 C 42 17.2 74.8 1100 8 US-10-10-10 C 42 17.2 74.8 1100 8 US-10-10-10 C 42 17.2 74.8 1100 8 US-10-10-10 C 42 17.2 74.8 1100 8 US-10-10 C 42 17.2 74.8 1100 8 US-10-10-10 C 42 17.2 74.8 1100 B-0-9-94 C 39 17.2 74.8 1100 B-0-9-94 C 39 17.2 74.8 1100 C CMRENT APPLICANT ONLY ISOLATED NUMBER: US/09/270,4 CURRENT PILING DATE: 1999-03-16 C 7 TTLE OF INVENTION: ALIGABE NUMBER: US/09/270,4 CURRENT PILING DATE: 1999-04-17 C 7 TTLE OF INVENTION: ALIGABE NUMBER: US/09/270,4 CURRENT PILING DATE: 1999-04-17 C 7 TTLE OF INVENTION: AUGUST NUMBER: US/09/270,4 CURRENT PILING DATE: 1999-04-17 C 7 TTLE OF INVENTION: AUGUST NUMBER: US/09/270,4 CURRENT PILING DATE: 1999-04-17 C 7 TTLE OF INVENTION: AUGUST NUMBER: US/09/270,4 CURRENT PILING DATE: 1999-04-17 C 7 TTLE OF INVENTION: AUGUST NUMBER: US/09/270,4 C 7 TTLE OF INVENTION: AUGUST NUMBER: US/09/270,4 C 7 TTLE OF INVENTION: AUGUST NUMBER: US/09/270,4 C 7 CURRENT PILING DATE: US/09/270,4 C 7 TTLE OF INVENTION: AUGUST NUMBER: US/09/270,4 C 7 TTLE OF INVENTION: AUGUST NUMBER: US/09/270,4 C 7 TTLE OF INVENTION: AUGUST NUMBER: US/09/270,4 C 7 TTLE OF INVENTION: AUGUST NUMBER: US/09/270,4 C 7 TTLE OF INVENTION: AUGUST NUMBER: US/09/270,4 C 7 TTLE OF INVENTION: AUGUST NUMBER: US/09/270,4 C 7 TTLE OF INVENTION: AUGUST NUMBER: US/09/270,4 C	1 US-60-436-641-4108 Sequence 4108, Ap US-10-401-229-9790 Sequence 41211, A US-10-401-229-1037 Sequence 51037, Ap US-10-391-399-522 Sequence 51037, Ap US-10-401-229-9654 Sequence 520973, Ap US-10-401-229-9659 Sequence 9610, Ap US-10-401-229-9630 Sequence 9654, Ap US-04-947-907-9990 Sequence 9306, Ap US-09-949-016-33069 Sequence 33068, A US-09-949-016-33069 Sequence 33068, A US-09-949-016-33069 Sequence 33070, Ap US-09-949-016-33070 Sequence 33070, Ap US-09-949-016-33081 Sequence 138582, US-09-949-016-138582 Sequence 138584, US-09-949-016-138584 Sequence 138584, US-09-949-016-138584 Sequence 12897, App US-10-329-624-752 Sequence 12897, App US-10-329-624-18990 Sequence 1287, App US-10-170-235-17364 Sequence 13, Appl US-10-170-235-17364 Sequence 13, Appl US-10-170-235-17364 Sequence 133, Appl	ALIGNMENTS	437D Leic Acid Molecules Encoding Cancer Associated Antiger : Se, And Uses Thereof 7/270,437D	Score 23; DB 5; Length 23; Pred. No. 0.34; ; Mismatches 0; Indels 0; Gaps 0; 23	JD
C 24 17.2 74.8 C 25 17.2 74.8 C 26 17.2 74.8 C 28 17.2 74.8 C 29 17.2 74.8 C 29 17.2 74.8 C 29 17.2 74.8 C 31 17.2 74.8 C 33 17.2 74.8 C 33 17.2 74.8 C 33 17.2 74.8 C 33 17.2 74.8 C 34 17.2 74.8 C 34 17.2 74.8 C 35 17.2 74.8 C 38 17.2 74.8 C 38 17.2 74.8 C 39 17.2 74.8 C 39 17.2 74.8 C 39 17.2 74.8 C 39 17.2 74.8 C 38 17.2 74.8 C 39 17.2 74.8 C 42 17.2 74.8 C 39 17.2 74.8 C 39 17.2 74.8 C 39 17.2 74.8 C 39 17.2 74.8 C 39 17.2 74.8 C 39 17.2 74.8 C 38 17.2 74.8 C 39 17.2 74.8 C 38 17.2 74.8 C 38 17.2 74.8 C 38 17.2 74.8 C 38 17.2 74.8 C 38 17.2 74.8 C 38 17.2 74.8 C 38 17.2 74.8 C 38 17.2 74.8 C 17.2 74.8 C 38 17.2	100 100 100 100 100 100 100 100 100 100		con US/09270 Treng Late	υ—υ	uS/0927043 Beng am Elisabeth e
	23 26 27 26 27 28 29 20 20 20 20 20 20 20 20 20 20		RESULT 1  US-09-270-437D-12  S Gequence 12, Applicati GENERAL INFORMATION: APPLICANT: Chen, Yal- APPLICANT: Gure, Ali APPLICANT: Gure, Ali APPLICANT: Gradger, SI APPLICANT: Tsang, So APPLICANT: Tsang, So APPLICANT: Trang, So APPLICANT: Aloue, Ali APPLICANT: Aloue, Ali APPLICANT: CONCERT, Aloue TITLE OF INVENTION: II TITLE OF INVENTION: II TITLE OF INVENTION: II TITLE OF INVENTION: II TITLE OF INVENTION: II TITLE OF INVENTION: II TITLE OF INVENTION: II NUMBER OF SEQ ID NOS: SEQ ID NO 12 IENGTH: 23 ITYPE: DNA ONGANISM: Homo sapien FEATURE: FEATURE: SEATURE: CONGANISM: Homo sapien SEATURE: CONGANISM: Homo sapien	Query Mat Best Loca Matches 1 C	RESULT 2 (S-09-270-437D-5/c (S-09-270-437D-5/c (SEQUENCE 5, Application) (GENERAL INFORMATION: (APPLICANT: Chen, Yao-T) (APPLICANT: Tang, Soli (APPLICANT: Stockert, S

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 23; DB 6; Length 2040; 100.0%; Pred. No. 0.55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 23; DB 6; Length 1990; 100.0%; Pred. No. 0.55;
                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 23; DB 6; Length 1990; Best Local Similarity 100.0%; Pred. No. 0.55; Matches 23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
US-09-724-676-6/C
Sequence 6, Application US/09724676
Sequence 6, Application US/09724676
GENERAL INFORMATION:
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 6
LENGTH: 2040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OBNIGHMENT IN COMPUSED LTD
TITLE OF INVENTION: Variants of alternative splicing
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT PELLING 128 1000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
LENGTH: 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
CURRENT APPLICATION NUMBER: US/09/124,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
US-09-724-676A-7/c
US-09-724-676A-7/ Application US/09724676A
; GEGNERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ccaacregreeccarreactric 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               442 ccaachddredccarrcadcrrc 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   442 ccaacregreeccarrcacrrc 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 23, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
CRGANISM: Homo Bapiens
US-09-724-676-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
CORGANISM: Homo sapiens
US-09-724-676A-7
                                                                                                                                                                                                                   TYPE: DNA
CORGANISM: Homo sapiens
US-09-724-676-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
US-09-724-676A-6/C
                                                                                                                                                                                          1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09270437D

Sequence 7, Application US/09270437D

Sequence 7, Application US/09270437D

GENERAL INFORMATION:

APPLICANT: Gene, Ali

APPLICANT: Teang, Solam

APPLICANT: Teang, Solam

APPLICANT: Applicant: Alexander

APPLICANT: Knuth, Alexander

APPLICANT: Applicant: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

MUMBER OF SEQ ID NOS: 23

FELOR APPLICANT: Alexander

NUMBER OF SEQ ID NOS: 23

FELOR APPLICANT: Alexander

NUMBER OF SEQ ID NOS: 23

FELOR APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Alexande
                                APPLICANT: Old, Lloyd J.

TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Antige
TITLE OF INVENTION: Antigens Per Se, And Uses Thereof
TITLE OF INVENTION: Antigens Per Se, And Uses Thereof
TITLE OF INVENTION: Antigens Per Se, And Uses Thereof
CURRENT APPLICATION NUMBER: US/09/270,437D
CURRENT FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 09/061,709
PRIOR PILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 23
SEQ ID NO 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Score 23; DB 5; Length 1946;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 23; Conservative 0; Mismatches 0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Score 23; DB 5; Length 1708;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Compugen LTD TITLE OF INVENTION: Variants of alternative splicing FILE REFERENCE: 129181.4 Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: CDS
LOCATION: 1622,1702,1771,1809,1833
LOCATION: 1622,000 unsure of nucleotide
US-09-270-437D-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS

1. CCATTON: 1384,1464,1533,1571,1595

1. CTHER INFORMATION: unsure of nucleotide

18.09-270-437D-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-09-724-676-7/c Sequence 7, Application US/09724676; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306 cchachdardacchrichadric 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
Query Match
100.0%; Score 23; DB 6; Length 2119;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 23; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 23; DB 6; Length 2119;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
US-09-724-676A-5/C
i Sequence 5, Application US/09724676A
i GENERAL INFORMATION:
i TITLE OF INVENTION: VATIONE OF ALL OF INTENTION: VATION OF INTENTION: VATION OF INTENTION: VATION OF INTENTION: VATION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION OF INTENTION O
                                                                                                                                                                                                  Sequence 5, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION WUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
                                       442 CCAACTGGTGGCCATTCAGCTTC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    442 ccaacredredccarrcaecrrc 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       442 CCAACTGGTGGCCATTCAGCTTC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
CORGANISM: Homo sapiens
US-09-724-676-9
                                                                                                                                    RESULT 10
US-09-724-676-5/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 5
LENGTH: 2119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
US-09-724-676-9/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 5
LENGTH: 2119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-724-676-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 2158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Score 23; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 23; DB 6; Length 2069; 100.0%; Pred. No. 0.55; Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
US-09-724-676-10/C

Sequence 10, Application US/09724676
GENERAL INFORMATION:
HAPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT PELLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SEQ ID NO 10
LENGTH: 2069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-12-16-66A-10/C

Sequence 10, Application US/09724676A

GENERAL INFORMATION:
APPLICANT: Compugen LTD
ITILE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILIG DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 10
LENGTH: 2069
                                                     APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 6
LENGTH: 2040
Sequence 6, Application US/09724676A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            442 CCAACTGGTGGCCATTCAGCTTC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ccaacregregecarreagrire 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            442 CCAACTGGTGGCCATTCAGCTTC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 23, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA

ORGANISM: Homo sapiens
US-09-724-676-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-724-676A-10
```

g ઠે

ö

Gaps

ઠે

100.0%; Score 23; DB 6; Length 2158;

Query Match

Query Match

```
Search completed: April 18, 2003, 10:50:27 Job time : 257.311 secs
; TYPE: DNA; ORGANISM: Homo sapiens
US-09-724-676A-8
                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 23; DB 6; Length 2208;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 23; DB 6; Length 2158; Best Local Similarity 100.0%; Pred. No. 0.56; Matches 23; Conservative 0; Mismatches 0; Indels
                    Best Local Similarity 100.0%; Pred. No. 0.56; Matches 23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-09-724-676A-8/C
i Sequence 8, Application US/09724676A
i GENERAL INFORMATION:
A APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
TITLE OF INVENTION: Variants of alternative splicing
TITLE OF INVENTION: Variants of alternative splicing
TITLE OF INVENTION: Variants of alternative splicing
CURRENT PAPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 8
; LENGTH: 2208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GEGUALCE 8, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
TITLE OF INVENTION: Variants of alternative splicing
; TITLE REFERENCE: 129181.4 Compugen;
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT APPLICATION NUMBER: 2000-11-28
; SOFTWARE: PATENTION OS: 97222
; SOFTWARE: PATENTIN Version 3.2
; SEQ ID NO 8
; LENTH: 2208
                                                                                                                                                                                                                                                                                                     APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION WUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOCTHARE: Patentin version 3.2
SEQ ID NO 9
LENTH: 2158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      442 CCAACTGGTGGCCATTCAGCTTC 420
                                                                                                                                                                                                                                                                      ; Sequence 9, Application US/09724676A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               442 CCAACTGGTGGCCATTCAGCTTC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                442 cchacregredecchricherric 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo Bapiens
US-09-724-676-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
CRGANISM: Homo sapiens
US-09-724-676A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
US-09-724-676-8/c
                                                                                                                                                                                                                                    RESULT 13
US-09-724-676A-9/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                     g
                                                                                                                 ઠે
```

```
Gaрв
                                                    .<u>.</u>
Query Match 100.0%; Score 23; DB 6; Length 2208; Best Local Similarity 100.0%; Pred. No. 0.56; Marches 23; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                              442 CCAACTGGTGGCCATTCAGCTTC 420
                                                                                                          1 ccaacregreeccarreactre 23
```

BQ64966 AGENCOURT BQ648383 AGENCOURT	BO651655 AGENCOURT BO652180 AGENCOURT BO652180 AGENCOURT BO728196 AGENCOURT BO728196 AGENCOURT BO647561 AGENCOURT	BES41467 601067919 B08385 F18A15-T7.1 BM148903 TCAAPES52 AQ132664 HS 3058 A BM146309 TCAAPER43 BG025694 60227493 BF797894 602257293	A2901563 RPCT-24-2 BM475738 AGENCOURT BH315184 CH230-209 BE508123 dc26h02.y BG407307 dab17b05.	A1444993 BOHQB46TR BH054219 RPCT-24-3 AV952715 AV952715 AZ762364 IM0557F21	B140.1056 MI-P-CPO-B26736 T1867TF TAM BE231931 136808 MA B6231931 136808 MA B0603654 MI-P-CPO-AV825598 AL683579 AL683579 AL585504 AL595504 AU237120 AU237120 AL640616 AL640616 BF307752 601890820 B11622 F18A15-T7.3 AZ000183 RPCI-23-3 AQ482316 RPCI-11-2		(#937231) Homo sapiens cDNA (#937231) (#937231) (#937231) (#937231) (#937231) (#937231) (#937231) (#937231) (#937231) (#937231) (#937231) (#937231) (#937231)	ldo,M.F., Chiapelli,B., avello,A., Gish,W., Hawkins avello,A., Madis,E., Moore	RIKIN,L., KONLING,T., Therry-Meg,J., Trevaakia,E., R., Wilson,R. and Marra,M. an expressed sequence tags	ne . Louis, MO 63108 rough LLNL / contact the
7 23 100.0 940 1 8 23 100.0 950 1 9 23 100.0 953 1	10 23 100.0 955 1 11 23 100.0 982 1 12 23 100.0 1042 1 13 23 100.0 1042 1 14 23 100.0 1061 1 15 21.4 93.0 770 1	19.4 84.3 912 1 18.8 81.7 326 1 18.8 81.7 395 1 18.8 81.7 505 1 18.8 81.7 589 1 18.8 81.7 541 1	18.8 81.7 1095 1.18.2 79.1 155 17 18.2 18.2 79.1 508 12 18.2 79.1 508 12 18.2 79.1 508 12 18.2 79.1 588 13	18.2 79.1 719 17 18.2 79.1 776 17 17.8 77.4 325 10 17.8 77.4 412 17 17.8 77.4 482 13	34 17.8 77.4 551 17 B26736 35 17.8 77.4 552 10 BE231931 37 17.8 77.4 570 14 B0603654 38 17.8 77.4 604 10 AV825598 c 39 17.8 77.4 621 9 AL683579 c 40 17.8 77.4 634 9 AL683579 c 41 17.8 77.4 657 9 AU337120 c 41 17.8 77.4 682 9 AL640516 c 43 17.8 77.4 74 74 12 BF307752 c 43 17.8 77.4 796 17 BF307752 c 43 17.4 75.7 401 17 AZ000183 c 45 17.4 75.7 597 17 AQ482316	ALIGNMENTS	RESULT 1  AA196774/C LOCUS LOCUS DEFINITION ZG60602.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA ACCESSION AA196774 AA196774.1 GI:1792476 EST. SOURCE Numan. ORGANISM Homo sapiens Chardata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria: Drimares: Craniata; Vertebrata; Euteleostomi;	REFERENCE 1 (bases 1 to 249) AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins ,M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Mardis, E., Moore ,B., Mooris, M., Parsons, J.	Schellenberg, K., Soares, M.B., Tan, F., Underwood, K., Wohldmann, P., Waterston, TITLE Generation and analysis of 280,000 hum: JOURNAL Genome Res. 6 (9), 807-828 (1996)	COMMENT Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LLNL
<u>-                                      </u>							EGHU G>KO	<u> </u>		· 
_p5_4578 gen_ttd.	Search time 800.818 Seconds (without alignments)	cerr updates/sec	32308132			·		y chance to have a e result being printed, distribution.	Description	AA196774 zq60f02.r AA196976 zq60h02.r BM006191 603614013 BG473949 602516444 BQ647425 AGENCOURT
GenCore version 5.1.4 p5_4 Copyright (c) 1993 - 2003 Compugen I	<ul> <li>nucleic search, using sw model</li> <li>April 18, 2003, 04:47:40;</li> </ul>	CORE: 23 1 ccaactggtggccattcagctc 2 able: IDENTITY_NUC Gapop 10.0 , Gabext 1 0	16154066 seqs, 809774. of hits satisfying choses	ub seq length: 2000000000 cessing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	m estba:* em_esthum:* em_esthum:* em_esthun:* em_estcov:* em_estpl:* em_estpl:* em_htc:* gb_estl:* gb_estl:* gb_estl:*	12: gD e8t3:* 13: gD_e8t4:* 14: gD e8t5:*	15: em_estfun:* 16: em_estom:* 17: 9b gas:* 19: em_gss_inv:* 20: em_gss_inv:* 21: em_gss_inv:* 22: em_gss_inv:* 23: em_gss_inv:* 24: em_gss_inv:* 25: em_gss_inv:* 26: em_gss_inv:* 27: em_gss_inv:* 27: em_gss_inv:* 26: em_gss_inv:* 27: em_gss_inv:* 26: em_gss_inv:* 27: em_gss_inv:*	No. is the numb greater than or derived by ana	i	23 100.0 249 9 AA196774 23 100.0 466 9 AA196774 23 100.0 764 13 BM006191 23 100.0 877 12 BG473949 23 100.0 896 14 BQ647425 23 100.0 929 14 BQ652586
	OM nucleic Run on:	Title: Perfect s Sequence: Scoring t		Post-processing:	<b>Database</b>			Pred. BCore and 1s	Bult No.	0 0 0 0 0 0 4 0 w 4 w w

```
mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                 121 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BM00619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Si
Matches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
BM006191/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
VERSION
KEYWORDS
                                                                                                                                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                  / Udb_xrefe="taxon:900"
/ db_xrefe="taxon:960"
/db_xrefe="taxon:960"
/db_xrefe="taxon:960"
/clone="inbacs:4601"
/clone=lib="stratagene neuroepithelial cells"
/clone=lib="stratagene neuroepithelial cells"
/dev stage="Ntera-2/RA neuroepithelial cells"
/dev stage="Ntera-2/RA neuroepithelial cells"
/dev stage="Ntera-2/RA neuroepithelial cells"
/dev stage="Ntera-2/RA neuroepithelial cells"
/dev stage="Ntera-2/RA neuroepithelial cells"
/dev stage="Ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/dev stage="ntera-2/RA neuroepithelial cells"
/d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ma. (Dases 1 to 466)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Hillier, L., Dennon, G., Becker, M., Edw., Le, N., Mardis, E., Moore, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA196976
466 bp mRNA linear EST 22-JAN-1997 ag60h02.rl Stratagene neuroepithelium (#937231) Homo sapiens CDNA clone IMAGE:646035 5', mRNA sequence.
AA196976
AA196976.1 GI:1792567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: esc@watcon.wustl.edu
Email: esc@watcon.wustl.edu
This clone is available royalty-free through LLNL ; contact the
This clone is available royalty-free through LLNL ;
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /oranism="Homo sapiens"
/bxref="CDB:5216286"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="INAGE:646035"
/clone lib="Stratagene neuroepithelium (#937231)"
/dev_stage="Ntera-2/RA neuroepithelial cells"
/deb_nost="NoLE (kanamycin resistant)"
/note="vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dr. NT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 23; DB 9; Length 249; Best Local Similarity 100.0%; Pred. No. 2.8; Matches 23; Conservative 0; Mismatches 0; Indels
       IMAGE Consortium (info@image.llnl.gov)
Seg primer: -28M13 rev2 from Amersham
High quality sequence stop: 119.
Location/Qualifiers
                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ccaactggrggccarrcagcrrc 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 CCAACTGGTGGCCATTCAGCTTC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
AA196976/C
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                             FEATURES
```

g à

```
ö
                                                                                                                                                                                             BM006191
603614013F1 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:5433698 5',
ö
                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 764)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 23; DB 13; Length 764; 100.0%; Pred. No. 4.6;
                                                                              Query Match 100.0%; Score 23; DB 9; Length 466; Best Local Similarity '100.0%; Pred. No. 3.7; Matches 23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                           1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                               42 ccaaciderescentrascric 20
                                                                                                                                                                                                                                              BM006191.1 GI:16520545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Library.
```

ğ

BG473949/c

```
1. .896
/organism="Homo sapiens"
/db xref="texacon:9606"
/clone="IMAGE:6283876"
/clone="IMAGE:6283876"
/clone="IMAGE:6283876"
/clone="IMAGE:6283876"
/clone="IMAGE:6283876"
/clone="IMAGE:6283876"
/clone="IMAGE:6283876"
/clone="IMAGE:6283876"
/clone="IMAGE:6283876"
/clone="IMAGE:6283876"
/clone="IMAGE:6283876"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376"
/clone="IMAGE:628376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ICSM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; CE I (bases 1 to 929)

RS NIH-MGC http://mgc.nci.nth.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nth.gov

Tissue Procurement: CGAP (Stanford)

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium

CLONE distribution: MGC clone distribution information can be http://image.llnl.gov

Plate: LLCM2497 row: k column: 24

High quality sequence stops: 533.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BQ652586

AGENCOURT_8490818 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6293903
5', mRNA sequence.
BQ652586
GG52586.1 GI:21776758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .929
/organism="Homo sapiens"
/db_xref="taxon.9606"
/dlone="likakGE:6293003"
/clone=lib="NIH MGC_100"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepatcocallular carcinoma, cell line"
/tisue_type="hepatcocallular carcinoma, cell line"
/tissue_type="hepa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://imago.llnl.gov
blate: LLCM2480 row; j column: 05
High quality sequence stop: 421.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 23; DB 14; Length 896;
100.0%; Pred. No. 5;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             354 CCAACTGGTGGCCATTCAGCTTC 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 23, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                    Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
BQ652586/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                  SM Homeosapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukheria; Primates; Catarrhini; Hominidae; Homo.
Bulle (1999)
National Institutes of Health, Mammalian Gene Collection (MGC)
Conteact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement. ATC:
CONA Library Preparation: Ling Hong/Rubin Laboratory
CONA Library Preparation: Ling Hong/Rubin Laboratory
CONA Library Arrayed by: Incyte Genomics, Inc.
CONA Library Arrayed by: Incyte Genomics, Inc.
Conne distribution: MGC clone distribution information can be Found through the I.M.A.G.E. Consortium/LiNL at: image.llnl.gov
High quality sequence stop: 673.

High quality sequence stop: 673.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db xref="texon: organizer..."
/db xref="texon: organizer..."
/clone="IMAGE:4647994"
/clone=lib="NIH MGC_16"
/tissue_type="retinoblastoma"
/lab_host="UH108" (phage-resistant)"
/note="Organ: eye; Vector: poTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA.made by oligo-dT priming. Directionally-
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BG473949

877 bp mRNA linear EST 21-MAR-2001

RNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BQ647425

BQ647425

BQ647425.1 GI:21771597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Division of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 23; DB 12; Length 877;
100.0%; Pred. No. 4.9;
Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
cDNA Library Preparation: Rubin Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       690 CCAACTGGTGGCCATTCAGCTTC 668
                                                                                                                                                                                       BG473949.1 GI:13406226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 a
                                                                                                                                                                                                                                                                                        human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bource
                                                                                                                          ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
BQ647425/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
```

셤

ö

Gaps

ö

```
Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human.
                                                                                                                                                                                                         human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BQ647360/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                     RESULT 8
BQ648383/c
LOCUS
                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                          ORGANISM
                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
                                                                                                                                            ACCESSION
                                                                                                                                                             VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGIN
                                                                                                                                                                                                         SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="rwAGS:129693"
/clone="rwAGS:129693"
/clone="rwAGS:129693"
/clone="rwAGS:129693"
/clone="rwAGS:129693"
/clone="rwAGS:129693"
/clone="rwAGS:1296940"
/clone="rwAGS:1296940"
/clone="rwAGS:100"
/clone="organ: liver; vector: pormy; site_1: xhol; site_2: /note="organ: liver; vector: pormy; site_1: xhol; site_2: /note="organ: liver; vector: priming. Directionally cloned EcoRi; cDNA made by oligo-dT priming. Directionally cloned EcoRi; cDNA made by oligo-dT priming. Directionally cloned EcoRi; cDNA made by oligo-dT priming. Directionally cloned EGORCAG(G): Size-selected >500bp for average insert size GGCACGAG(G): Size-selected by Ling Hong in the laboratory of Garald M: Rubin (University of California, Berkeley) of Garald M: Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kt (Stratagene) and Superscript in RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                            AGENCOURT 8286221 NIH MGC_100 Homo sapiens cDNA clone IMAGE:6299693 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbe-remail.nih.gov
Tissue Procurement: CGAP (Stanford)
Tissue Procurement: CGAP (Stanford)
Tissue Proparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM2512 row: column: 06
High quality sequence stop: 395.
Location/Qualifiers
                                                                                                                                                                                                                                                       ö
into EcoRI/Xhol sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RI (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 940)
Nath-MGC http://mgc.ncl.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 23; DB 14; Length 940;
Pred. No. 5.1;
                                                                                                                                                                                                               Length 929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                    100.0%; Score 23; DB 14; 100.0%; Pred. No. 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                           158 t
                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262 9
                                                                                                                                                             264 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            337 CCAACTGGTGGCCATTCAGCTTC 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                               417 CCAACTGGTGGCCATTCAGCTTC 395
                                                                                                                                                                                                                                                                                                       1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
Local Similarity 100.0%;
les 23; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BQ649666.1 GI:21773838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Library."
269 c
                                                                                                                                                             247 C
                                                                                                                                                                                                                                                Local Similarity 100.
                                                                                                                                              Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Н
                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                          BQ649666/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                    ₽
```

```
/organism="Homo sapiens"
/db_xref="taxon:966"
/db_xref="taxon:966"
/clone="InAGRES 1626202"
/clone="InAGRES 1626200"
/clone=lib="NHH MGC_100"
/clone lib="NHH n: liver; vector: porms; site_1: xhol; site_2: /note="Organ: liver; vector: priming. blretchnally cloned EcoRi; cDNA made by oligo-dT priming. blretchnally cloned EcoRi; cDNA made by oligo-dT priming. blretchnally cloned GGCACGAG(G): Size-selected by Ling Hong in the laboratory of Garald M. Rubin (University of California, Berkeley) of Garald M. Rubin (University of California, Berkeley) using ZAP-cDNA, synthesis kit (Stratagene) and Superscript IRT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                               And septens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mational to 950)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

And Library Eregarian (1990)

Tissue Procurement: CGAP (Stanford)

Tissue Procurement: CGAP (Stanford)

Tissue Procurement: MGC (Stanford)

The Sequencing by: Agencourt Bioscience Corporation

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

CONA Library Arrayed by: Agencourt Bioscience Corporation

NA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov m column: 03

Plate: LLCM2439 row m column: 03

High quality sequence stop: 599.

SS 1...550

Nurce //warniem="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BQ647360 953 bp mRNA linear BST 15-JUL-2002 AGENCOURT 8443628 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6284231 5', mRNA Sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
950 bp mRNA linear EST 15-JUL-2002 55, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NH+MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 18 100.0%; Score 23; DB 14; Length 950; Similarity 100.0%; Pred. No. 5.1; 23; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 CCAACTGGTGGCCATTCAGCTTC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BQ647360
BQ647360.1 GI:21771532
                                                                                                                                                                                                                      BQ648383.1 GI:21772555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 953)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         278 c
```

```
/clone lib="NIH_MGC_100"
/tissue_type="hepatocellular carcinoma, cell line"
/lab_host="NHIOB (phage-resistant)"
/lab_host="NHIOB (phage-resistant)"
/noce="Organ: liver; Vector: porPay; Site_1: XhoI, Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >SODDp for average insert size
I.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Strategene) and Superscript
II.RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                157 t
                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 t
                                                                                                                                                                                                                                                                                             253 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            267 g
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 CCAACTGGTGGCCATTCAGCTTC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BQ652180
BQ652180.1 GI:21776352
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                  Library."
a 313 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                           232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
BQ652180/c
LOCUS
                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                           1. 953
/ Organism="Homo sapiens"
/ Ab xxce="axxon:9606"
/ Clone="InAGE:628431"
/ Clone="InAGE:628431"
/ Clone="InAGE:628431"
/ Clone="InDex="Blide"
/ Lissue type="hepat_cellular carcinoma, cell line"
/ Lissue type="hepat_cellular carcinoma, cell line"
/ Lissue type="hepat_cellular carcinoma, cell line"
/ Lissue type="hepat_cellular carcinoma, cell line"
/ Lissue type="hepat_cellular carcinoma, cell line"
/ Lissue type="hepat_cellular carcinoma, cell line"
/ Lissue type="hepat_cellular carcinoma, site_2:
/ Rcorl; cDNA made by oligo-dr priming. Directionally cloned
/ Lisko Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
Listue type="hepat_cellular carcinoma"
/ Listue Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1to 955)
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: Capaba-remail.nih.gov/.
Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be http://image.llnl.gov
Plate: LLCM2444 row: a column: 11
High quality sequence stop: 588.
                    Contect: Robert Strausberg, Ph.D.
Email: gapbs-r@mail.nih.gov
Tissue Prourement: CGAP (Stanford)
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Flate: LLCM2481 row: h column: 24
High quality sequence stop: 651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              955 bp mRNA linear EST 15-JUL-2002
5', mRNA Bequence.
BQ651665.1 GI:21775837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 23; DB 14; Length 953;
100.0%; Pred. No. 5.1;
tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone="IMAGE:6269842"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             336 ccaacrddreccarrcagrrc 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 23; Conservative
      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo saptens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human.
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
BQ651665/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEATURES
```

δ 엄

/ Old xref="texon: begins: but the control of the c Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 92)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: Capaba-rémail.nih.gov

Tissue Procurement: CGAP (Stanford)

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be http://image.llnl.gov

Clone distribution: MGC clone distribution information can be http://image.llnl.gov

Right quality sequence stop: 667.

High quality sequence stop: 667.

Incention/Qualifiers

Incention/Qualifiers

Incention/Qualifiers

Incention/Qualifiers

Incention/Qualifiers ö BQ652180 AGENCOURT\_8188778 NIH\_MGC\_100 Homo sapiens cDNA clone IMAGE:6282804 Gapa ò Query Match
100.0%; Score 23; DB 14; Length 955;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 23; Conservative 0; Mismatches 0: Indels Score 23; DB 14; Length 982; Pred. No. 5.2; 0; Indels

8

```
1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 CCAACTGGTGGCCATTCAGCTTC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0uery Match
Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
BQ647561/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
                            REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="INAGE=626913"
/clone="INAGE=626913"
/clone="INAGE=626913"
/clone="INAGE=626913"
/clone="INAGE=626913"
/clone="INAGE=626913"
/clone="INAGE=626913"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="DHN made by oligo-df priming. Directionally cloned EcoR; cDNA made by oligo-df priming. Directionally cloned EcoR; cDNA made by oligo-df primings. Directionally cloned EcoR; cDNA made by oligo-df primings. Directionally cloned EcoR; cDNA costructed by ling Homig in the laboratory of Garald M. Rubin (University of California, Berkeley) of Garald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript IRT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                     Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Mamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 983)

INIH-MG http://mgo.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)

IU Unpublished (1999)

IL Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: GAPP (Stanford)

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Http://image.llnl.gov

Llocation/Qualifiers

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGENCOURT 6715416 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:5797961
5', mRNA sequence.
                                                                                                                                                   983 bp mRNA linear EST 15-JUL-2002
AGENCOURT 8303966 NIH MGC_100 Homo sapiens cDNA clone IMAGE:6269413
5', mRNA Sequence.
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Score 23; DB 14; Length 983;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 23; Conservative 0; Mismatches 0; Indels Aatches 23; Conservative 0; Mismatches 23; Conservative
    Indels
        ö
        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   274 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43 CCAACTGGTGGCCATTCAGCTTC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BM928196.1 GI:19378575
                                                                       336 CCAACTGGTGGCCATTCAGCTTC 314
                                               1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                          BQ643920.1 GI:21768092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Library."
279 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 983
             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human.
                                                                                                                                                                                                                                                                                                                          human.
                 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
BM928196/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                     LOCUS
                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                   BQ643920/c
                   Matches
                                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                            RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
```

δ 셤

```
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1061)

NH-MGC http://mgc.nci.nih.gov/.

NRTional Institutes of Health, Mammalian Gene Collection (MGC)

NRTional Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Lonact: Robert Strausberg; Ph.D.

Contact: Robert Strausberg; Ph.D.

Email: cgapberfemill.nih.gov

Email: cgapberfemill.nih.gov

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lln.gov

Plate: LLCM2482 row: o column: 08

High quality sequence stop: 443.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1042)

2S NIH-MGC http://mgc.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Locatet: Robert Strausberg, Ph.D.

Email: cgapbs-rømil.nih.gov

Tissue Procurement: GGAP (Stranford)

CONTACTOR Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

CONTA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

CONTACTOR Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Http://image.llnl.gov

Plate: LLCM2025 row: c column: 18

High quality sequence stop: 662.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGENCOURT 8349614 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6284767 .5', mRNA sequence.
BQ647561.
BQ647561.1 GI:21771733
BST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 23; DB 14; Length 1042; 100.0%; Pred. No. 5.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286 9
```

ö

```
Matches
                                                                  ઠે
                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/dlone="Index:6284767"
/clone="toks:6284767"
/clone lib="NIH_MGC_100"
/tissue_type="hepatocellular carcinoma, cell line"
/lab host="hylloB (phage-resistant)"
/note="Organ: liver; Vector: porPs; Site_l: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >SoDbp for average insert size
into EcoRI, cDNA made by cligo-dT priming. Directionally cloned
GGCACGAG(G). Size-selected >SoDbp for average insert size
of Gerald M Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Strategene) and Superscript
iler...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
B. 1 (bases 1 to 770)
S. 1 (bases 1 to 770)
S. MH-MGC http://mgc.nci.nih.gov/
L. Dnpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
CDNA Library Arrayed by: Locyte Genomics, Inc.
Clond chrough the I.M.A.G.E. Consortium/LLNL at:
Plate: LiANMags.llnl.gov
High quality sequence stop: 631.
Location/Qualifiers
Irce
1...770
L...770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           770 bp mRNA linear EST 09-AUG-2000 mRNA sequence.
BE541467.1 GI:9770112
BS541467.1 GI:9770112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5 kb. Library prepared by Life Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
100.0%; Score 23; DB 14; Length 1061;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 21.4; DB 10; Length 770; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                         179 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:966"

clone="IMAGE:3454085"

/clone lib="NIH MGC_10"

/cell line="MGC36"

/lab_fost="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                     282 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               224 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CCAACTGGTGGCCATTCAGCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43 ccaacredrescearreascric 21
                                                                                                                                                                                                                                                                                                                                                                                     323 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                     277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             221
                       Bource
                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
BES41467/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
```

```
        Matches
        22;
        Conservative
        0;
        Mismatches
        1;
        Indels
        0;
        Gaps

        Qy
        1
        CCAACTGGTGCCATTCAGCTTC
        23

        Db
        305
        CCCACTGGTGGCCATTCAGCTTC
        283
```

Search completed: April 18, 2003, 07:31:57 Job time: 804.985 Becs

				· .		
		•		·		
						•
***						
il Nama						e v
				•		
						100 mg (100 mg) 100 mg (100 mg) 100 mg (100 mg) 100 mg (100 mg) 100 mg (100 mg) 100 mg) 100 mg (100 mg) 100 mg
p p				AT A T		
	ī			e e a Turke		
*						
	•					
k .						
Column St.					# V.	
er fam 32 deur			11 14		<b>,                                    </b>	
er kun 18 den er en en en en en en en en en en en en en						
· · · · · · · · · · · · · · · · · · ·						

```
RESULT 1
AC113611
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                  April 18, 2003, 04:46:26 ; Search time 292 Seconds (without alignments) 2192.677 Million cell updates/sec
GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                           2054640 segs, 14551402878 residues
                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                          OM nucleic - nucleic search, using sw model
                                                                                                                                              1 gctctttggggacaggaaggtc 22
                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                     IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            em_ro:*
em_gts:*
em_vi:*
em_vi:*
em_vi:*
em_htg_hum:*
em_htg_lnv:*
em_htg_other:*
em_htg_pun:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         em_htgo_mus:*
em_htgo_other:*
                                                                                                                      US-09-270-437D-13
                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            htgo_hum: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         em_htg_rod:*
em_htg_mam:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 em_htg_vrt:*
                                                                                                                                                                                                                                                                                                                                                                                                            gb_ov: *
gb_par: *
gb_pl: *
gb_pl: *
gb_pr: *
gb_pr: *
gb_ro: *
gb_ats: *
gb_ats: *
gb_un: *
em_ba: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             em_hum: +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             # # # #
B B B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             em_ov:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  em or:
                                                                                                                    Title:
Perfect acore:
                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                              Sequence:
                                                                                                                                                                                                         Searched:
                                                                     Run on:
```

AC113611 Homo sapi AC105949 Mus muscu AR015949 Mus muscu AR083389 Sequence AR083389 Sequence 115470 Sequence 115470 Sequence 115470 Sequence 115470 Sequence AR171865 Sequence 125471 Homo sapi AC05579 Homo sapi AC05579 Homo sapi AC05547 Homo sapi AC05547 Homo sapi AC05547 Homo sapi AC05548 Mus muscu AC118527 Rattus no AC118527 Rattus no AC11852 Rattus no AC11852 Rattus no AC113909 Rattus no AC113909 Rattus no AC113909 Rattus no AC113909 Rattus no AC113909 Rattus no AC113909 Rattus no AC113909 Rattus no AC113909 Rattus no AC113909 Rattus no AC113909 Rattus no AC113909 Rattus no AC113909 Rattus no AC11391 Homo sapi AC107385 Homo sapi AC107385 Homo sapi AC107385 Homo sapi AC110819 Mus muscu ACS2710 Homo sapi AC110819 Mus muscu ACS2710 Homo sapi AC115117 Homo sapi AC113611 198623 bp DNA 11near HTG 11-APR-2002 Homo sapiens chromosome 4 clone RP11-421M20, WORKING DRAFT SEQUENCE, 4 unordered pieces. Human DNA Homo sapi Mus muscu Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 198623) Waterston, R.H. score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. AC113611.2 GI:20136967 HTG; HTGS PHASE1; HTGS\_DRAFT; HTGS\_ACTIVEFIN. Homo sapiens. Homo sapiens SUMMARIES ALIGNMENTS DB \* Query Match Length D REFERENCE AUTHORS TITLE

The sequence of Homo sapiens clone

chance to have a

Pred. No. is the number of results predicted by

```
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
AC105949
               Characteristics of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of th
                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (11-APR-2002) Genome Sequencing Center, Washington Submitted (11-APR-2002) Genome Sequencing Center, Washington Office (11-APR-2002) Genome Sequence Version replaced gi:19073839.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing vector: N13; 0% Sequencing vector: plasmid; 100% Sequencing vector: plasmid; 100% Sequencing vector: plasmid; 100% Sequencing vector: plasmid; 100% of reads Chemistry: Dye-primer F1; 0% of reads Chemistry: Dye-primer E1; 0% of reads Chemistry: Dye-primer E1; 0% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 100% of 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Washington University Genome Sequencing Center Center code: WidSC Web site:http://genome.wustl.edu/gsc/index.shtml Contact: submissions@watson.wustl.edu
Center project Information
Center project name: H_NH0421M20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 26542: contig of 26542 bp in length 5543 26642: gap of unknown length 5643 57247: contig of 30605 bp in length 1248 57347: gap of unknown length 1348 108935: contig of 51588 bp in length 1036 198623: contig of 89588 bp in length 1036 198623: contig of 89588 bp in length 1036 100036: gap of unknown length 1036 198623: contig of 89588 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_name:Contig15"
47163 a 53839 c 54375 g 42946 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26643. .57247
/note="assembly_name:Contig13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57348...108935
/note="assembly_name:Contig14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. 198623
/organism="Homo sapiens"
/db xref="taxon:9606"
/chromosome="4"
/clone="RP11-421M20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----- Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vector side:right"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26543
26643
57248
57348
108936
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                        REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                        REFERENCE
               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
```

```
DORST MARCH

Deat Local Similarity 100.09; Midmatche 7 0; Indels 0; Gaps 0;

REMITION

1 GENTIFICAGE MAGET 9900

1 GENTIFICAGE MAGET 9900

1 GENTIFICAGE MAGET 9900

2 CONTRICTOR MAGET 9900

2 CONTRICTOR MAGET 9900

2 CONTRICTOR MAGET 9900

2 CONTRICTOR MAGET 9900

3 CONTRICTOR MAGET 9900

3 CONTRICTOR MAGET 9900

3 CONTRICTOR MAGET 9900

3 CONTRICTOR MAGET 9900

3 CONTRICTOR MAGET 9900

3 CONTRICTOR MAGET 9900

3 CONTRICTOR MAGET 9900

3 CONTRICTOR MAGET 9900

3 CONTRICTOR MAGET 9900

3 CONTRICTOR MAGET 9900

3 CONTRICTOR MAGET 9900

3 CONTRICTOR MAGET 9900

3 CONTRICTOR MAGET 9900

3 CONTRICTOR MAGET 9900

3 CONTRICTOR MAGET 9900

3 CONTRICTOR MAGET 9900

3 CONTRICTOR MAGET 9900

3 CONTRICTOR MAGET 9900

4 CONTRICTOR MAGET 9900

4 CONTRICTOR MAGET 9900

4 CONTRICTOR MAGET 9900

4 CONTRICTOR MAGET 9900

4 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONTRICTOR MAGET 9900

5 CONT
```

```
AF117107 26-JAN-1999
Homo sapiens IGF-II mRNA-binding protein 2 (IMP-2) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50. .1846

gate="IMP-2" | Agene | IMP-2"  IMP-2" | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | Agene | A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nelsen, J., Christiansen, J., Lykke-Andersen, J., Johnsen, A.H., Wewer, U.M. and Nielsen, F.C.
Direct Submission
Submitted (30-DEC-1998) Institute of Molecular Biology, University of Copenhagen, Soelvgade 83H, Copenhagen DK-1307, Denmark
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2010)
Nieleen,J., Christianen,J., Lykke-Andersen,J., Johnsen,A.H., Wewer,U.M. and Nielsen,F.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A family of insulin-like growth factor II mRNA-binding proteins represses translation in late development MOI. Cell. Biol. 19 (2), 1262-1270 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="alternative start-codon gives an additional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 90.9%; Score 20; DB 2; Length 184582; Best Local Similarity 100.0%; Pred. No. 16; Matches 20; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly fragment"
53205 a 38803 c 37801 g 53673 t
                                                                                                                                                                                .7842. .30472
'note="assembly_fragment"
                                                                                                                                                   'note="assembly_fragment"
                                                                                        note="assembly_fragment"
                                                                                                                                                                                                                                           30573, .49894 //note="assembly_fragment"
                                                                                                                                                                                                                                                                                              19995. .69993 -/
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                         70094. .89184
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                               89285. .106186 // hote="assembly_fragment"
| 106287. .184582

    .2010
    /organism="Homo sapiens"
/db_xref="taxon:9606"
    .2010

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 139851 ĠĊİĊİİİĞĠĞAÇAĞĞAĞĞ 139870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF117107.1 GI:4191609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="IMP-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="IMP-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 2010)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GCTCTTTGGGGACAGGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF117107
                                                                  misc_feature
                                                                                                                       misc_feature
                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
AF117107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                  Submitted (14-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON Apr 14, 2002 this sequence version replaced gi:18129448. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker:html
                                                                                                                                                                                                                                     Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced

by the finished sequence as soon as it is available and the accession number will be preserved.

1 1013: contig of 1013 bp in length

1114 2223: contig of 110 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                     Center Choose name: 217 C 15

Summary Statistics
Squencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 187431 bases at least Q40
Consensus quality: 183090 bases at least Q30
Insert size: 1833000; agarose-fp
Insert size: 183402; sum-of-contigs
Quality coverage: 6.9 in Q20 bases; sum-of-contigs
Quality coverage: 6.9 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                          Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig of 12631 bp in length p of 100 bp contig of 13322 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4328 4427: gap of 100 bp 4428 6625: contig of 2198 bp in length 6726 10222: contig of 3507 bp in length 10233 10332: gap of 100 bp 100 bp 10333 17741: contig of 7409 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49895 49994: gap of 100 bp
49995 69993: contig of 19999 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6994 70033; gap of 100 bp 70094 89184; contig of 100 bp in length 89185 89284; gap of 100 bp 89285 106186; contig of 16902 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106187 106286: gap of 100 bp
106287 184582: contig of 78296 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 bp
f 1110 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 bp
f 2004 bp in length
Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone_lib="RPCI-24 Male Mouse BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note≃"assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .114. .2223
note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2324. .4327
/note="assembly_fragment"
4428. .6625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: L18821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:10090"
clone="RP24-217C15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17742 17841: gap of
17842 30472: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30473 30572: gap of
30573 49894: con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2224 2323: gap of
2324 4327: con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                      TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bource
                                                                                                              COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
```

ô

```
Pred. No. 37;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2006 CTCTCTGGGGACAGGAAGGTC 2026
                                                      2006 CTCTCTGGGACAGGAAGGTC 2026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
                                                                                                                                                                    AR164498.1 GI:16237546
                                                                                                                                                                                                                                                                                                                                                                                                              2 CTCTTTGGGGACAGGAGGTC 22
                                       22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 CICITIGGGGACAGGAAGGIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115470.1 GI:1250378
  ilarity 95.2%;
Conservative
                                         CTCTTTGGGGACAGGAAGGTC
                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 95.2
Matches 20, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
 Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                            697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unknown
                                                                                                                                                                                                Unknown.
                                                                                                                                                                                                              Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Simi
Matches 20;
                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2006
                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
132484
                                                                                                                                              DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
115470
                                           ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
                                                                                                          RESULT 6
AR164498
LOCUS
                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <del>Q</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                     g
      PDONWAIRALETLSGKVELHGKIMEVDYSVSKKLRSRKIQIRNIPPHLQWEVLDGLLA
QYGTVENVEQVNTDTETAVNNYTYATREEAKIAMEKLSGHQPENYSFKISYIPDEEVS
SPSPPQRAQRODHSSREQGHAPGGTSQARQIDPPLAILVPTQFVGALIGKEGALITIKNI
SPSPPQRAQRODHSSREQGHAPGGTSQARQIDFPLAILLIMQKEADETTKLAEEIPL
TKQTQSRVDJHKKENSGAARKYTHIAVTBEGTSEACRMILEIMQKEADETKLAEEIPL
KILAHUGLVGRLIGKEGRNLKKIEHETGTKITISSLQDLSIYNBFRETTITVKGTVEACA
SAEIEMKKLEAFBROMLANQQANLIPGLNLSALGIFSTGLSVLSPPAGERGAPPA
APYHPPTTHSGYFSSLYPHHQPGPFPHHHSYPEQEIVNLFIPTGVAGAIIGKGAHIK
QLARFRAGAIKTARA PABGPDVSERWVIITGPPEAQFKAQGRIFGKLKEENFFNRKEEVK
LEAHIRVPSSTAGRVIGKGGKTVVNELQNLTSBAVIVPRQQTPDENEEVIVRIIGHFFA
SQTAQRKIREIVQQVKQDEQKYPQGVASQRSK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAT 01-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                     PAT 29-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 2935)
Jones, S. and Tang, J.
Methods comprising calcium independent cytosolic phospholipase A/B
                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unitabilities 1 to 2935)
Jones, S. and Tang, J.
Calcium independent cytosolic phospholipase A.sub.2 /B
Patent: 18 5976854-A 1 02-NOV-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 19.4; DB 6; Length 2935;
Pred. No. 37;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                       ö
                                                                                                                                                                                Length 2010;
                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
9
                                                                                                                                                                                   DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 19.4; DB
                                                                                                                                                                                                                                                                                                                            DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2935 bp
Sequence 1 from patent US 5976854.
AR083389
AR083389.1 GI:10010179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  572
                                                                                                                                                                                 ch
1 Similarity 95.2%; Pred. No. 37;
20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent: US 5840511-A 1 24-NOV-1998;
Location/Qualifiers
1. 2935
                                                                                                                                                                                                                                                                                                                     2935 bp
Sequence 1 from patent US 5840511.
AR059699 1 GI:5986149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="unknown"
856 c 810 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="unknown"
856 c 810 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2006 CICTCTGGGGACAGGAAGGTC 2026
                                                                                                                                                                                                                                                    109 GCTCTTTGGGGACAGGAAGCT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 88.2%;
Best Local Similarity 95.2%;
Matches 20; Conservative (
                                                                                                                                                                                                                                        2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 CTCTTTGGGGACAGGAAGGTC
                                                                                                                                                                                                                                       1 GCTCTTTGGGGACAGGAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                           Unknown.
Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unknown
                                                                                                                                                                                                                                                                                                                                                                                                Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                        Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
AR083389
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                       RESULT 4
AR059699
LOCUS
                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                     엄
                                                                                                                                                                                                                                              ઠે
```

```
PAT 06-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAT 02-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                      PAT 17-0CT-2001
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unclassified.
Unclassified.
1 (bases 1 to 2935)
1 (bases 1 to 2935)
20nes, 2.
Calcium independent cytosolic phospholipase A2/B enzymes
Calcium independent cytosolic phospholipase A2/B enzymes
Calcium independent cytosolic phospholipase A2/B enzymes
Calcium independent cytosolic phospholipase A2/B enzymes
Calcium independent cytosolic phospholipase A2/B enzymes
1.0.2935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2935;
  ö
                                                                                                                                                                                                                                                                                                                                                                           Length 2935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.2%; Score 19.4; DB 6;
ilarity 95.2%; Pred. No. 37;
Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                      1;
       ;
                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA
                                                                                                                             DNA
                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2935 bp
Sequence 1 from patent US 5589170.
132484
132484.1 GI:1823275
                                                                                                                                                                                                                                                                                                                                                                           88.2%; Score.19.4; E 95.2%; Pred. No. 37; Eive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     572
                                                                                                                                                                                                                                                                                                                                    572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2935 bp
Sequence 1 from patent US 5466595.
115470
                                                                                                                          AR164498 2935 bp
Sequence 1 from patent US 6274140.
AR164498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="unknown"
856 c 810 g
                                                                                                                                                                                                                                                                                                                         /organism="unknown"
856 c 810 g
```

Ŋ

ö

us-09-270-437d-13.rge

```
3642 bp mRNA linear PRI 22-JAN-2002 IMAGE:5090334, mRNA, complete cde.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 39 Row: o Column: 21 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5729883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MXKLYIGNLSPAVTADDLRQLFGDRKLPLAGQVLLKSGYAFVDY PDQNWAIRAIETELSGKVELHGKIMEVDYSVSKKLRSRKIQIRNIPPHLQWEVLDGLLA QYGTVENVEGVNTDYETAVVNVTYATREEAKIAMEKLSGHQFENYSFKISYIPDEEVS SPSPPQRAQRGDHSSREQGHAPGGTSQARQIDFPLRILVVPTQFVGAIIGKEGLTIKNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3642)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Straubberg, R.
Direct Submission
Submitted (14-JAN-2002) National Institutes of Health, Mammalian
Submitted (14-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Prayeration: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing Center (NISC).
Galthersburg, Maryland! Institutes of Health Intramural
Galthersburg, Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Maryland:
Marylan
                                                                                                                                       ö
                                                                       Query Match 88.2%; Score 19.4; DB 6; Length 3412; Best Local Similarity 95.2%; Pred. No. 37; Matches 20; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epithelioid carcinoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           product="IGF-II mRNA-binding protein 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="LocusID:10644"
/db_xref="taxon:9606"
/clone="MGC:29539 IMAGE:5090334"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein_id="AAH21290.1"
db_xref="GI:18204201"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Pancreas,
/clone_lib="NIH MGC_42"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="Vector: pOTB7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                              132 GCTCTTTGGGGACAGGAAGCT 152
                                                                                                                                                                                                                                                                                                                                                                                                                 BC021290
BC021290.1 GI:18204200
                                                                                                                                                                             21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
                                                                                                                                                                      1 GCTCTTTGGGGACAGGAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                    LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                      RESULT 11
BC021290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REMARK
COMMENT
                            ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAT 17-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acid molecule encoding cancer associated antigen, the antigen itself, and uses thereof
Patent: US 6297364-A 8 02-OCT-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAT 17-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 3283)
Chen,Y.-T., Gure,A., Tsang,S., Stockert,E., Jager,E., Alexander,K.
and Old,L.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 3412)
Chen, Y.-T., Gure, A., Tsang, S., Stockert, B., Jager, B., Alexander, K. and Old, L.J.
Isolated nucleic acid molecule encoding cancer associated antigen, the antigen itself, and uses thereof
Patent: US 6297364-A 6 02-0CT-2001;
Location Qualifiers
            Unknown.
Unclassified.
Unclassified.
1 (bases 1 to 2935)
Jones, S. and Tang, J.
Calcium independent cytosolic phospholipase A.sub.2 /B enzymes
Patent: US 5589170-A 1 31-DEC-1996;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                          6; Length 2935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6; Length 3283;
                                                                                                                                                                                                                                                                                                                                                                        Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 others
                                                                                                                                                                                                                                                                                                                          B
                                                                                                                                                                                                                                                                                                     Query Match

88.2%; Score 19.4; Dest Local Similarity
95.2%; Pred. No. 37;
Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.2%; Score 19.4; D
95.2%; Pred. No. 37;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3283 bp
Sequence 8 from patent US 6297364.
AR171867.1 GI:17910817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AR171865 3412 bp
Sequence 6 from patent US 6297364.
AR171865 AR171865.1 GI:17910815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="unknown"
833 c 779 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="unknown"
887 c 804 g
                                                                                                                                                                                                                                                                                                                                                                                                                                             2006 CTCTCTGGGGACAGGAGGTC 2026
                                                                                                                                                                                                                                                                                                                                                                                                    2 CTCTTTGGGGACAGGAC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 GCTCTTTGGGGACAGGAAGCT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GCTCTTTGGGGACAGGAAGGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 95.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           945 a
Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              970 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unknown
                                                                                                                                                                                             Bource
                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE
ORGANISM
                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
ACCESSION
                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bource
                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
AR171865
LOCUS
                                                                                                                TITLE
                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
AR171867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

21

```
1 GCTCTTTGGGGACAGGAAGGT
                 1 GCTCTTTGGGGACAGGAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                   SOURCE
                                                                                                                                                                                        ALS96177
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                RESULT 13
                                                                                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AdD31596.1"
/pb.xref="G1:4883681"
/db.xref="G1:4883681"
/db.xref="G1:4883681"
/db.xref="G1:4883681"
/drinnlaredelinen-"whwikijitanispavtadderolegderolegovilksgyafvu
/translation="whwikijitanispavtadderolegovily"
/drinnlaredelinen-"who with the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AFUS7352
Homo sapiens hepatocellular carcinoma autoantigen (p62) mRNA,
complete cds.
TKQTQSRVDIHRKENSGAAEKPUTIHATPEGTSEACKMILEIMQKEADETKLAEEIPL
KILAHNGLVGKLIGKEGRNLKKIEHETGTKITISSLQDLSIYNPERTITVKGTVERACA
SAEIEIMKKLREAFENDMLANNQQANLIPGINLEALGIFSTGLSVLESPAGPRGAPPA
SYPYPETHYGSYSELYPHHQFOPPHHHSYPEQEIVNLFIPTQAVGAIIGKKGAHIK
QLARFAGASIKIAPAGEPDVSREMVIITGPPEAQFKAQGRIFGKLKEENFENPKEEVK
LEAHIRVPSSTAGRVIGKGGKTVNELQNLTSAEVIVPRDQTPDENEEVIVRIGHFFA
SQTAQRKIREIVQQVKQQEOKYPQGNSK<sup>N</sup>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (baese I to 3667)
Zhang, J.Y., Chan, E.K., Peng, X.X. and Tan, E.M.
A novel cytoplasmic protein with RNA-binding motifs is an autoantigen in human hepatocellular carcinoma J. Exp. Med. 189 (7), 1101-1110 (1999)
                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (03-APR-1998) Molecular & Experimental Medicine, The Scripps Research Institute, 10550 N. Torrey Pines Road, La Jolla, CA 92037, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon start=1
product="hepatocellular carcinoma autoantigen"
                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 9; Length 3667;
                                                                                                                                                                                                                                                                                     Length 3642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 3667)
Zhang,J.Y., Chan,B.K.L., Peng,X.X. and Tan,B.M.
Direct Submission
                                                                                                                                                                                                                                                                                        Score 19.4; DB 9;
Pred. No. 37;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.2%; Score 19.4; D
95.2%; Pred. No. 37;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     436. .2106
/gene="p62"
/note="RNA-binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 gcrcrrrddddacaddaagcr 156
                                                                                                                                                                                                                                                                                                                                                                                                          1 GCTCTTTGGGGACAGGA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF057352.1 GI:4883680
                                                                                                                                                                                                                                                                                              88.2%;
nilarity 95.2%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                882 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match . 88.2
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                     919 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10190901
                                                                                                                                                                                                                        1077
                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF057352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                           ઠ
```

```
Direct Submission

AL Submission

Submitted (10e-SEPP-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk

requests: clonerequest@sanger.ac.uk

requests: clonerequest@sanger.ac.uk

requests: clonerequest@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.

During sequence as found these are annotated as variations

Where differences are found these are annotated as variations

variation annotation may not be found in the sequence submission

variation annotation may not be found in the sequence submission

variation annotation may not be found in the sequence submission

variation annotation may not be found in the sequence submission

variation annotation may not be found in the sequence only a small overlapping clone, as we submit sequences with

sequence was fainished as follows unless otherwise noted: all

redions were either double-stranded or sequencing problems, such

schemistry or covered by high quality data (i.e., phred quality >=

chamistry or covered by high quality data (i.e., phred quality >=

chamistry or covered by high quality data (i.e., phred quality >=

chamistry or covered by high quality data (i.e., phred quality >=

chamistry or covered by high quality data (i.e., phred quality >=

chamistry or covered by the secritical on digest. The following

assembly was confitmed by restriction digest. The following

assembly was confitmed by restriction digest. The following

abbreviations are used to associate primary accession numbers given

abbreviations are used to associate primary accession numbers fatabase can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence

was generated from part of bacterial choe contigs of human

drought proper database. Brown the library RPCI-11.2 constructed by the group

of pieter de long. Per further details see

of pieter de long. Per further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                            ALSWE177 91084 bp DNA linear PRI 08-SEP-2001
Human DNA sequence from clone RP11-325P15 on chromosome 1, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VECTOR: packed.

VECTOR: packed.

IMPORTANT: This sequence is not the entire insert of clone IMPORTANT: This sequence is not the entire overlapping sections only once, except for a short overlap. The true left end of clone RP11-325P15 is at 1 in this sequence. The true left end of clone RP11-337C18 is at 89085 in this sequence. The true right end of clone RP4-704D21 is at 41034 in this sequence. The true right end of clone RP4-704D21 is at 41034 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 91084)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88.2%; Score 19.4; DB 9; Length 91084; 95.2%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25047 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .91084
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /chromosome="1"
/clone="RP11-325P15"
/clone_lib="RPCI-11.2"
a 19586 c 19377 g 25(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21
                                                                                                                                                                                                                                                                                                                                      AL596177
AL596177.4 GI:15552942
498 GCTCTTTGGGGACAGGAAGCT 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clark, S.
Direct Submission
```

Locus

요

```
9571 9670; gap of 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 10055; contig of 685 bp in length 10055 10455; gap of 100 bp 100 bp 10055; 1162; contig of 700 bp in length 1163 11262; gap of 100 bp in length 1163 12662; gap of 100 bp in length 12063 12593; contig of 694 bp in length 13534 13533; gap of 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100
                                                                                                                                                 contig or ...
of 100 bp
contig of 671 bp in length
p of 100 bp
contig of 707 bp in length
ap of 100 bp
ap of 100 bp
ap of 696 bp in length
                                                                                                                                                                                                                                                                                                                                        100 bp

25 723 bp in length

100 bp

100 bp in length

100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 bp
f 698 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ap of 100 bp contigor of 683 bp in length ap of 100 bp in length ap of 690 bp in length ap of 100 bp in length contigor of 708 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28853: gap of 100 bp 29563: contig of 710 bp in length 29663: gap of 100 bp 30312: contig of 718 bp in length 30481: gap of 100 bp 31201: contig of 720 bp in length
                                                                                                                                100 bp
f 712 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15: gap of 100 b
18753: contig of 708
                                                                                                    contig of
                                                                                                                                                                                                                                                                                                                                                                      contig of
                                                                                                                                                                                                                                                                                                                                                                                                                contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig of
                                                                                                                                                                                                                                                                                                                                                                                  7252: gap of
7978: con
8078: gap of
8772: con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap of
                                 1642
2330 2429: gap c
3143:
                                                                                                                     3144 3243: gap o
3244 3955: c
3956 4055: gap o
4056 4727 4826: c
4827 4826: gap o
                                                                                                                                                                        4055; gap
4726;
4826; gap
7 4826; gap
7 5533;
6329; c
                                                                                                                                                                                                                                                                                                                               6429: gap c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8872: gap c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26472:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27255:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28045;
                                                                                                                                                                                                                                                                               5534
5634
6330
6430
7153
7253
7979
8079
8873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Upbullshap

Orbases 1 to 11259)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Balren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Boguslavkiy, L., Baldwin, J., Barria, N., Bastien, V., Beda, F., Campopiano, A., Costel, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Domino, W., Doyle, M., Perreira, P., Fitzhugh, W., Gage, D., Grand, C., Lau, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Letu, C., Liu, G., Looke, K., Macdonald, P., Marquis, N., McMarn, R., McMereers, R., Letu, C., Liu, G., Looke, K., Macdonald, P., Marquis, N., Meneus, L., Millo, L., Looke, K., Macdonald, P., Marquis, N., Maylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Plsani, C., Pollara, V., Norman, C.H., O'Connor, T., O'Donnell, P., Plsani, C., Pollara, V., Norman, C.H., O'Connor, T., O'Donnell, P., Plsani, C., Pollara, V., Naymond, C., Riley, R., Rogov, P., Rothman, D., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talanas, J., Vessiltev, H., Vtel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, Wallited, 12-MAR-2000 Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using Repeatwasker: httl

Center: Whitehead Center

Center: Whitehead Institute/ MIT Center for Genome Center: Whitehead Institute/ MIT Center for Genome Center.

Center: Whitehead Conter MIT Center for Genome Center.

Center: Whitehead Institute/ MIT Center for Genome Center.
                                                                                                                                                             ACUZEST9 112259 bp DNA linear HTG 28-NOV-2001 SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: This record contains 139 individual
* sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 15, clone RP11-76D16 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 714: contig of 714 bp in length 715 814: gap of 100 bp 815 1541: contig of 727 bp in length 1542 1641: gap of 100 bp
AC026579.2 GI:17048293
HTG; HTGS PHASE0.
Homo Bapiens.
Homo Bapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 112259)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        be preserved.
                                                                                                          RESULT 14
AC026579/c
                                                                                                                                                                                                                                        ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
```

COMMENT

```
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhin; Hominidae; Homo.

Mammalia; Butheria; Primates; Catarrhin; Hominidae; Homo.

I (bases I to 142971)

Bodota; Manay, D. M., Adams, C., Buhay, C., Bunac, C.,

Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C.,

Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C.,

Burkett, C., Burrows, J., Fernandez, C., Pomah-Rashid, N.,

David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N.,

David, R., Delgado, O., Teantz, P., Ganesh, R., Gorrell, J.H., Gorrell, L.L.,

Forcum-Tansey, J., Frantz, P., Ganesh, R., Gorrell, J.H., Gorrell, L.L.,

Forcum-Tansey, J., Frantz, P., Ganesh, R., Gorrell, J.H., Gorrell, L.L.,

Forcum-Tansey, J., Frantz, P., Landson, L., Jackson, L., Jackson, L., Jackson, L.,

Hollows, K., Kelly, S., Kneitz, S., Kondejewski, N., Kong, Y.,

Jones, M., Kelly, S., Kneitz, S., Kondejewski, N., Kong, Y.,

Lau, S., Leal, B., Lee, E., Li, Z., Lichtarge, O., Liu, J., Martin, R.,

Martinez, C., McLeod, M.P., Mel, G., Merscher, S., Miller, A.,

Martinez, C., McLeod, M.P., Mel, G., Merscher, S., Miller, A.,

Rayton, R., Nguyen, N., Nguyen, S., Oswal, G., Parish, B., Paxton, S.,

Rayton, B., Perez, L., Pu, E.L., Quiles, M., Reiter, D., Rives, M.,

Samuel, S., Say, J., Scherer, S., Shen, H., Shim, C., Simon, W., Samuel, S., Say, A., Sucgang, R., Tabor, P., Taylor, T., Vasquez, L.,

Khang, A., Yang, A., Yang, R., Yu, W., Zhou, X., Kucherlapati, R., Welson, D. and

Athar, M., Yang, R., Vu, W., Zhou, X., Kucherlapati, R., Nelson, D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Direct Submission
Submitted (27-APR-2000) Human Genome Sequencing Center, Departmen
Submitted (27-APR-2000) Human Genetics, Baylor College of Medicine, One
of Molecular and Human Genetics, Baylor College of Medicine, One
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wollet Submission
Submitted (07-JAN-2000) Human Genome Sequencing Center, Departmen Submitted (07-JAN-2000) Human Genetics, Baylor College of Medicine, One of Molecular and Human Genetics, Baylor College of Medicine, One
Homo sapiens 12q BAC RP11-76E16 (Roswell Park Cancer Institute
Human BAC Library) complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baylor Plaza, Houston,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baylor Plaza, Houston,
4 (bases 1 to 142971)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Unpublished
2 (bases 1 to 142971)
Worley, K.C.
                                                                            AC020629.6 GI:7656675
                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                            ACCESSION
VERSION
KEYWORDS
SOURCE
                        DEFINITION
                                                                                                                                                    ORGANISM
                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 112259;
                                                                                                           4956
50251
50350; gooding of vo pp in length
50251
51091; contig of 741 bp in length
51092
51192; gap of 100 bp
51192
51190; contig of 718 bp in length
51190
52010
52713; contig of 706 bp in length
52010
52714
52814
53826; contig of 718 bp in length
53827
53827
54337; contig of 718 bp in length
53827
54337; contig of 711 bp in length
5438
55155; contig of 718 bp in length
5438
55155; contig of 718 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                          1989 32088: gap of 100 bp
(2089 32777: contig of 689 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.2%; Score 19.4; Dl
95.2%; Pred. No. 33;
ive 0; Mismatches
                                      gap of 100 bp
18: contig of 687 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GCTCTTTGGGGACAGGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
```

```
CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANNOTATION OF FEATURES:
STSS are identified using ePCR (Genome Res. 7:541-550) searches
STSS are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green,
                                                                                                                                                                                                                                        Direct Submission
Submission (07-MAR-2002) Human Genome Sequencing Center, Department
Submitted (07-MAR-2002) Human Genetics, Baylor College of Medicine, One
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 7010, USA
Baylor Plaza, Houston, TX 7010, USA
On Apr 27, 2000 this sequence version replaced gi:7025656.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
gc-help@bcm.tmc.edu
                                 Department
Submitted (28-APR-2000) Human Genome Sequencing Center, Departmer of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 5 (bases 1 to 142971)
```

PRI 07-MAR-2002

linear

DNA

142971 bp

AC020629

RESULT 15 AC020629 LOCUS

Db 77783 GCTCTTTGGGGACAGGAAGCT 77763

ઠે

Department

Department

unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 18-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.

QUALSTAT-REPORT------

142971 140680 0.000118703 0.0433608 31 ----- Summary Statistics -----Phrap values in estimate:
Average error rate (BCM-Phrap estimate):
Fraction of Phrap values less than 40:
Number of consensus changing edits:
Number of N's in consensus Contig length:

gaccagoctg (a) ocaacatggt gtgtcggccc (c) ccgcccgcgc taaatgaggg (c) agaccagtgg gcaggaggcg (c) agaccagtgg gtgtcctga (t) gctctcctgc gtccatggt (t) ctcattgttc accagoctgg (c) caacatggod ttacatctag (t) totttgcaaa actttgtoto (a) aaaaaaaaaa ccatgific(t) catigiticas catgifict(c) attgiticas atgigitice(a) tigiticaset aaaaaaaa (a) aattaaaaca aaaaaaaaa (a) attaaaacag aaaaaaaaa (a) ttaaaacagg cctaggtccc (a) cttaaatgag catotoaaa (a) aaaaaagaac tctcaaaaaa (a) aaaagaactc ttītīttag (t) acagacaggg (c) ccaaagtgtt tcaaaaaaa (a) aagaactctt --- Consensus changing edits Original+Context gaccagcctg (n) ccaacatggt gtgtcggccc (n) ccaacatggt taaatgaggg (n) agaccagtgg gcagtgaggcc (n) agaccagcg ttgttcctga (n) gcctcctgc gtccatggt (n) cnnnttgttc gtcttctgga (n) caaaaaaaaa tatctatctg (n) ctatatctat tccactctaa (n) agttccatt aaaaaaaaaa (n) nnttaaaaca aaaaaaaaan (n) nttaaaaacag aaaaaaaan (n) ttaaaacagg cctaggtccc (n) cttaaatgag accagcctgg (n) caacatggcg ttacatctag (n) tctttgcaaa acttgtctc (n) aaaaaaaaa goccaggtot (n) ccaaagtgtt catotcaaaa (n) ananangaac totcaaaana (n) anangaacto atgigincm (n) tigitcaact tittitiag (n) acagacaggg catgtgtncn (n) nttgttcaac accgtgccca (n) cagaatagaa tggaacaatt (n) gatacccaca aaaanana (n) gaactettee attaccatta (n) aatatggtat tcaaaanana (n) angaāctett gccatggngg (n) Position 11171 20976 120980 139505 18168 22169 38915 55675 7658 1906 5228 20974 8021

Bases -- Distribution of Quality < 40

ö 5553. .5859 /note="Region similar to Hs#S1195593 gt69f10.x1 Homo sapiens cDNA: A1285403" Gaps / Typt family="(TA) n" complement (3917. .4030) / Typt family="AluJb" / Typt family="AluJb" / Typt family="MIR" 5145. .5510 / Note="Region similar to Hs#5953417 0a06g05.81 Homo 3585. .3735 /note="Region similar to Hs#S936143 aj27d02.81 Homo sapiens colNA: AA789222" Length 142971; ô 40 35 Indele 15 20 25 : Phrap Value Range ä DB 9; Score 19.4; DI Pred. No. 32; 0; Mismatches 3497. 3490 /standard\_name="CdaOybO4" /db\_xref="GDB:446196" 3585. 3735 /rpt\_family="Alusx"
complement(1722. 2137)
/rpt\_family="figgerza"
complement(3161. 3584)
/rpt\_family="MSTD"
3228. 3502 /organism="Homo sapiens" /db\_xref="taxon:9606" /chromosome="12" /clone="RP11-76E16" /Btandard\_name="G05956" /db\_xref="dbSTS:11453" 347. .3490 CDNA: AA765439" 147. .236 /rpt\_family="A-rich" 258. .378 Location/Qualifiers family="AluJb" Db 133084 GCTCTTTGGGGACAGGAAGCT 133104 10 /rpt\_family="A complement(537 gxfo. 95.28; 1 GCTCTTTGGGGACAGGAAGGT Query Match Best Local Similarity 95.2 Matches 20; Conservative 1.01 Version: # bases repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region misc\_feature misc\_feature misc\_feature FEATURES STS

Search completed: April 18, 2003, 06:27:37 Job time : 414, secs

											•
								•			
					•						
	• ,	,							P <sub>in</sub> k		
									•		
						*					
						λ.,					
							•				
•											
								•			
	· 										
				-							
							•			• .	
				•				V.	an i		
										4	
			•		•						
	.*									 1	
									i ya .		
								•	<u> </u>	,	
					· .'			F			
							14				
						vi a		* * *			As Ar
				4	i de la companya de l				목소 - 1 · · · · · · · · · · · · · · · · · ·		
		•				7.4		*	· š		
	•										
											•••
				•							•
		,									
•											
									•	w	7.1

.

```
April 18, 2003, 04:12:35; Search time 98 Seconds (without alignments) 505.551 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT.
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT.
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT.*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /geneseqn-embl/NA1992.DAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /=====/3594aca/yeneseqn-emb1/NA1993.DAT:
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /SIDS2/gcgdata/geneseg/genesegn-embl/NA1991.
/SIDS2/gcgdata/genesegn-embl/NA1992.
/SIDS2/gcgdata/genesegn-embl/NA1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985./SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /SIDS2/gcgdata/geneseq/geneseqn-embl/Na1986.
/SIDS2/gcgdata/geneseq/geneseqn-embl/Na1987.
/SIDS2/gcgdata/geneseq/geneseqn-embl/Na1988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        geneseqn-embl/NA1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genesegn-emp1/NA1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gcgdata/geneseq/geneseqn-emb1/NA1980.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        geneseqn-emp1/NA1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                4370478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gcgdata/geneseq/geneseqn-embl/NA1983.
GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                               2185239 seqs, 1125999159 residues
                                                                                  OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                              1 gctctttggggacaggaaggtc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cgdata/geneseg
                                                                                                                                                                                                                                                                                                                           IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N_Geneseq 101002:*
.: /SIDS2/gcgdata/
                                                                                                                                                                                                                                   US-09-270-437D-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIDS2,
                                                                                                                                                                                                                                                       Perfect score:
                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                                              Seguence:
                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                    Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description		יייים יייים מטע	FOR PILMET TOY DNA	Human secreted pro	DNA propositor and	ביין היינים יינים אינים	Calcium-independen	. Calcium-independen	The Hopkonophinal	oud principality by	Hamster cytosolic	Chinese hampton	ביידיים מווופרבו כש	An alternative for
SUMMARIES		ΔI		1 AAZ36159	44003267	1000000	2 AAS/0981	7 AAT44578	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	7400010	3 AAT59199	A AATERS 7	/700057	AAV64840	AA236154	*CTOCRUS
		e Match Length DB I		22	364 2	0.00	2 0102	2935 1.	2035 1	1	2935 IL	2935 16	2020	2000	3283 21	:
*	Query	Match L		700	88.2	28.2		88.2	88.2		7.00	88.2	0 00		88.2	
		Score		77	19.4	19.4		19.4	19.4	0 -		19.4	19.4		19.4	
	Result	Š.	-	4	~	m	•	3"	S	¥	•	7	80	•	ת	

DNA encoding cance DNA encoding novel Human cDNA encodin Human RAD54 nuclei Human LOBO homolog Human COBO no cancer	Fugarium venenatum Human neuroblastom Human type IX aden DNA encoding novel Human polynucleoti		Alpha galactosidas Human polynucleoti Human polynucleoti Human immune/haema Human MNTF-1-927 D Human pancreatic c Human digestive sy Human lohancata	
	1 AAF07623 2 AAI95925 5 AAX00463 3 AAK376845 2 AAK53086			
	778 21 801 22 8085 20 5526 23 5778 22 5804 22		4 4 9 9 5 5 4 4 4 5 5 5 5 5 5 5 5 5 5 5	
0000010	000000	Cl dt dt dt dt dt		10.10.10.10.10.10.10.10.10.10.10.10.10.1
	,,,,,,,,,	~ ~ ~ ~ ~ ~ ~ ~ ~	) CO CO 4 4 4 4 4 4 4 .	ST ST ST ST ST ST ST ST ST ST ST ST
0 0 112.	C 18 C 20 C 21 C 21		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

## ALIGNMENTS

Cancer associated antigen; KOC-1; cancer; vaccine; CT7; PCR primer; ss. Knuth A, Old LJ; Nucleotides representing cancer-associated genes, used to develop products for the diagnosis, monitoring and treatment of cancers -PCR primer for DNA encoding cancer associated antigen KOC-3. Jager E, Gure A, Tsang S, Stockert E, (LUDW-) LUDWIG INST CANCER RES. AAZ36159 standard; DNA; 22 BP. 99WO-US05766. 98US-0061709 (first entry) WPI; 2000-013284/01. Homo sapiens. WO9954738-A1. 16-MAR-1999; 17-APR-1998; 11-FEB-2000 28-OCT-1999. Synthetic. AAZ36159; Chen Y, 

```
The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well sulted for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID 3265; 71pp + CD-ROM; English.
                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                               AAC03267
                                                                                                                                                                                                                                                                                                   g
&$66666666666666688%
                                                                                                                                                                                                                         ઠે
```

```
mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS70981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS7098.
                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                ប្តស្តប្តស្ត្រស្ត
                                                                                                       per primers AAZ36159-60 were used to amplify a cancer associated antigen concer designated XCC-3. The specification also describes a cancer associated antigen designated CT7. The CT7 polymucleotide was isolated associated antigen designated CT7. The CT7 polymucleotide was isolated from SK-MEL-37 melanoma cells. The polymetide has some homology with from SK-MEL-10, imited to about 210 carboxy terminal amino acids. The amino cerminal of the protein has a repetitive pattern, with repeats rich in terminal of the protein has a repetitive pattern, with repeats rich in the peptide given in AAY43877. The CT7 polymetide can be processed to the peptides which provoke lysis by cytolytic T cells. The polymucleotides peptides which provoke lysis by cytolytic T cells. The polymucleotides and polymetides can be used for treating a cancerus condition and antigens can be used as an immunogenic or vaccine composition with an artigens can be used as an immunogenic or vaccine composition with an actigens can be used as an immunogenic or vaccine composition with an extigens can be used as an immunogenic or vaccine composition with an extigens can be used as an immunogenic or vaccine composition with an extigens can be used as an amount or granulocyte macrophage-colony containing factor (GM-CSF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; 8s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 22; DB 21; 100.0%; Pred. No. 0.46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein 5' EST, SEQ ID NO: 3265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 22 BP; 4 A; 4 C; 9 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                   Claim 108; Page 13; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC03267 standard; cDNA; 364 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GCTCTTTGGGGACAGGTC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTCTTTGGGGACAGGAGGTC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 Similarity 100.0%;
22; Conservative <sup>6</sup>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0122487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-500381/45.
P-PSDB; AAG03261.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP1033401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC03267;
```

```
The invention relates to isolated polymucleotide (I) and probes, complyeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome composed enem mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The composed enes. (I) is useful in gene therapy techniques for identifying expressed genes. (I) is useful in gene therapy techniques (I) is useful for generating antibodies against it, detecting or (II). (II) is useful for generating antibodies against it, detecting or (II). (II) is useful for generating antibodies against it, as useful in medical afor shopping of superating in tissue, as molecular weight markers and as function of supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. Composition, forensics, gene mapping, identification of mutations capanostics, forensics, gene mapping, identification of mutations of materials of and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human cut diagnostic coding sequences of the invention.
                                                                        ö
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                        ;
0
                                      DB 21; Length 364;
                                                                          Indels
Sequence 364 BP; 84 A; 101 C; 118 G; 59 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                           DNA encoding novel human diagnostic protein #6785.
                                                          Pred. No. 11;
0; Mismatches
                                        88.2%; Score 19.4; 95.2%; Pred. No. 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID No 6785; 103pp; English.
                                                                                                                                                                                                                                                     AAS70981 standard; cDNA; 2010 BP
                                                                                                                                          Tang YT;
                                                                                                                  1 GCTCTTTGGGGACAGGAAGGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                   (first entry)
                                    Query Match
Best Local Similarity 95.2*
....hag 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-639362/73.
P-PSDB; ABG06794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYSE-) HYSEQ INC
```

Conservative

20;

Matches

ö

Gaps

°;

Indele

```
The present sequence encodes a calcium-independent cytosolic phospholipase A2/B (cPLA2/B) enzyme. cPLA2/B is important in the release of arachidonic acid in specific tissues characterised by unique membrane phospholipids. The invention provides a process for producing such an enzyme. The enzyme as mol. wt. of 86 kD on SDS-PAGE and the presence has a crivity in a mixed micelle assay with has activity in a mixed micelle assay with lass activity in a mixed micelle assay with useful for screening anti-inflammatory agents mediated by the arachidonic acid cascade, for treating, e.g. rheumatoid arthritis
Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                  cPLA2/B; calcium-independent cytosolic phospholipase A2/B;
arachidonic acid; 1-palmitoy1-2-[14C]-arachidony1-phosphatidylcholine;
anti-inflammatory; screen; rheumatoid arthritis; ds.
                                                                                                                                                                                                                                                                                                                                    Calcium-independent cytosolic phospholipase A2/B coding sequence.
                                                                                              DB 23; Length 2010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prodn. of a Ca-independent cytosolic phospholipase A(2)/B - by culturing host cells contg. the phospholipase gene, useful for screening anti-inflammatory agents for treating e.g. rheumatoid
                                                         Sequence 2010 BP; 565 A; 552 C; 532 G; 361 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2935 BP; 697 A; 856 C; 810 G; 572 T; 0 other;
                                                                                                                           1;
                                                                                           Score 19.4; DB
Pred. No. 13;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Column 15-22; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
96..2354
/*tag= a
                                                                                                                                                                                                                                               AAT44578 standard; cDNA; 2935 BP.
                                                                                                                        ö
                                                                                                                                                                       109 GCTCTTTGGGGACAGGAAGCT 129
                                                                                                                                                      5
                                                                                           88.2%;
                                                                                                                                               1 GCTCTTTGGGGACAGGAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94US-0281193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94US-0281193
95US-0422420
                                                                                 Query Match
Best Local Similarity 95.21
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-424653/42.
P-PSDB; AAW01479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang J;
                                                                                                                                                                                                                                                                                                            11-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-JUL-1994;
14-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US5554511-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-SEP-1996.
                                                                                                                                                                                                                                                                                AAT44578;
                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jones S,
   SKSSS
                                                                                                                                                                          g
                                                                                                                                               6
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
     Gaps
                                                                                                                                                                                                                            CHO; calcium-independent cystolic phospholipase-A2/B; enzyme; phospholipase-A2; phospholipase-B; drug screening; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This cDNA was prepared from RNA isolated from CHO-DUX cells. The CDNA may be ligated into predigested lambda phage ZAPI/EcoRI vector and packaged into phage particles. The CDNA library was screened using oligonucleotide probes based on peptide sequences of calcium-perably linked to an expression control sequence such as pWT2 or PED expression vectors in order to produce the phospholipase enzyme recombinantly. Host cells include animal cells, insect cells, eukaryotes, prokaryotes, etc. The sequence may also be expressed in transgenic animals (e.g. milk of transgenic cow). The encoded protein is used to screen for agents which inhibit phospholipase activity for use as antiinflammatory agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         isolated polynucleotide encoding cytosolic phospholipase A2/8 for producing enzyme for use in screening anti-inflammatory agents and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                Calcium-independent cytosolic phospholipase-A2/B enzyme cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.2%; Score 19.4; DB 17; Length 2935; 95.2%; Pred. No. 14; 1. Indels 0; Mismatches 1; Indels 0;
     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2935 BP; 697 A; 856 C; 810 G; 572 T; 0 other;
    ä
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Column 15-22; 24pp; English.
                                                                                                                                                                                                                                                                                                                Location/Qualifiers
96..2352
/*tag= a
                                                                                                                 AAT05842 standard; cDNA; 2935 BP
                                             Crcrcrededacadearc 2026
ö
                          22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2006 CTCTCTGGGGACAGGAC 2026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22
                       CTCTTTGGGGACAGGAGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                          94US-0281193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ilarity 95.2%;
Conservative
                                                                                                                                                                      15-JUN-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 CTCTTTGGGGACAGGAGGTC
                                                                                                                                                                                                                                                                                 Cricetulus griseus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          producing enzyme for produce of antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-009526/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jones S, Tang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AARS3018
                                                                                                                                                                                                                                                        antibody; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                       27-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                   US5466595-A.
                                                                                                                                                                                                                                                                                                                                                                                              14-NOV-1995.
                                                                                                                                             AAT05842;
                     N
                                                2006
                                                                                                   AAT05842
ID AAT0
                                                                                                                                          ò
                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
```

RESULT

DB 17; Length 2935;

Score 19.4; I Pred. No. 14;

88.2%; 95.2%;

Query Match Best Local Similarity

AAT59199;

```
Calcium independent; cytosolic phospholipase A2/B; cPLA2/B; screening; anti-inflammatory; arachidonic acid cascade; chinese hamster; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A cDNA clone (AAT68827), deposited as ATCC 69669, codes for a cytosolic phospholipase A2/B (sPLA2/B) (AAW17849) that is thought to extrosolic phospholipase A2/B (sPLA2/B) (AAW17849) that is thought to screening a cho-bux cDNA library with probes based on isolated screening a CHO-DUX cDNA library with probes based on isolated cos and CHO cells. Probes based on the hamster sPLA2/B was expressed in CNS and CHO cells. Probes based on the hamster sPLA2/B clone AAT68823-26).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Calcium independent phospholipase A2/B - used to reduce inflammation
                                                                                             Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade; inflammation; inhibitor; antiinflammatory; CHO; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 19.4; DB 18; Length 2935;
Pred. No. 14;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2935 BP; 697 A; 856 C; 810 G; 572 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chinese hamster calcium independent cPLA2/B cDNA.
                                                                Hamster cytosolic phospholipase A2/B cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
96..2354
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; Page 33-36; 74pp; English.
                                                                                                                                                                                                    Location/Qualifiers
96..2354
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV64840 standard; cDNA; 2935 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2006 crcrcrededeacaddarc 2026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 95.2%;
Matches 20; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 CTCTTTGGGGACAGGAAGGTC
                                                                                                                                                                                                                                                                                                                                                                96WO-US17794
                                                                                                                                                                                                                                                                                                                                                                                                       95US-0555568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              (GEMY ) GENETICS INST INC
                                 07-AUG-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in a mammalian subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cricetulus griseus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-281037/25.
P-PSDB; AAW17849.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jones S, Tang J;
                                                                                                                                                                                                                                                                                                                                                                    07-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                           38-NOV-1995;
                                                                                                                                                                                                                                                                                           WO9717448-A2
                                                                                                                                                                                                                                                                                                                                15-MAY-1997
                                                                                                                                                                             Cricetus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV64840;
AAT68827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is the mucleotide sequence encoding the Ca-independent

Chospholipase Az/B from Chinese hamster ovary cells. The protein was

phospholipase Az/B from Chinese hamster ovary cells. The protein methods e.g.

isolated from these cells by conventional chromatographic methods e.g.

DEAR anion exchange, hydrophobic interaction, heparin Toyopearl and Mono

Charles anion exchange, hydrophobic interaction, heparin Toyopearl and Mono

Charles from withor pools of degenerate probes were synthesised. The

sequencing from withor pools of degenerate probes were synthesised. The

probes were used to screen a CHO cell cDNA library in lambda ZAPII

probes were used to screen a CHO cell cDNA library in lambda ZAPII

probes were used to compinant phages screened, 12 positive plaques were

vector. Of 400000 recombinant phages screened, 12 positive plaques were

check the phospholipase gene can be inserted into eukaryotic vectors for

The phospholipase gene can be inserted into eukaryotic vectors for

check AANI3164.76, can be used to identify phospholipase inhibitors that

can be used as anti-inflammatory agents, esp. against components of the

can be used as anti-inflammatory agents, esp. against components of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                Ca-independent phospholipase A2/B; Chinese hamster ovary cell; probe; chromatography; DEAE anion exchange; hydrophobic interaction; lambda; heparin Toyopearl; chromatofocussing; eukaryotic expression vector; COS; CHO; inhibitor; anti-inflammatory agent; arachidonic acid cascade; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Compsn. comprising calcium-independent phospholipase enzyme - for screening for anti-inflammatory agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.2%; Score 19.4; DB 18; Length 2935; 95.2%; Pred. No. 14; tive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product= ca-independent phospholipase A2/B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2935 BP; 697 A; 856 C; 810 G; 572 T; 0 other;
                                                                                                                                                   Ca-independent phospholipase A2/B gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Column 15-22; 24pp; English.
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
96..2354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2026
                                   AAT59199 standard; cDNA; 2935 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 CTCTTTGGGGACAGGAGGTC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2006 CTCTCTGGGGACAGGAAGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94US-0281193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94US-0281193
95US-0422106
                                                                                                                                                                                                                                                                                           Chinese hamster ovary cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-076789/07.
P-PSDB; AAW13163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JUL-1994;
14-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                    US5589170-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-DEC-1996.
                                                                                                                      20-MAY-1997
```

Jones S,

ö

Gaps

AAT68827 standard; cDNA; 2935 BP.

RESULT 7 AAT68827

Query Match

Matches

ઠે 셤

```
ö
                                                                                                                                                                                                                                                      This sequence encodes a novel calcium independent cytosolic phospholipase A2/B enzyme isolated from chinese hameter ovary cells. This protein can be used for screening unknown compounds for anti-inflammatory activity mediated by the arachidonic acid cascade.
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An alternative form of DNA encoding cancer associated antigen KOC-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            old LJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotides representing cancer-associated genes, used to develop products for the diagnosis, monitoring and treatment of cancers
                                                                                                                                                                                                     Screening assay for phospholipase inhibitors - using specified phospholipase polypeptide
                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                     DB 20; Length 2935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gure A, Tsang S, Stockert E, Jager E, Knuth A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cancer associated antigen; KOC-3; cancer; vaccine; CT7; ss.
                                                                                                                                                                                                                                                                                                                                                          1; Indels
  /product= "calcium independent cPLA2/B"
                                                                                                                                                                                                                                                                                                          Sequence 2935 BP; 697 A; 856 C; 810 G; 572 T; 0 other;
                                                                                                                                                                                                                                                                                                                                  88.2%; Score 19.4; D
95.2%; Pred. No. 14;
ive 0; Mismatches
                                                                                                                                                                                                                                   Claim 1b(i); Column 15-22; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 55; Page 42-43; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
                                                                                                                                                                                                                                                                                                                                                                                       2006 CTCTCTGGGGACAGGAAGGTC 2026
                                                                                    94US-0281193.
95US-0422106.
96US-0735716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                           CTCTTTGGGGACAGGAGGTC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ36154 standard; DNA; 3283
                                                                 96US-0735716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US05766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0061709.
                                                                                                                            (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                   WPI; 1999-034032/03.
P-PSDB; AAW81825.
                                                                                                                                                                                                                                                                                                                                            Local Similarity
es 20, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-013284/01
                                                                                                                                                 Tang J;
                                                                                   27-JUL-1994;
14-APR-1995;
23-OCT-1996;
                                                              23-OCT-1996,
                       US5840511-A
                                         24-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9954738-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-OCT-1999
                                                                                                                                                   Jones S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ36154;
                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen Y,
                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                           N
                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                          ઠે
```

```
The present sequence represents an alternative form of a cancer associated antigen gene designated KOC-3. The specification also describes a cancer associated antigen designated CT7. The CT7. The CT7 colphyptide has some homology with MAGE-10, limited to about 210 carboxy terminal anno acids. The amino terminal of the protein has a repetitive pattern, with repeats rich in serine, proline, glutamine and lencine, and an almost invariable core of the peptide given in AAX43877. The CT7 colphyptide can be processed to peptides which provoke lysis by cyclytic T cells. The polynucleotides and polypeptides can be used for treating a cancerous condition and screening for or disgnosing cancerous conditions. The cancer associated antigens can be used as an immunogenic conditions. The cancer associated antigens can be used as an immunogenic creation ecomposition with an adjuvant, e.g. a cytokine, a saponin, or cycle macrophage-colony stimulating factor (GM-CSF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           designated KCC-3. The specification also describes a cancer associated antigen designated CT7. The CT7 polynucleotide was isolated from antigen designated CT7. The CT7 polynucleotide was isolated from SK-MEL-37 melanoma cells. The polypeptide has some homology with terminal of the protein has a repetitive pattern, with repeats rich in the peptide given in AAY43877. The CT7 polypeptide core of peptides given in AAY43877. The CT7 polypeptide core of peptides which provoke lysis by cytolytic T cells. The polynucleotides and polypeptides can be used for treating a cancerous condition and accepting for or diagnosting cancerous conditions. The cancer associated antigens can be used as an immunogenic or vaccine composition with an adjuvant, e.g. a cytokine, a saponin, or granulocyte macrophage-colony etimulating factor (GM-CSF).
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Old LJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotides representing cancer-associated genes, used to develop products for the diagnosis, monitoring and treatment of cancers
                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                          Score 19.4; DB 21; Length 3283; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cancer associated antigen; KOC-3; cancer; vaccine; CT7; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a cancer associated antigen
                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                              Sequence 3283 BP; 945 A; 833 C; 779 G; 725 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tsang S, Stockert E, Jager E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding cancer associated antigen KOC-3.
                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 55; Page 41; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ36152 standard; DNA; 3412 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 GCTCTTTGGGGACAGGAAGCT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                     1 GCTCTTTGGGGACAGGA 21
                                                                                                                                                                                                                                                                                                                                        88.2%;
95.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0061709.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-013284/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gure A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9954738-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L7-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-OCT-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ36152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      888888888888888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                    요
```

ö

Length 3667;

DB 23;

```
g
                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated polymucleotide (I) and polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The chair control of the control of the chair control of the chair chair control of the chair chair control of (II) is useful in gene therapy techniques (II). It is useful to generating antibodies against it, detecting or control of (II) and its binding partners are useful in medical a food supplement. (II) and its binding partners are useful in medical contents involving aberrant protein expression or biological activity. (I) and polymeptide and polymolectide sequences have applications in the polypeptide and polymolectide sequences have applications in content protein content traits to assess biodiversity and to produce other types of data and products dependent on DNR and cannot content types of data and products dependent on DNR and diagnostic coding sequences of the invention.

Content of produce data for this patent did not appear in the printed of the chair of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content o
                                                                  ö
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                    ö
                                   DB 21; Length 3412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3667 BP; 1081 A; 882 C; 846 G; 858 T; 0 other;
                                                                     Indels
     Sequence 3412 BP; 970 A; 887 C; 804 G; 750 T; 1 other;
                                                                                                                                                                                                                                                                                                              DNA encoding novel human diagnostic protein #6786.
                                                                     7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at ftp.wipo.int/pub/published_pct_sequences.
                                     Score 19.4; DE
Pred. No. 14;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID No 6786; 103pp; English.
                                                                                                                                                                                                                    AAS70982 standard; cDNA; 3667 BP.
                                                                                                                                      132 GCTCTTTGGGGACAGGAAGCT 152
                                                                                                         21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT;
                                        Query Match

Best Local Similarity 95.2%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                       1 GCTCTTTGGGGACAGGAAGGT
                                                                                                                                                                                                                                                                                     13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-639362/73.
P-PSDB; ABG06795.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-OCT-2001.
                                                                                                                                                                                                                                                          AAS70982;
                                                                                                                                                                                            RESULT 11
                                                                                                                                                                                                            g
                                                                                                                ઠ
XXX
```

```
Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virtudie; fungicide; opthalmalogical; undinerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrouscular disorder; cerebral ischaemia; angiogenesis; erebrouscular disorder; Alzheimer's disease; infection; ocular disorder; corebral infection; ocular disorder; skin ageing; food additive; preservative; antiproliferation;
                                   ő
                                       Gaps
                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                            Human cDNA encoding a novel secreted protein, Seq ID 329.
                                          Indels
                                            1;
88.2%; Score 19.4; D
95.2%; Pred. No. 14;
iive 0; Mismatches
                                                                                                                                                                                                                                               AAS26150 standard; cDNA; 3694 BP.
                                                                                                                                   498 GCTCTTTGGGGACAGGAAGCT 518
                                                                                           21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0227009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  000US-0217496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JAN-2001; 2001WO-US01341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              000US-0205515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0190076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       000US-0189874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    000US-0198123
                                                                                             1 GCTCTTTGGGGACAGGAAGGT
                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                   20; Conservative
  Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200155322-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                             07-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-AUG-2001
                                                                                                                                                                                                                                                                                                   AAS26150;
                                                                                                                                                                                                         RESULT 12
AAS26150
```

```
2000US-0241809.
2000US-0241826.
2000US-0244617.
2000US-0246474.
2000US-0246475.
                                                                                                                                            08-NOV-2000; 2
08-NOV-2000; 2
08-NOV-2000; 2
08-NOV-2000; 2
08-NOV-2000; 2
08-NOV-2000; 2
08-NOV-2000; 3
08-NOV-2000; 3
                                                                                                      02-OCT-2000;
02-OCT-2000;
13-OCT-2000;
```

(HUMA-) HUMAN GENOME SCI INC 2000US-0249299 2000US-0249300 2000US-0250391 2000US-0251030 2000US-0251988 2000US-0256719 2000US-0251479 05-DEC-2000; 05-DEC-2000; 05-DEC-2000; 06-DEC-2000; 17-NOV-2000; 

Ruben SM Rosen CA, Barash SC,

WPI; 2001-488783/53. P-PSDB; AAU16163.

New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -

Claim 1; SEQ ID No 329; 980pp; English.

The invention relates to isolated nucleic acid molecules and their chocded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliotate a medical condition in e.g. humans, mice, crabbits, goats, horses, cats, dogs, chickens or sheep. They to a pathological condition. Antibodies to the proteins can also to a pathological condition. Antibodies to the proteins can also condition. Antibodies to the proteins can also diagnostic immunoassays e.g. radiolumnoassays or enzyme linked immunoassays [ELISA]. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, cardiovascular disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac of the polypeptides and fungi c.g. disorders listed in the specification, and many other disorders listed in the specification, end many other c.c. transplantation, for supporting cell culture of primary tissues, to cream a food additive or preservative to increase storage c.c. regenerate tissues and in chemotaxis. The polypeptides can also be used c.g. a food additive or preservative to increase or decrease storage c.g. as food additive or preservative to increase or decrease storage c.g. minerals, cofactors and other nutritional components. The present

Gaps ö Length 3694; Indels DB 22; 88.2%; Score 19.4; D 95.2%; Pred. No. 14; tive 0; Mismatches Query Match Best Local Similarity 95.21 Matches 20; Conservative

ö

GCTCTTTGGGGACAGGAAGGT 21 Н

ò

Human LOBO homologue genomic DNA fragment 7.

(first entry)

25-JAN-2000

AAZ23905;

AAV39294 standard; cDNA; 1212 BP.

RESULT 13 AAV39294

155 GCTCTTTGGGGACAGGAAGCT 175

심

```
The present sequence represents a specifically claimed partial nucleic caid sequence encoding human RAD54 (hRAD54). A method for analysing a sample for mutation of DNA encoding hRAD54 has been developed using a sample for mutation of DNA encoding hRAD54 has been developed using a complete that the last 15 and no more than 30 consecutive bases of the DNA sequence encoding hRAD54. hRAD54 is a gene thought to be present in tumours that display allelic imbalance at 1p32, the chromosomal band in the intended as one of four minimal regions of chromosome 1 deletion in dentified as one of four minimal regions of chromosome 1 deletion in alia, that have been identified as novel hRAD54 by homology between the alia, that have been identified as novel hRAD54 by homology between the such as yeast RAD54. hRAD54 proteins are used in the treatment of such as yeast RAD54. hRAD54 proteins are used in the treatment of sundromes and X-linked mental retardation with alpha-thalassaemia syndrome and breast cancer. hRAD54 polynucleotides are also useful for despecially useful for diagnosis of disease or susceptibility to diseases. hRAD54 polynucleotides are also useful for diseases. hRAD54 polynucleotides are also useful for diseases or susceptibility to diseases. PRAD54 polynucleotide, proteins, agonists and antagonists which are broteins are useful in gene therapy.
                                                                                                                               Human; RAD54; hRAD54; cancer; xeroderma pigmentosum; Bloom syndrome; Werner's syndrome; ATR-X; diagnosis; detection; SNF2 superfamily; X-linked mental retardation with alpha-thalassemia syndrome; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human hRAD54 DNA and polypeptide - and agonists, antibodies, antagonists, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1212 BP; 241 A; 360 C; 287 G; 322 T; 2 other;
                                                                                                Human RAD54 nucleic acid sequence comprising exon 1-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.9%; Score 17.8; DB 19;
90.5%; Pred. No. 71;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Robbins DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ23905 standard; DNA; 11849 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rasio D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 25; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     (SMIK ) SMITHKLINE BEECHAM CORP. (UYJE-) UNIV JEFFERSON THOMAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GCTCTTTGGGGACAGGAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 GCGCTTTGGGAACAGGAAGGT
                                                                                                                                                                                                                                                                                                                                                  97EP-0308998.
                                                                                                                                                                                                                                                                                                                                                                                   96US-0030676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 90.5'
Matches 19; Conservative
                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fishel RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-274189/25
                                                                                                                                                                                                      qene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                  10-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                         13-NOV-1996;
                                                                      16-SEP-1998
                                                                                                                                                                                                                                          sapiens
                                                                                                                                                                                                                                                                             EP844305-A2.
                                                                                                                                                                                                                                                                                                                27-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Croce CM,
                                   AAV39294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
AAZ23905/c
ID AAZ23
                                                                                                                                                                                                                                            Ношо
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
```

```
This invention describes novel nucleic acids (I; designated LOBO (long Dones)) encoding proteins influencing bone development in mammals. The proteins of the invention reduce and/or inactivate bone extension (i.e. proteins of the invention of the skull and have osteopathic activity. The nucleic acid molecules, proteins and antibodies can be used in diagnostic or pharmaceutical compounds e.g. for gene therapy. The methods and nucleic acid molecules, etc. are useful for production of transgenic animals, especially a transgenic animals, especially a transgenic acidonder especially a transgenic encodes a sasociated with bone development, e.g. spondyloepiphysal dysplasia and achondroplasia. This sequence encodes a human LOBO protein described in the method of the invention.
                                                                                    osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding proteins which influence bone development, useful for treating and studying bone disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

80.9%; Score 17.8; DB 20; Length 11849;
Best Local Similarity 90.5%; Pred. No. 93;
Matches 19; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11849 BP; 2693 A; 3311 C; 3343 G; 2502 T; 0 other;
                                                                                      LOBO; long bones; bone development; bone extension; skull;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human colon cancer antigen encoding cDNA SEQ ID NO:1373.
                                                                                                   diagnostic; pharmaceutical; gene therapy; transgenic ar spondyloepiphysal dysplasia; achondroplasia; human; ds
                                                                                                                                                                                                                                                                                                                        Aigner T, Wirth T;
                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Page 384-391; 391pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH34291 standard; cDNA; 3036 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7320 GCTCTTTGGGGTCAGGAGAT 7300
                                                                                                                                                                                                                                                                                                                              Hess J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21
                                                                                                                                                                                                                                                                        98DE-1013799,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GCTCTTTGGGGACAGGAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            colorectal carcinoma; ss.
                                                                                                                                                                                                                                                                                                                               Rump A,
                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-601320/51.
                                                                                                                                                                                                                                                                                                    (ROSE/) ROSENTHAL A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200122920-AZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-SEP-2001
                                                                                                                                                                                     WO9950284-A2.
                                                                                                                                                                                                                                            26-MAR-1999;
                                                                                                                                                                                                                                                                          27-MAR-1998;
                                                                                                                                                                                                                                                                                                                                 Rosenthal A,
                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                 17-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH34291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
AAH34291/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ద
ö
```

ö

ö

Gaps

ö

Indels

Length 1212;

```
PX 28-SEP-2000; 2000WO-US26524.

PR 29-SEP-1999; 99US-0157137.

PR 29-SEP-1999; 99US-0157137.

PR 29-SEP-1999; 99US-0152280.

PR 29-SEP-1999; 99US-0152280.

PR 29-SEP-1999; 99US-0152280.

PA (HUMA-) HUMAN GENOME SCI INC.

PA WPI; 2001-235357/24.

PR PEDB; AAG74886.

XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides, XX VAH32943 to AAH37195 and AAG73514 to AAG77708 represent human colon cancer-associated mulciples acid molecules (N) and proteins (P), Where Cancer-associated mulciples acid molecules (N) and proteins (P), Where the proteins are collectively known as colon cancer antigens. The colon therapy and vaccine production. N and P may be used in the prevention, classociated with decreased expression by rectifying mutations or deletions contacted with decreased expression by rectifying mutations or deletions in an patient spenome that affect the activity of P by expressing CC and treatment of diseases associated with inappropriate P associated with honored activity of P by expressing CC and treatment of colorectal carcinomas and cancer-associated PS of the proteins or the supplement the patients of produce the colon cancer-associated PS of the proteins or the supplement the patients on Production of PC and treatment of colorectal carcinomas and cancer-associated PS of the activity of P by expressing and AAB7789 represent sequences used in the exemplification of the CC N Bagges 66 to 682 and page 7035 of the sequence are present for XX SEC ID NO:1027 to 1052, 7921 and 7922.
```

Sequence 3036 BP; 961 A; 603 C; 633 G; 830 T; 9 other;
Query Match
Best Local Similarity 94.7%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0;

ö

0; Gaps

Db 2881 GCACTTTGGGGACAGGAAG 2863

දු ද

1 GCTCTTTGGGGACAGGAAG 19

Search completed: April 18, 2003, 05:45:32 Job time : 104 secs

48	

```
2112
3240
70000
1641
1662
1662
1662
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
96..2352
                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY:
; LOCATION:
US-08-281-193-1
                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
16.2
16.2
16.2
16.2
16.2
                                                                   15.8
115.8
115.8
115.8
115.8
115.8
115.8
                                                                                                                                                                                                            JS-08-281-193-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-422-106-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local
Matches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 1, Appli
                                                 April 18, 2003, 04:53:41 ; Search time 21.5 Seconds (without alignments) 313.809 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1
Sequence 1
Sequence 2
GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                                     /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTuS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTuS_COMB.seq:*
                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                               US-08-912-794-1
US-08-555-568B-20
                                                                                                                                                441362 segs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                - nucleic search, using sw model
                                                                                                     1 gctctttggggacaggaaggtc 22
                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                      IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                Issued_Patents_NA:*
                                                                                    US-09-270-437D-13
                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                       Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                 2935
2935
2935
2935
2935
2935
3418
3418
3418
3515
1680
1680
1680
1680
1680
1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1680
1277
1277
1707
1707
1710
2109
                                                                                                                                                                                                                                                                                4.0.0
                                                                                                                      Scoring table:
                                                                                             Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                OM nucleic
                                                                                                                                                                                                                                               Database :
                                                                                                      Sequence:
                                                                                                                                                Searched:
                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                         Result
```

```
ö
                                                                                      9, Appli
5, Appli
40, Appl
500, App
13, Appl
94, Appl
94, Appl
3, Appli
3, Appli
                                                                                                                                                                                                                                                     , 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                     Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08281193
Fatent No. 546595
FATEL INFORMATION:
APPLICANT: Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/281,193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08422106
Patent No. 589170
GENERAL INFORMATION:
APPLICANT: Jones, Simon
APPLICANT: Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
US-09-519-223-20
US-08-555-56BB-22
US-09-519-223-22
US-09-851-896-30
US-08-951-896-30
US-08-7071-9
US-08-705-771-9
US-08-705-771-9
US-09-443-0418-5
US-09-443-0418-13
US-09-443-0418-13
US-09-443-0418-13
US-09-328-775-3
US-09-221-0775-3
US-08-775-3
US-08-841-483-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 88.2%; Score 19.4; DE Similarity 95.2%; Pred. No. 1.3; 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2006 CTCTCTGGGGACAGGAAGGTC 2026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2935 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CTCTTTGGGGACAGGAGGTC 22
```

```
B: Genetics Institute,
87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . Sequence 1, Application US/09519223
; Patent No. 6274140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION UNDBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPAK: (617) 498-8224
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2935 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2006 crcrcrddddacaddaadgrc 2026
   PGGGGACAGGAAGGTC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 87 CambridgePar
CITY: Cambridge
STATE: Massachusetts.
COUNTRY: U.S.A.
ZIP: 02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-519-223-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
                                                                                                                                                                              RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.2%; Score 19.4; DB 2; Length 2935;
ilarity 95.2%; Pred. No. 1.3;
Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.2%; Score 19.4; DB 1; Length 2935; 95.2%; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Jones, Simon
APPLICANT: Tang, Jim
TITLE OF INFORMION: Calcium Independent Phospholipase A2/B
TITLE OF INFORMION: SI
NUMBER OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM TYPER: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: SYSTEM:
COMPUTER: COMPATION OF COMPATION OF COMPATION OF CAMPUTER OF COMPATION OF CAMPUTER OF COMPATION OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER OF CAMPUTER O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION Telease #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735,716
FILLING DATE: 23-OCT-1996
FILLING DATE: 424
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,106
CILING DATE: 14-APR-1995
CILASSIFCATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/281,193
FILING DATE: 27-UUL-1994
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2935 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/281,193
FTLING DATE: 27-UUL-1994
INPORMATION FOR SEQ ID NO: 1:
ESCUENCE CHARACTERISTICS:
LENGTH: 2935 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08735716
Patent No. 5840511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2006 crcrcrededacaddaderc 2026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96..2352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
HYPOTHETICAL: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
US-08-735-716-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , NAME/KEY:
LOCATION:
US-08-422-106-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 88.2%; Score 19.4; DB 2; Length 2935; Best Local Similarity 95.2%; Pred. No. 1.3; Matches 20; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INCOLLES.
GENERAL INCOLLES.
SIMON
APPLICANT: Jones, Simon
APPLICANT: Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
Sequence 1, Application US/0855568B
Patent No. 5976854
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Jones, Simon
APPLICANT: Tang, Jim
TITLE OF INVENTION:
Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION NUMBER: US/08/555,568B
FILING DATE:
```

Massachusetts

```
Sequence 8, Application US/09061709B
Sequence 8, Application US/09061709B
Patent No. 6297364
GENERAL INFORMATION
APPLICANT: Chen, Yao-Tseng
APPLICANT: Tsang, Solam
APPLICANT: Tsang, Solam
APPLICANT: Stocker, Elisabeth
APPLICANT: Stocker, Elisabeth
APPLICANT: Much, Alexander
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Thereof
TITLE OF INVENTION: Isolated Nucleic And Uses Thereof
CURRENT APPLICATION NUMBER: US/09/061,709B
CURRENT FILING DATE: 1998-04-17
MURBER OF SEQ ID NOS: 8
SEQ ID NO 8
LENGTH: 3283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-061-709-6

i Sequence 6, Application US/09061709B

i Patent No. 6297364

i GENERAL INFORMATION:

APPLICANT: Chen, Yao-Tseng

APPLICANT: Tsang, Ali

APPLICANT: Tsang, Solam

APPLICANT: Tsang, Solam

APPLICANT: Tsang, Solam

APPLICANT: Tsang, Solam

APPLICANT: Tsang, Solam

APPLICANT: Jager, Elke

APPLICANT: Jager, Elke

APPLICANT: Original Antion

TILLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated

TILLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof

CURRENT PILLING DATE: 1998-04-17

NUMBER OF SEQ ID NOS: 8

SEQ ID NO 6

LENGTH: 3412

TYPE: NAN
                                                                               Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                             ö
              Query Match 88.2%; Score 19.4; DB 5; Length 2935; Best Local Similarity 95.2%; Pred. No. 1.3; Matches 20; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 88.2%; Score 19.4; DB 4; Length 3283; Best Local Similarity 95.2%; Pred. No. 1.4; Matches 20; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

88.2%; Score 19.4; DB 4; Length 3412;
Best Local Similarity 95.2%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                       Db 2006 CTCTCTGGGGACAGGAAGGTC 2026
                                                                                                             2 CTCTTTGGGGACAGGAGGTC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GCTCTTTGGGGACAGGAAGGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-061-709-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-061-709-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oʻ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: GENERICS INSTITUTE, INC.

TITLE OF INVENTION:

CAMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

TITLE OF INVENTION NUMBER: PCT/US95/08069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 88.2%; Score 19.4; DB 4; Length 2935; Best Local Similarity 95.2%; Pred. No. 1.3; Matches 20; Conservative 0; Mismatches 1; Indels 0.
              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIVE STEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
SOFTWARE: PatentIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE:
CLASSIFICATION
PRIOR APPLICATION
PRIOR APPLICATION
PRIOR APPLICATION
PRIOR APPLICATION
TELEBOWN: SCOLE A.
REGISTRATION UNMBER: 32,724
FILEDCOMMUNICATION INFORMATION:
TELEBOWN: (617) 876-5851
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2935 base pairs
TYPE: nucleic acid
STRANDEDRESS: double
TOMBER: 1 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2006 CTCTCTGGGGACAGGAC 2026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2935 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 CTCTTTGGGGACAGGAGGTC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: CDS
; LOCATION: 96.2352
US-09-519-223-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96..2352
U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL: NANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 11r
MOLECULE TYPE:
HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
PCT-US95-08069-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  // NAME/KEY:
// LOCATION:
PCT-US95-08069-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
```

ö

4273 GCACTTTGGGTACAGGTAGGTC 4252

g ઠ

```
Gaps
           Sequence 2, Application US/08928862
; Patent No. 630897
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: 1801ation and Use of Motoneuronotrophic Factors
FILE REFERENCE: 12592-2
CURRENT APPLICATION NUMBER: US/08/928,862
CURRENT FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DEADOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/140,729A
FILING DATE: 20 OCT 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5658/82.nad, Kevin E
REGISTRATION NUMBER: 35,303
REPERBUCE/DOCKET NUMBER: 39,509
TELEFRAM: 312-715-1000
TELEFRAM: 312-715-11000
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
TELEFRAM: 312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Amara, Susan G
APPLICANT: Ariza, Jeffrey L
TITLE OF INVENTION: Amino Acid Transporters and Uses
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUDRESSEE: AUDRESS:
AUDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPITED: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-08-140-729A-2/C
US-08-140-729A-2/C
; Sequence 2, Application US/08140729A
; Patent No. 5658782
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 74.5%;
[1 Similarity 94.4%;
17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 CTTTGGGGACAGGAAGGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: 5'UTR
LOCATION: 1..30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 17; Conserv
RESULT 11
US-08-928-862-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-928-862-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            엄
                                                                                                                                                                GENERAL INC. 83/44/5

GENERAL INCRMATION:
APPLICANT: Recker, Beth
APPLICANT: Tomlinson, James E.
APPLICANT: Tomlinson, James E.
APPLICANT: Tomlinson, James E.
APPLICANT: Tomlinson, General E.
APPLICANT: COR Therapeutics, Inc.
APPLICANT: COR Therapeutics, Inc.
APPLICANT: COR Therapeutics, Inc.
APPLICANT: COR Therapeutics, Inc.
APPLICANT: COR THERENCE: 44481-5029-01-05
FILE REFERENCE: 44481-5029-01-05
FILE REFERENCE: 1999-07-01
FRIOR APPLICATION NUMBER: 60/998,559
FRIOR APPLICATION NUMBER: 60/998,559
FRIOR APPLICATION NUMBER: 08/886,440
FRIOR APPLICATION NUMBER: 08/886,440
FRIOR PILING DATE: 1999-07-01
FRIOR PILING DATE: 1999-07-01
SEQ ID NOS: 3
SOFFWARE: PatentIn Ver: 2.0
SEQ ID NO 1
LENGTH: 4985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 5515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 98, Application US/09398193
Sequence 98, Application US/09398193
Patent No. 6197581
GENERAL INFORMATION:
TITLE OF INVENTION: Ademylate cyclase and uses therefor TITLE OF INVENTION: Ademylate cyclase and uses therefor CURENT PEPLICATION NUMBER: US/09/398,193
CURENT FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 104
SOFTWARE PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
78.2%; Score 17.2; Dl
Best Local Similarity 86.4%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 17.2; Di
Pred. No. 18;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: human type IX adenylyl cyclase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3751 GCACTITGGGTACAGGTAGGTC 3730
                                                                                                                          Sequence 1, Application US/09473717
Patent No. 6372475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 86.4%;
Matches 19; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GCTCTTTGGGGACAGGAAGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , NAME/KEY: CDS
; LOCATION: (539)..(4600)
US-09-398-193-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: (17)...(3898)
US-09-473-717-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 98
LENGTH: 5515
TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SULT 10
-09-398-193-98/c
```

Š

```
Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 1680;
         IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                       Sequence 2, Application US/08916745
Patent No. 5840516
GENERAL INFORMATION:
APPLICANT: Arriza, Jeffrey L
TITLE OF INVENTION: Amino Acid Transporters and Uses
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/916,745

FILING DATE: 19-AUG-1997

CLASSIFICATION NUMBER: US 08/140,729

FILING APPLICATION NUMBER: US 08/140,729

FILING DATE: 20-CC-1993

ATTORNEY/AGENT INFORMATION:

NAME: NO. 5840516nan, Kevin E

REGISTRATION NUMBER: 93,509

TELECOMMUNICATION INFORMATION:

REGISTRATION NUMBER: 93,509

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-715-1000

TELEFAX: 312-715-1234

TELEFAX: 312-715-1234

TELEMOTH: 1680 base pairs
     Mismatches
     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-09-042-929-2/c
; Sequence 2, Application US/09042929
                                                            528 CTCTTTGGGGACAGGAGG 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   528 CTCTTTGGGGACAGGAGG 511
17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 CTCTTTGGGGACAGGAAG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3'UTR
1626..1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31..1626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                           STATE: IL
COUNTRY: USA
                                                                                                                       RESULT 14
US-08-916-745-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:

LOCATION:

US-08-916-745-2
 Matches
                                    ઠે
                                                                                                                                                                          ô
                                                                                                                                                                          Gaps
                                                                                                                                                                         ö
                                                                                                                               Score 16.4; DB 1; Length 1680;
Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 1680;
                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08546666
Patent No. 5776774
GENERAL INFORMATION:
APPLICANT: Amara, Susan G
APPLICANT: Arriza, Jeffrey L
TITLE OF INVENTION: Amino Acid Transporters and Uses
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GETWALING SYSIEM: PC-DOS/MS-DOS
GOFFWARE: PAtentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/546,666
FILING DATE:
CLASSIFICATION DATA:
PRELICATION NUMBER: US/08/140,729
FILING DATE: 20 OCT 1993
ATTORNEY/ACENT INFORMATION:
NAME: 00.5776774ann, Kevin B
REGISTRATION NUMBER: 35,303
REGISTRATION NUMBER: 35,303
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAK: 312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 16.4; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELERAX: 312-712-11
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERICS:
LENGTH: 1680 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                     Query Match

Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.58;
                                                                                                                                                                                                                    528 CTCTTTGGGACAGGAGG 511
                                                                                                                                                                                             2 CTCTTTGGGGACAGGAG 19
                                                     3'UTR
1626..1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3'UTR
1626..1680
   CDS
31..1626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31..1626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                              | FEATURE:
| NAME/KEY:
| LOCATION:
| US-08-140-729A-2
 NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                       RESULT 13
JS-08-546-666-2/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY:
; LOCATION:
US-08-546-666-2
                                                                                                                                                                                               δ
                                                                                                                                                                                                                            셤
```

```
Particlar in Arrita, Susan G
Applicant Marita Arrita, Susan G
Applicant Arrita, Jefffrey L
Title OF INTENTION: Amino Acid Transporters and Uses
NUMBER OF SECTIONES:
CORRESPONDENCE ANISTS.
TITLE OF INTENTION: Amino Acid Transporters and Uses
NUMBER OF SECTIONES:
CORRESPONDENCE ANISTS.
TITLE OF INTENTION: Amino Acid Transporters and Uses
CONDITIONES:
TITLE OF INTENTION OF A CONDITION:
CONDITIONES:
COMPUTENT SECTION OF A CONDITION:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
CONDITIONES:
C
```

Oy 2 CTCTTTGGGGACAGGAAG 19
Db 528 CTCTTTGGGGACAGGAGG 511

Search completed: April 18, 2003, 07:34:33
Job time : 24.5 secs

```
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1
US-09-927-180-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Appli
Sequence 1, Appli
Sequence 129, Appl
Sequence 10, Appli
Sequence 702, Appl
Sequence 702, Appl
Sequence 702, Appl
Sequence 600, Appl
Sequence 600, Appl
Sequence 600, Appl
Sequence 600, Appl
Sequence 500, Appl
Sequence 500, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 9511, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18, Appl
Sequence 20, Appl
Sequence 22, Appl
                                                                                       April 18, 2003, 06:35:31; Search time 91.3333 Seconds (without alignments) 241.975 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                              1279498
GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0. US-09-927-180-1

0. US-09-99-651-8

0. US-09-764-864-329

2. US-10-71-223-1

0. US-09-764-807-702

0. US-09-946-807-702

0. US-09-946-807-702

0. US-09-946-807-702

0. US-09-95-668-702

0. US-09-95-668-702

0. US-09-95-668-702

0. US-09-95-68-702

0. US-09-95-68-702

0. US-09-858-546-801

0. US-09-878-574-4815

0. US-09-878-574-4815

0. US-09-878-574-4815

0. US-09-877-180-18

0. US-09-977-180-18
                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                       639749 seqs, 502280978 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                          1 gctctttggggacaggaaggtc 22
                                                        OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                        IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                           US-09-270-437D-13
                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15531
15531
659158
256
275
                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                       Searched:
                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
```

	Sequence 1339, Ap Sequence 1339, Ap Sequence 132, App Sequence 132, App Sequence 132, App Sequence 67, App Sequence 67, App1 Sequence 3, App1 Sequence 3, App1
US-09-864-864-306 US-10-274-968-3 US-09-740-027-3 US-09-736-457-1159 US-09-92-941-1159 US-09-94-626-1159 US-09-917-800A-392 US-09-917-800A-392 US-09-917-800A-392 US-09-917-800A-392 US-09-917-800A-392 US-09-917-800A-392 US-09-917-800A-392 US-09-917-800A-392 US-09-917-800A-392 US-09-917-800A-392 US-09-9131-313-313-313-313-313-313-313-313-3	<del></del>
100 00 00 00 00 00 00 00 00 00 00 00 00	200000000000000000000000000000000000000
3231 24707 24707 361 361 361 437 439 401 401 401 401 401 401	527 689 787 787 787 1369 1787
73.6 72.7 72.7 72.7 72.7 72.7 72.7 72.7 71.8 71.8 71.8 71.8 71.8 71.8	71.8
16.2 16.2 16.2 16.2 16.2 16.2 16.8 15.8 15.8 15.8 15.8 15.8	15.8 15.8 15.8 15.8 15.8 15.8
34 3 3 3 3 3 3 3 4 3 3 5 5 5 5 5 5 5 5 5	8 6 6 4 4 4 4 4 4 4 6 6 6 6 6 6 6 6 6 6
000000 000	υυ

## ALIGNMENTS

```
WESULT IN APPLICATION US/09927180

Sequence 1, Application US/09927180

Patent No. US20020106364A1

GENERAL INFORMATION: Calcium Independent Phospholipase A2/B

INTIE OF INVENTION: Calcium Independent Phospholipase A2/B

INTRESPONDENCE: 25

CORRESPONDENCE: 25

COUNTRY: US.A.

ZIP: 02140

COUNTRY: US.A.

ZIP: 02140

COMPUTER: IBM PC COMPATIBLE

CONPUTER: IBM PC COMPATIBLE

COMPUTER: PatentIn Release #1.0, Version #1.25 (EPO)

MEDIUM TYPE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION NUMBER: 09/519,223

FILING DATE: 09-A49-Z001

CRASTIFICATION NUMBER: 09/519,223

APPLICATION NUMBER: 09/519,223

APPLICATION NUMBER: 09/519,223

APPLICATION NUMBER: 09/519

REGISTRATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2915 base pairs

TELEPRONE (617) 498-824

TELEPRONE CHARACTERISTICS:

LENGTH: 2915 base pairs

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917) BASE INFORMATION:

TELEPRONE (1917)
```

```
Conservative
                                                                                                                                                                                          Query Match
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
CORGANISM: Homo sapiens
US-09-764-864-329
                                                                     TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 20; Conserva
NUMBER OF SEQ ID NOS:
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
US-09-764-864-329
                                                                                                                                             US-09-899-651-6
                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Tsang, Solam
APPLICANT: Tsang, Solam
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Mutth, Alexander
APPLICANT: Mutth, Alexander
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: Associated
TITLE OF INVENTION: Associated
TITLE OF INVENTION: Associated
TITLE OF INVENTION: Associated
TITLE OF INVENTION: Associated
TITLE OF INVENTION: Associated
TITLE OF INVENTION: Associated
TITLE OF INVENTION: Associated
TITLE OF INVENTION: Associated
TITLE OF INVENTION: UNBER: US/09/899,651
CURRENT FILING DATE: 2001-07-06
PRIOR FILING DATE: 1998-04-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Teang, Solam
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Jack.
APPLICANT: Jack.
APPLICANT: Malesander
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: Associated
TITLE OF INVENTION: Associated
TITLE OF INVENTION: Associated
TITLE OF INVENTION: Associated
TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
TITLE OF INVENTION: ANDER: US/09/899,651
CURRENT APPLICATION NUMBER: US/09/061,709
PRIOR APPLICATION NUMBER: US/09/061,709
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 8
IENGTH: 3283
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 19.4; DB 10; Length 3283; Pred. No. 4.3;
                                                                                                                                                                                                                             ;
0
                                                                                                                                                                              Length 2935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                Indels
                                                                                                                                                                                   DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                              Query Match

Best Local Similarity 95.2%; Pred. No. 4.
Matches 20; Conservative 0; Mismatche
                                                                   DOCATION: 96..2352
sequence description: Seq ID NO: 1: US-09-927-180-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/09899651
Patent No. US20020111470A1
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/09899651
Patent No. US20020111470A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 gererriegegekekekeker 152
                                                                                                                                                                                                                                                                                                                            2006 crcrcreedeacaddadcre 2026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GCTCTTTGGGGACAGGAGGT 21
                                                                                                                                                                                                                                                                                 2 CICITIGGGGACAGGAAGGIC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 95.2%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Chen, Yao-Teeng
APPLICANT: Gure, Ali
APPLICANT: Tsang, Solam
APPLICANT: Stockert, Elsab
APPLICANT: Jager, Elke
APPLICANT: Knuth, Alexander
APPLICANT: Old, Lloyd J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Chen, Yao-Tseng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                        ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠ
                                                                                                                                                                                                                                                                                              ઠ
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                         Sequence 319, Application US/09764864
; Sequence 329, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICATION: Rosen et al.
; TITLE OF INVENTION: NUMBER: US/09/764,864
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper; NUMBER OF SEQ ID NOS: 1792
; SEQ ID NO 329
; SEQ ID NO 329
; LENGTH: 3364
                                                                                                                                                                                                                                                                                                                                                                           88.2%; Score 19.4; DB 10; Length 3694; 95.2%; Pred. No. 4.3; tive 0; Mismatches 1; Indels 0;
                         ö
Length 3412;
                           Indels
 Score 19.4;
Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/10071223
Patent No. US20020137174A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 gcrcrrrggggacaggagcr 175
                                                                                132 GCTCTTTGGGGACAGGAAGCT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GCTCTTTGGGGACAGGAAGGT 21
                                                         1 GCTCTTTGGGGACAGGAAGGT 21
    88.2%;
95.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Storm, Daniel R. APPLICANT: Hacker, Beth
```

ORGANISM: human type IX adenylyl cyclase

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10;
                                                                                                                                     Sequence 702, Application US/09795668
Patent No. US202045577A1
GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn.
APPLICANT: Stefansson, Hreinn.
APPLICANT: Stefanthoredottir, Valgerdur
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHERNIA GENE
FILE REFERENCE: 2345,2004-001
CURRENT APPLICATION NUMBER: US/09/795,668
CURRENT FILING DATE: 2000-02-28
PRIOR FILING DATE: 2000-02-28
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 702, Application US/09795686

Patent No. US20020094954A1

GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn
APPLICANT: Stefansson, Hreinn
APPLICANT: Glother, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345,2005-001
CURRENT APPLICATION NUMBER: US/09/795,686
PRIOR PILING DATE: 2000-02-28
PRIOR FILING DATE: 2000-02-28

NUMBER OF SEQ ID NOS: 1531
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
76.4%; Score 16.8; Dest Local Similarity 90.0%; Pred. No. 75; Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.4%; Score 16.8; D
90.0%; Pred. No. 75;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-09-858-546-3/c
; Sequence 3, Application US/09858546
; Patent No. US20020172995A1
; GENERAL INFORMATION:
                                          98 rerrradedacaddadedre 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 TGTTTAGGGACAGGAAGGTC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 TCTTTGGGGACAGGAAGGTC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 TCTTTGGGGACAGGAGGTC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 rerrragedacaddaadgrc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 90.03
Matches 18, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-795-668-702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-09-795-686-702
                                                                                                                      JS-09-795-668-702/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
US-09-795-686-702/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                      원
      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                   ö
                                                                                             Length 4985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10; Length 5515;
                                                                                                                                                                                                                                                                  VESULI. 98. Application US/09751100B

Sequence 98, Application US/09751100B

Petent No. US2020142436A1

GENERAL INFORMATION:

APPLICANT: Medical Research Council

TITLE OF INVENTION: Human Adenylate Cyclase and Use Therefor FILE REFERENCE: P27948A

CURRENT APPLICATION NUMBER: US/09/751,100B

CURRENT FILING DATE: 2000-12-28

NUMBER OF SEQ ID NOS: 104

SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 9; Length 401;
                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                    Score 17.2; DB 12;
Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 702, Application US/09946807
Patent No. US20020165144A1
GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn
APPLICANT: Stefansson, Hreinn
APPLICANT: Guicher, Jeffrey, R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004-001
CURRENT FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US/09/795,668
PRIOR PILING DATE: 2001-02-28
PRIOR RELING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
SOFTHARE: FastSEQ for Windows Version 4.0
                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17.2; DE
Pred. No. 44;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
76.4%; Score 16.8; D
Best Local Similarity 90.0%; Pred. No. 75;
Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                              3751 GCACTTTGGGTACAGGTAGGTC 3730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4273 GCACTTTGGGTACAGGTC 4252
                                                                                                                                                        1 GCTCTTTGGGGACAGGAC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GCTCTTTGGGGACAGGAGGTC 22
                                                                          Query Match 78.2%;
Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAMEKKY: CDS
LOCATION: (539)..(4600)
OTHER INFORMATION:
US-09-751-1008-98
) NAME/KEY: CDS
) LOCATION: (17)..(3898)
US-10-071-223-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-946-807-702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-946-807-702/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 98
LENGTH: 5515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                          g
                                                                                                                                                            ઠે
```

ò 셤

ô

ö

Gaps

ö

Indels

Length 15531;

```
74.5%; Score 16.4; DB 9; Length 659158;
                                                                                                                                                                                                                                                                                                                     APPLICANT: MERCANO, JUAN
APPLICANT: MERCANO, JUAN
APPLICANT: HORVAI, SIMON
TITLE OF INVENTION: CLONING OF A HIGH-GROWTH GENE
FILE REFERENCE: 407T-923710US
FILE REFERENCE: 407T-923710US
CURRENT PILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 08/999,477
PRIOR APPLICATION NUMBER: US 08/999,477
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VERSION 3.0
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 2010
LENGTH: 659158
                                DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ຫ້
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ຫ້
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   c, g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 တ်
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ϋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ϋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ů
                                  74.5%; Score 16.4; D
94.4%; Pred. No. 99;
cive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (546598)..(547017)
OTHER INFORMATION: n is unidentified a, c,
NAME/KEY: misc feature
LOCATION: (494715)..(494814)
OTHER INFORMATION: n is unidentified a, c,
NAME/KEY: misc feature
LOCATION: (390586)..(391005)
OTHER INFORMATION: n is unidentified a, c,
NAME/KEY: misc feature
LOCATION: (390586)..(391005)
OTHER INFORMATION: n is unidentified a, c,
OTHER INFORMATION: n is unidentified a, c,
OTHER INFORMATION: n is unidentified a, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (271829)..(271848)
OTHER INFORMATION: n is unidentified a,
NAME/KEY: misc feature
LOCATION: (183872)..(183891)
OTHER INFORMATION: n is unidentified a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (132680)..(132700)
OTHER INFORMATION: n is unidentified a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (170625)..(170645)
OTHER INFORMATION: n is unidentified a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (602466)..(602485)
OTHER INFORMATION: n is unidentified a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (123459)..(123478)
OTHER INFORMATION: n is unidentified a,
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (317174)..(317193)
OTHER INFORMATION: n is unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (280353)..(280373)
OTHER INFORMATION: n is unidentified
                                                                                                                                                                                                                                                                  Sequence 20, Application US/09771208
Patent No. US20020155564A1.
GENERAL INFORMATION:
APPLICANT: MEDRANO, JUAN
                                                                                                                                                              Db 12698 TCTTGGGGGACAGGAAGG 12715
                                                                                                                       3 TCTTTGGGGACAGGAAGG 20
                                    Query Match
Best Local Similarity 94.4
Matches 17; Conservative
US-09-764-870-600
                                                                                                                                                                                                                                         RESULT 13
US-09-771-208-20
                    INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
INVENTION: USES THEREOF
ERENCE: CL001232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                          DB 9; Length 80959;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 9; Length 15531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Sequence 600, Application US/10125540

Sequence 600, Application US/10125540

Sequence 600, Application No. US20030059875A1

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

FILE REFERENCE: PTZ1401

CURRENT APPLICATION NUMBER: US/10/125,540

CURRENT APPLICATION NUMBER: US/10/125,540

CURRENT PILING DATE: 2002-04-19

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 646

SEQ ID NO 600

LENGTH: 15531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
TITLE REPERENCE: PTZ14
CURRENT APPLICATION NUMBER: US/09/764,870
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 646
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 76.4%; Score 16.8; D
Best Local Similarity 90.0%; Pred. No. 61;
Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 16.4;
Pred. No. 99
                                           Sequence 600, Application US/09764870 Patent No. US20020042386A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (1)...(80959)
OTHER INFORMATION: n = A,T,C or G
US-09-858-546-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 75694 GCTCTTTGGAGCCAGGAAGG 75675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 12698 rcrrgdddddddddd 12715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 TCTTTGGGGACAGGAAGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
US-10-125-540-600
                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 600
LENGTH: 15531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
US-09-764-870-600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
US-10-125-540-600
                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

or

တ်

or

ö

ö

ör

ö

```
Job time : 206.5 secs
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5931, Application US/09878574

Fatent No. US20020110548A1

GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rose, Thomas J.
APPLICANT: Thompson, Michael D.
ITILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
ITILE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B

CURRENT APPLICATION NUMBER: US/09/878,574

CURRENT PLING DATE: 1999-06-14

PRIOR PLING DATE: 1999-06-14

NUMBER OF SEQ ID NOS: 15775

LENGTH: 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5673, Application US/09878574
| Patent No. US200220110548A1
| Patent No. US200220110548A1
| Patent No. US200220110548A1
| APPLICANT: Byrum, Joseph R. APPLICANT: Plancas J. Thrib OF INVENTION: Michael D. TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE O
                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                              Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
73.6%; Score 16.2; DB 10; Length 256;
Best Local Similarity 85.7%; Pred. No. 1.48+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.6%; Score 16.2; DB 10; Length 275;
85.7%; Pred. No. 1.4e+02;
Live 0; Mismatches 3; Indels 0;
                                                                     1; Indels
                     Pred. No. 84;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA

ORGANISM: Glycine max

CTHER INFORMATION: Clone ID: 701097533H1

US-09-878-574-5931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701102760H1
US-09-878-574-9673
Best Local Similarity 94.4%; Promatches 17; Conservative 0;
                                                                                                                                                                             Db 39002 CTTTGGGACAGGAGGT 39019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 GCGCCTTGCGGACAGGAAGGT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GCTCTTTGGGGACAGGAAGGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GCTCTTTGGGGACAGGAAGGT 21
                                                                                                                             4 CTTTGGGGACAGGAAGGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 85.77
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                RESULT 14
US-09-878-574-5931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-878-574-9673
                                                                                                                         ሯ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
```

Search completed: April 18, 2003, 10:16:02

120 deserrecedacadea 140

g

	कुँद प्र -						
;¥ 							. !
	. *						
		•					
				*.			
			,			**************************************	
						•	¥
	*		y .				in the state of th
		en en en en en en en en en en en en en e					
		n to have the second					
			дч - -				
			· · · · · · · · · · · · · · · · · · ·		en en en en en en en en en en en en en e		
							\$
					:		
						•	
A.							•
		. *** . ***		n Amilyan in Angle Service			
	ें अ		•				
	11 B				a a		
						•	
						Richard Constitution (Constitution Constitution	
					4		. 9
					n		e e e e e e e e e e e e e e e e e e e

```
April 18, 2003, 05:48:17; Search time 1211 Seconds (Without alignments) 456.759 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49582208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pending Patents NA Main: *

1: \(\cggn2_6\)\(\text{ptodata}1/\text{pna}/\text{VSOOR}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\) \(\cdgrave{comp.}\)
GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24791104 segs, 12571243825 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cgn2_6/ptodata/1/pna/US102B
                                                                                                                      OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                gctctttggggacaggaaggtc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                             US-09-270-437D-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                        Run on:
```

```
| cgn2_6/ptodata/1/pna/US6000_COMB.seq:*
| cgn2_6/ptodata/1/pna/US6001_COMB.seq:*
| cgn2_6/ptodata/1/pna/US6001_COMB.seq:*
| cgn2_6/ptodata/1/pna/US6003_COMB.seq:*
| cgn2_6/ptodata/1/pna/US6004_COMB.seq:*
| cgn2_6/ptodata/1/pna/US6004_COMB.seq:*
| cgn2_6/ptodata/1/pna/US6005_COMB.seq:*
| cgn2_6/ptodata/1/pna/US6005_COMB.seq:*
| cgn2_6/ptodata/1/pna/US6005_COMB.seq:*
| cgn2_6/ptodata/1/pna/US6010_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/1/pna/US6041
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Special of the special state o			200	Sequence 322, App	Semience 7233, Ap	7 6 6 6	Segretaries 7233, Ap	3 0		Sednence 54639, A	Sequence 3999, Ap	Sequence 369, App	Seguence 369. App	Seguence 48934		Section of Appara	Segrence Figure 5	מלוש ידר מייים מדיי	Sednence /PIA, Ap	Sequence 7619, Ap	Sequence 7619, Ap	Sequence 7619, Ap
ID	US-09-540-229-481	US-08-903-802-1160	US-09-540-210B-29243	US-08-993-774-322	US-09-539-800-7233	US-09-539-800B-727	US-09-539-800C-727	US-60-034-975-322	US-09-644-871-2566	TIS-09-540-208-54629	CO-C- 000 000 000 011	0866-386-86-80-80	PCT-US01-01307-369	US-10-092-302-369	US-09-528-409-48934	US-09-933-524-48934	US-09-933-524A-48934	US-09-721-589-51	0137-4636-361-80-811	CT07 - C707 - C77 - C77	US-US-136-362D-7619	US-08-196-362E-7619	US-08-196-362F-7619
8	21	13	21	13	20	20	20	47	25	2	1 -	7,	-	33	19	35	35	29	ď		n 1	'n	ഗ
% Query Match Length DB	231	237	237	270	270	270	270	270	321	345	700	***	408	408	417	417	417	440	458	0 0	0 0	458	458
Query Match	88.2	88.2	88.2	88.2	88.2	88.2	88.2	88.2	88.2	88.2	0 0		7.88	88.2	88.2	88.2	88.2	88.2	88.2	C	9 0	7.88	88.2
Score	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4		4.4	19.4	19.4	19.4	19.4	19.4	19.4	10.4		L 7.	19.4
Result No.	-	7	m	4	Ŋ	<b>9</b>	7	80	σı	10	11	1.5	7 .	ີ .	T .	15	91	17	18	13	1 6	2 6	77

Sequence 7619, Ap

```
Sequence 22243, Application US/09540210B

Sequence 22243, Application US/09540210B

Sequence 22243, Application US/09540210B

GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
ITLE REFERENCE: PD-1037 CIP 2002-04-03
CURRENT APPLICATION NUMBER: 108/972,899
PRIOR APPLICANTION NUMBER: 08/972,899
PRIOR APPLICANTION NUMBER: 08/395,244
APPLICANT: Stuart, Susan G.
APPLICANT: Ito, Laura Y.
APPLICANT: Akerblom, Ingrid E.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Naughton, Rebecca E.
TILLE OF INVENTION: POLYMOCLEOTIDES AND POLYPEPTIDES
TITLE OF INVENTION: DERIVED FROM HUMAN BLADDER
NUMBER OF SEQUENCES: 1441
CORRESPONDENCE ADDRESS:
ADDRESSES: ANGYTE PHARMACEUTICALS, INC.
STREET: 31.7 PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA.
TITLE CALIFORNIA
COUNTRY: 18404
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/903,802
FILING DATE: HERRWITH
FILING DATE: HERRWITH
FILING DATE: HERRWITH
FILING DATE: HORRY: 00/023,308
FILING DATE: ULLY 31, 1996
CLASSIFICATION NUMBER: 60/023,308
FILING DATE: JULY 31, 1996
CLASSIFICATION NUMBER: 90.020
REGISTRATION NUMBER: 99.132
REFERENCE/DOCKET NUMBER: PD-0202 US
REFERENCE/DOCKET NUMBER: PD-0202 US
REFERENCE/DOCKET NUMBER: PD-0202 US
TELEFRAION (415) 845-4166
INFORMATION FOR SEQ ID NO: 1160:
SEQUENCE CHARACTER STICS:
LENGTH: 237 base pairs
TYPE INUCLEIC acid
STREET DATE BINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 19.4; DB 13;
Pred. No. 1.3e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 ĠĊTĊŤŤŤĠĠĠĠĠĊĠĠĠĀĠĠŤ 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.2%;
Best Local Similarity 95.2%;
Matches 20; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linea
MOLECULE TYPE: CL
IMMEDIATE SOURCE:
CLONE: 1322001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
US-09-540-210B-29243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-903-802-1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature;
NAME/KEY: misc_feature;
NOTHER INFORMATION: Incyte ID No: hu00195332
NOTHER INFORMATION: 23-24, 33, 35, 39, 54, 94-95, 101, 113-114, 173, 182, 194, 198, 10CATION: 2, 11, 23-24, 33, 35, 39, 54, 94-95, 101, 113-114, 173, 182, 194, 198, 10CATION: 2, 11, 23-24, 33, 35, 39, or other
US-09-540-229-481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Scilhamer, Jeffrey J.
APPLICANT: Scilhamer, Angelo M.
APPLICANT: Scilhamer, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuare L.
APPLICANT: Mudlahy, Sara J.
APPLICANT: Mudlahy, Sara J.
APPLICANT: Mudlahy, Sara J.
APPLICANT: Mudlahy, Sara J.
APPLICANT: Mudlahy, Sara J.
APPLICANT: Mudlahy, Sara J.
APPLICANT: Mudlahy, Sara J.
APPLICANT: Mudlahy, Sara J.
APPLICANT: Mudlahy, Sara J.
APPLICANT: Mudlahy, Sara J.
APPLICANT: Mudlahy, Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J.
APPLICANT: Mudlahy Sara J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Appli
Sequence 113, App
Sequence 113, App
Sequence 6, Appli
Sequence 6, Appli
Sequence 27652, A
                                                                                                            Sequence 49810, A
Sequence 49810, A
Sequence 49810, A
Sequence 410, Appl
Sequence 6785, Ap
Sequence 6785, Ap
Sequence 1, Appli
Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6786, Ap
Sequence 146, App
Sequence 146, App
Sequence 48, App
Sequence 329, App
                                      Sequence 7619, Ap
Sequence 680, App
Sequence 680, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                               Sequence 1,
Sequence 8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 88.2%; Score 19.4; DB 21; Length 231; Best Local Similarity 95.2%; Pred. No. 1.38+02; Matches 20; Conservative 0; Mismatches 1; Indels 0;
                                                                  US-10-097-340-146
US-60-406-385-48
PCT-US01-01341-329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
US-08-903-802-1160
; Sequence 1160, Application US/08903802
; GENERAL INFORMATION:
APPLICANT: Gooding, Douglas H.
; APPLICANT: Stuve, Laura L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 481, Application US/09540229
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 GCTCTTTGGGGACAGGAAGCT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GCTCTTTGGGGACAGGAAGGT 21
                                                   458
465
465
467
467
698
6010
2010
2035
2035
2035
33283
3374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Homo sapiens
```

ö

ö

셤 ð

Length 237;

```
PRIOR APPLICATION NUMBER: 08/72, 925
PRIOR APPLICATION NUMBER: 08/026, 586
PRIOR APPLICATION NUMBER: 08/026, 586
PRIOR APPLICATION NUMBER: 08/024, 1995
PRIOR APPLICATION NUMBER: 08/024, 1995
PRIOR APPLICATION NUMBER: 08/024, 1995
PRIOR APPLICATION NUMBER: 08/024, 1997
PRIOR PILING DATE: MATCH 25, 1997
PRIOR PILING DATE: MATCH 25, 1996
PRIOR PILING DATE: MATCH 26/026, 447
PRIOR PELICATION NUMBER: 06/021, 308
PRIOR PILING DATE: JULY 31, 1997
PRIOR PILING DATE: JULY 31, 1996
PRIOR PILING DATE: JULY 31, 1996
PRIOR PILING DATE: JULY 31, 1996
PRIOR PILING DATE: JULY 31, 1996
PRIOR PILING DATE: JULY 31, 1997
PRIOR PILING DATE: JULY 31, 1997
PRIOR PILING DATE: JULY 31, 1997
PRIOR PILING DATE: JULY 31, 1997
PRIOR PILING DATE: JULY 31, 1997
PRIOR PILING DATE: JULY 31, 1997
PRIOR PILING DATE: JULY 31, 1997
PRIOR PILING DATE: JULY 31, 1997
PRIOR PILING DATE: JULY 31, 1997
PRIOR PILING DATE: JULY 31, 1997
PRIOR PILING DATE: JULY 31, 1997
PRIOR PILING DATE: JULY 31, 1997
PRIOR PILING DATE: JULY 31, 1997
PRIOR PILING DATE: JULY 31, 1997
PRIOR PILING DATE: JULY 31, 1997
PRIOR PILING DATE: JULY 31, 1997
PRIOR PILING DATE: JULY 31, 1997
PRIOR PILING DATE: JULY 31, 1997
PRIOR PILING DATE: JULY 31, 1997
PRIOR PILING DATE: JULY 31, 1997
PRIOR PILING DATE: JULY 31, 1997
PRIOR PILING DATE: JULY 31, 1997
PRIOR PILING DATE: JULY 31, 1997
PRIOR PILING DATE: JULY 31, 1997
PRIOR PILING DATE: SEPTEMER: 60/025, 524
PRIOR PELICATION NUMBER: 60/025, 524
PRIOR PELICATION NUMBER: 60/025, 524
PRIOR PELICATION NUMBER: 60/025, 524
PRIOR PELICATION NUMBER: 60/025, 524
PRIOR PELICATION NUMBER: 60/025, 524
PRIOR PELICATION NUMBER: 60/025, 524
PRIOR PELICATION NUMBER: 60/025, 524
PRIOR PELICATION NUMBER: 60/025, 524
PRIOR PELICATION NUMBER: 60/025, 524
PRIOR PELICATION NUMBER: 60/025, 524
PRIOR PELICATION NUMBER: 60/025, 524
PRIOR PELICATION NUMBER: 60/025, 524
PRIOR PELICATION NUMBER: 60/025, 524
PRIOR PELICATION NUMBER: 60/025, 525
PRIOR PELICATION NUMBER: 60/025, 525
PRIOR PELICATION NUMBER: 60/025, 525
PRIOR PELICATION NUMBER: 60/025, 525
PRIOR PE
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gooding, Douglas H.
APPLICANT: Stuve, Laura L.
APPLICANT: Stuve, Laura L.
APPLICANT: Stuart, Susan G.
APPLICANT: Ito, Laura Y.
APPLICANT: Ito, Laura Y.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Naughton, Rebect
APPLICANT: Naughton, Rebect
APPLICANT: Naughton, Rebect
APPLICANT: Naughton, RESINTENT TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM TITLE OF INVENTION: MESENTENT TWOR MESENTENT TWOR MESENGES.
ADDRESSES: INCTE PHARMACCUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.2%; Score 19.4; DB 21; Length 237; 95.2%; Pred. No. 1.3e+02; Live 0; Mismatches 1; Indele 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTER: USAN
ZIP: 94304
COMPOTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC Comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,774
CLASSIFICATION: 336
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 99,132
REFERENCE/DOCKET NUMBER: 99-0300P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION PROPRATION:
TELECOMMUNICATION PROPRATION:
TELECOMMUNICATION PROPRATION:
TELECOMMUNICATION PROPRATION:
TELECOMMUNICATION PROPRATION:
TELECOMMUNICATION PROPRATION:
TELECOMMUNICATION PROPRATION:
TELECOMMUNICATION PROPRATION:
TELECOMMUNICATION PROPRATION:
TELECOMMUNICATION PROPRATION:
TELECOMMUNICATION PROPRATION:
TELECOMMUNICATION PROPRATION:
TELECOMMUNICATION PROPRATION:
TELECOMMUNICATION PROPRATION:
TELECOMMUNICATION PROPRATION:
TELECOMMUNICATION PROPRATION:
TELECOMMUNICATION PROPRATION:
TELECOMMUNICATION PROPRATION:
TELECOMMUNICATION PROPRATION:
TELECOMMUNICATION PROPRATION:
TELECOMMUNICATION PROPRATION:
TELECOMMUNICATION PROPRATION:
TELECOMMUNICATION PROPRATION:
TELECOMMUNICATION PROPRATION:
TELECOMMUNICATION PROPRATION:
TELECOMMUNICATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPRATION PROPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: hu00029997
US-09-540-210B-29243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
STATE: CALIFORNIA
COUNTRY: USA
                                                                                              PRIOR PILING DATE: May 29, 1997
PRIOR PILING DATE: May 29, 1997
PRIOR APPLICATION NUMBER: 09/107,592
PRIOR APPLICATION NUMBER: 60/052,751
PRIOR PILING DATE: July 1, 1997
PRIOR PILING DATE: July 1, 1997
PRIOR PILING DATE: July 1, 1997
PRIOR PILING DATE: June 9, 1998
PRIOR PILING DATE: June 13, 1997
PRIOR PILING DATE: June 13, 1997
NUMBER OF SEQ ID NOS: 35654
SOFTWARE: PERL PROGRAM
SOFTWARE: PERL PROGRAM
SEQ ID NO 29243
09/074,999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 322, Application US/08993774
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MATION:
Gooding, Douglas H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 GCTCTTTGGGGACAGGAAGCT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GCTCTTTGGGGACAGGAAGGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
```

```
111 GCTCTTTGGGGACAGGAAGCT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
US-09-539-800C-7233
                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88.2%; Score 19.4; DB 20; Length 270; 95.2%; Pred. No. 1.3e+02; ive 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNCLECTIDES OF CONNECTIVE TISSUE
FILE REFERENCE: PD-1023 CIP
CURRENT APPLICATION NUMBER: US/09/539,800
PRIOR APPLICATION NUMBER: 2000-03-30
PRIOR PLING DATE: 2000-03-30
PRIOR PLING DATE: August 16, 1995
PRIOR PLING DATE: August 16, 1995
PRIOR APPLICATION NUMBER: 08/271,217
                                                                                                                                                                                                                                                                                                                      Query Match

88.2%; Score 19.4; DB 13;
Best Local Similarity 95.2%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER:

PRIOR FILING DATE:
PRIOR FILING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
PRIOR PILING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DATE:
PRIOR PELING DA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: hu00328727
US-09-539-800-7233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: December 10, 1998
NUMBER OF SEQ ID NOS: 19698
SEQ ID NO 7233
LENGTH: 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09539800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seilhamer, Jeffrey J.
Delegeane, Angelo M.
Stuart, Susan G.
Stuye, Laura L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 95.2
The Conservative
                 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                         TOPOLOGY: linear MOLECULE TYPE: CDNA IMMEDIATE SOURCE: CLONE: 2502822H1 US-08-993-774-322
                                                                                                                                            CDNA
```

```
Length 270;
                                                                                                                                                                                                                                               APPLICANT: BLUNE, MALLAHY, SAIA J.
APPLICANT: MULAHY, SAIA J.
APPLICANT: MAUGHTON Rebecca E.
TITLE OF INVENTION: POLINUCLEOTIDES OF CONNECTIVE TISSUE
FILE REFERENCE: PD-1023 CIP
CURRENT APPLICATION NUMBER: US/09/539,800B
CURRENT FILING DATE: A00-03-30
PRIOR APPLICATION NUMBER: 08/521,383
PRIOR PILING DATE: JUME 27, 1994
PRIOR PILING DATE: JUME 27, 1994
PRIOR PLING DATE: JUME 7, 1994
PRIOR PLING DATE: OCCODER 4, 1994
PRIOR PLING DATE: OCCODER 4, 1996
PRIOR PLING DATE: OCCODER 4, 1996
PRIOR PLING DATE: OCCODER 4, 1996
PRIOR PLING DATE: OCCODER 4, 1996
PRIOR PLING DATE: OCCODER 4, 1996
PRIOR PLING DATE: OCCODER 4, 1996
PRIOR PLING DATE: DECEMBER 109/27, 74
PRIOR PLING DATE: DCCODER 4, 1996
PRIOR PLING DATE: DCCODER 4, 1999
PRIOR PLING DATE: DCCODER 19, 1999
PRIOR PLING DATE: PEDRUARY 12, 1998
PRIOR PLING DATE: PEDRUARY 12, 1998
PRIOR PLING DATE: PEDRUARY 12, 1998
PRIOR PLING DATE: PEDRUARY 12, 1998
PRIOR PLING DATE: PEDRUARY 12, 1998
PRIOR PLING DATE: DECEMBER 10, 1999
PRIOR PLING DATE: DECEMBER 10, 1999
PRIOR PRIOR DATE: DECEMBER 10, 1999
PRIOR PLING DATE: DECEMBER 10, 1999
PRIOR PRIOR DATE: DECEMBER 10, 1999
PRIOR PLING DATE: DECEMBER 10, 1999
PRIOR PLING DATE: PEDRUARY 12, 1998
PRIOR PLING DATE: PEDRUARY 12, 1998
PRIOR PLING DATE: PEDRUARY 12, 1998
PRIOR PLING DATE: PEDRUARY 12, 1998
PRIOR PLING DATE: PEDRUARY 12, 1998
PRIOR PLING DATE: PEDRUARY 12, 1998
PRIOR PLING DATE: PEDRUARY 12, 1998
PRIOR PLING DATE: PEDRUARY 12, 1998
PRIOR PLING DATE: PEDRUARY 12, 1998
PRIOR PLING DATE: PEDRUARY 12, 1998
PRIOR PLING DATE: PEDRUARY 12, 1998
PRIOR PLING DATE: PEDRUARY 12, 1998
PRIOR PLING DATE: PEDRUARY 12, 1998
PRIOR PLING DATE: PEDRUARY 12, 1998
PRIOR PLING DATE: PEDRUARY 12, 1998
PRIOR PLING DATE: PEDRUARY 12, 1998
PRIOR PLING DATE: PEDRUARY 12, 1998
PRIOR PLING DATE: PEDRUARY 12, 1998
PRIOR PLING DATE: PEDRUARY 12, 1998
PRIOR PLING DATE: PEDRUARY 12, 1998
PRIOR PLING DATE: PEDRUARY 12, 1998
PRIOR PLING DATE: PEDRUARY 12, 1999
PRIOR PLING DATE: PEDRUARY 12, 1999
PRIOR PLING DATE: PEDRUARY 12, 1999
PRIOR PLING DATE: PED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.2%; Score 19.4; DB 20;
95.2%; Pred. No. 1.3e+02;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu00328727
US-09-539-800B-7233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7233, Application US/09539800C GENERAL INFORMATION:
Sequence 7233, Application US/09539800B
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 gcrcrrrddddacaddaadcr 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GCTCTTTGGGGACAGGAAGGT 21
                                                                                      APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 95.2
Matches 20; Conservative
```

Gaps

```
Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.2%; Score 19.4; DB 47; Length 270; 95.2%; Pred. No. 1.3e+02; Live 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

88.2%; Score 19.4; DB 25; Length 321;
Best Local Similarity 95.2%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: HOLTEMATION:
APPLICANT: HOLTEMAN, Douglas A.
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES;
TITLE OF INVENTION: HEREPOR;
FILE REPERENCE: 1600.1167-001
CURRENT APPLICATION NUMBER: US/09/644,871
CURRENT FILING DATE: 2000-08-28
PRIOR APPLICATION NUMBER: 60/151,059
PRIOR PILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 9739
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2566
LENGTH: 321
                                                                                                                       **MEDIUM ITEE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
PILING DATE:
CLASSIFICATION:
MAME: CERRONE, MICHAEL C.
REGISTRATION:
MAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: 39,132
REFERENCE/DOCKET NUMBER: 9D-0300P
TELECPHONE: (415) 845-4166
INFORMATION FOR SEQ ID NO: 322:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 Dass pairs
TYPE: nucleic acid
SEQUENCE CHARACTERISTICS:
LENGTH: 270 Dass pairs
MOLECULE TYPE: CDNA
MOLECULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOLECULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE TYPE: CDNA
MOMESCULE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-644-871-2566; Sequence 2566, Application US/09644871; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
US-09-540-208-54639
; Sequence 54639, Application US/09540208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(321)

OTHER INFORMATION: n = A,T,C or G
US-09-644-871-2566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 GCTCTTTGGGGACAGGAGCT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 GCTCTTTGGGGACAGGAAGCT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GCTCTTTGGGGACAGGAGGT 21
                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 95.2
Matches 20, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gooding, Douglas H.
APPLICANT: Stuve, Laura L.
APPLICANT: Stuve, Laura L.
APPLICANT: Stuart, Susan G.
APPLICANT: Ito, Laura B.
APPLICANT: Akerblom, Ingrid E.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM TITLE OF INVENTION: MESENTERY TUMOR NOW PROCESSIONE FROM TITLE OF SEQUENCES: 4086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

88.2%; Score 19.4; DB 20; Length 270;
Best Local Similarity 95.2%; Pred. No. 1.38+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0
APPLICANT: Naughton, Rebecca E.

TITLE OF INVENTION: POLYNUCLEOTIDES OF CONNECTIVE TISSUE
CURRENT APPLICATION NUMBER: US/09/539, 800C
CURRENT PILING DATE: 2000-03-30
PRIOR PLILING DATE: 1000-03-30
PRIOR PLILING DATE: JUNE 27, 1994
PRIOR PLILING DATE: MUMBER: 08/521, 383
PRIOR PLILING DATE: MUMBER: 08/271, 217
PRIOR PLILING DATE: JUNE 27, 1994
PRIOR PLILING DATE: OF 1994
PRIOR PLILING DATE: OCCODER 4, 1997
PRIOR PLILING DATE: COCCODER 4, 1997
PRIOR PLILING DATE: COCCODER 4, 1997
PRIOR PLILING DATE: COCCODER 4, 1997
PRIOR PLILING DATE: COCCODER 4, 1997
PRIOR PLILING DATE: COCCODER 4, 1997
PRIOR PLILING DATE: COCCODER 4, 1997
PRIOR PLILING DATE: COCCODER 4, 1997
PRIOR PLILING DATE: COCCODER 4, 1997
PRIOR PLILING DATE: COCCODER 4, 1997
PRIOR PLILING DATE: COCCODER 4, 1997
PRIOR PLILING DATE: COCCODER 4, 1997
PRIOR PLILING DATE: COCCODER 4, 1997
PRIOR PLILING DATE: COCCODER 4, 1997
PRIOR PLILING DATE: PECCEMBER: 09/452, 774
PRIOR PLILING DATE: PECCEMBER: 09/452, 747
PRIOR PLILING DATE: PEDCEMBER: 09/452, 747
PRIOR PLILING DATE: PECCEMBER: 1, 1999
PRIOR PLILING DATE: DECEMBER: 1, 1999
PRIOR PLILING DATE: DECEMBER: 09/452, 747
PRIOR PLILING DATE: DECEMBER: 09/452, 747
PRIOR PLILING DATE: DECEMBER: 09/452, 747
PRIOR PRILING DATE: DECEMBER: 09/452, 747
PRIOR PLILING DATE: DECEMBER: 09/452, 747
PRIOR PLILING DATE: DECEMBER: 09/452, 747
PRIOR PLILING DATE: DECEMBER: 09/452, 747
PRIOR PRILING DATE: DECEMBER: 09/452, 747
PRIOR PRILING DATE: DECEMBER: 09/452, 747
PRIOR PRILING DATE: DECEMBER: 09/452, 747
PRIOR PRILING DATE: DECEMBER: 09/452, 747
PRIOR PRILING DATE: DECEMBER: 09/452, 747
PRIOR PRILING DATE: DECEMBER: 00/11, 910
PRIOR PRILING DATE: DECEMBER: 00/11, 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               i NAME/KEY: misc_feature
i OTHER INFORMATION: Incyte ID No: hu00328727
US-09-539-800C-7233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSER: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/60034975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db ' 111 GCTCTTTGGGACAGGAGCT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 322, Applica
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-60-034-975-322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
```

ö

```
PCT-US01-01307-369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
US-10-092-302-369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                  APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Laura L.
APPLICANT: Stuart, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
FILE REFERENCE: PD-1029 CIP
CURRENT APPLICATION NUMBER: US/09/540,208
CURRENT APPLICATION NUMBER: US/09/03-31
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 70811
SOFTWARE: PERL Program
SEQ ID NO 54639
LENGTH: 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 19.4; DB 17; Length 384;
Pred. No. 1.46+02;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFURGATION:
APPLICANT: HOIZMAN, DOUGIAS A.
APPLICANT: GEATING, DAVID P.
TITLE OF INVENTION: NUCLEIC AID MOLECULES DERIVED FROM A
TITLE OF INVENTION: HUMAN BURKITT'S LYMPHOWA LIBRARY
FILE REPERENCE: MAN98-47PM
CURRENT APPLICATION NUMBER: 06/100,464
PRIOR PELICATION NUMBER: 60/100,464
PRIOR PELICATION NUMBER: 60/101,670
PRIOR PELICATION NUMBER: 60/101,670
PRIOR APPLICATION NUMBER: 60/101,670
PRIOR PELICATION NUMBER: 60/106,456
PRIOR PELICATION NUMBER: 60/106,926
PRIOR PILING DATE: 1998-09-23
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1999-04-30
PRIOR PILING DATE: 1999-04-30
PRIOR PILING DATE: 1999-04-30
PRIOR PILING DATE: 1999-04-30
PRIOR PILING DATE: 1999-04-30
PRIOR PILING DATE: 1999-04-30
PRIOR PILING DATE: 1999-04-30
PRIOR PILING DATE: 1999-04-30
PRIOR PILING DATE: 1999-04-30
PRIOR PILING DATE: 1999-04-30
PRIOR PILING DATE: 1999-04-30
PRIOR PILING DATE: 1999-04-30
PRIOR PILING DATE: 1999-04-30
PRIOR PILING DATE: 1999-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 88.2%; Score 19.4; DB 21; Length 345; Best Local Similarity 95.2%; Pred. No. 1.4e+02; Matches 20; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature; OTHER INFORMATION: Incyte ID No: hu01153334 US-09-540-208-54639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 3999, Application US/09399932 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 dererrededakeksekser 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTCTTTGGGGACAGGAAGGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 GCTCTTTGGGGACAGGAAGCT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTCTTTGGGGACAGGAAGGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CRGANISM: Homo sapiens
US-09-399-932-3999
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
US-09-399-932-3999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 3999
LENGTH: 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
```

RESULT 12

```
Gaps
Sequence 369, Application PC/TUS0101307
; Sequence 369, Application PC/TUS0101307
; GENERAL INFORMATION:
   APPLICANT: Human Genome Sciences, Inc., et al.
   APPLICANT: Human Genome Sciences, Inc., et al.
   TILE REFERENCE: PT218PCT
; CURRENT APPLICATION NUMBER: PCT/US01/01307
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper; NUMBER OF SEQ ID NOS: 1040
; SEQ ID NO 369
; SEQ ID NO 369
; LENGTH: 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.2%; Score 19.4; DB 1; Length 408; 95.2%; Pred. No. 1.4e+02; 1ve 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PT21801
CURRENT APPLICATION NUMBER: US/10/092,302
CURRENT APPLICATION NUMBER: US/20-03-07
NUMBER OF SEQ ID NOS: 1040
Prior Application removed - See File Wrapper or Palm
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (328)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (337)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (363)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (1683)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (385)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OT. C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (363)
OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (385)
OTHER INFORMATION: n equals a,t,9, or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or
                                                                                                                                                                                                                                                                                                                                                                                                                                     or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (328)
OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 369, Application US/10092302
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (124)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
FOCATION: (328)
                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (124)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (337)
OTHER INFORMATION: n equals a,t,9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GCTCTTTGGGGACAGGAGGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 GCTCTTTGGGGACAGGAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
```

```
ö
                                                                                                                                      Gaps
                                                                                                                                    ..
0
                                                                                      Length 408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

88.2%; Score 19.4; DB 19; Length 417;
Best Local Similarity 95.2%; Pred. No. 1.48+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Generace 48934, Application US/09933524
GENERAL INFORMATION:
APPLICANT: Drmanac, Radoje T.
APPLICANT: Labar, Ivan
APPLICANT: Labar, Ivan
APPLICANT: Bickeor, Mark
APPLICANT: Dickson, Mark
APPLICANT: Jones, Lee W.
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: From Various Libraries
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 77
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 09/528,409
PRIOR APPLICATION NUMBER: 09/528,409
PRIOR APPLICATION NUMBER: 09/528,409
PRIOR APPLICATION NUMBER: 09/528,409
PRIOR APPLICATION VIBER: 2000-03-17
NUMBER OF SEQ ID NOS: 116231
SOFTWARE: Hy-patent.pl Version 3.1
LENTH: 417
                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Dramac, Radoje T.
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Jones, Lee W
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
FILE REFERENCE: 774
                                                                  Query Match

Best Local Similarity 95.2%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/528,409
CURRENT FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/125,453
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 116231
SOFTWARE: Hy-patent.pl Vergion 3.1
SEQ ID NO 48934
; OTHER INFORMATION: n equals a,t,g, or c
US-10-092-302-369
                                                                                                                                                                                                                                                                                                                                  Sequence 48934, Application US/09528409 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LCCATION: (1)...(417)
CTHER INFORMATION: n = A,T,C or G
US-09-528-409-48934
                                                                                                                                                                                              65 GCTCTTTGGGGACAGGAAGCT 85
                                                                                                                                                                     1 GCTCTTTGGGGACAGGAAGGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 Geretriegegacaggader 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GCTCTTTGGGGACAGGAAGGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
                                                                                                                                                                                                             g
                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         요
```

ô

Search completed: April 18, 2003, 09:35:47 Job time : 1212 secs

			·
			·
E.F.			
•			
a.			
*			
		and the second of the second o	
		the second secon	
	and the second of the second o		
<b>4</b>			
∰y Li			
	and the state of the state of the state of the state of the state of the state of the state of the state of the		en en en en en en en en en en en en en e
			•

Page

OM nucleic - nucleic search, using sw model

April 18, 2003, 06:35:28; Search time 245.167 Seconds (without alignments) 400.770 Million cell updates/sec Run on:

US-09-270-437D-13 22

1 gctctttggggacaggaaggtc 22 Perfect score: Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 5897297 seqs, 2233080881 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pending\_Patents\_NA\_New:\*

1: /cgn2\_6/ptodata/1/pna/PCT\_NEW\_COMB.seq:\*

2: /cgn2\_6/ptodata/1/pna/USG0\_NEW\_COMB.seq:\*

3: /cgn2\_6/ptodata/1/pna/USG0\_NEW\_COMB.seq:\*

4: /cgn2\_6/ptodata/1/pna/USG0\_NEW\_COMB.seq:\*

5: /cgn2\_6/ptodata/1/pna/USG0\_NEW\_COMB.seq:\*

6: /cgn2\_6/ptodata/1/pna/USG0\_NEW\_COMB.seq:\*

7: /cgn2\_6/ptodata/1/pna/USG0\_NEW\_COMB.seq:\*

8: /cgn2\_6/ptodata/1/pna/USG0\_NEW\_COMB.seq:\*

9: /cgn2\_6/ptodata/1/pna/USG0\_NEW\_COMB.seq:\*

10: /cgn2\_6/ptodata/1/pna/USG0\_NEW\_COMB.seq:\*

11: /cgn2\_6/ptodata/1/pna/USG0\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mo. Score Match Length DB ID  2 10.0  2 5 US-09-270-437D-13  2 19.4 88.2 364 6 US-09-513-999C-3265  3 19.4 88.2 364 6 US-09-513-999C-3265  5 19.4 88.2 1707 1 DCT-050-213-28701  8 19.4 88.2 1707 1 DCT-050-31357-39  9 19.4 88.2 1707 1 DCT-10-223-5179  10 19.4 88.2 3237 11 US-60-453-135-482  11 19.4 88.2 3237 11 US-60-453-135-482  12 19.4 88.2 3237 11 US-60-453-135-482  13 19.4 88.2 3237 11 US-60-453-135-482  14 19.4 88.2 3237 11 US-60-453-135-482  15 19.4 88.2 3237 11 US-60-453-135-482  16 19.4 88.2 3237 11 US-60-453-135-482  17 19.4 88.2 3427 11 US-60-453-135-3834  18 19.4 88.2 3427 11 US-60-453-135-3834  19 19 88.2 3427 11 US-60-453-135-3834  19 19 88.2 3427 11 US-60-453-135-3834  19 19 88.2 3427 11 US-60-453-135-3834  19 19 88.2 3427 11 US-60-453-135-3834  19 19 88.2 3427 11 US-60-453-135-3834  19 19 88.2 3427 11 US-60-453-135-3834  19 19 88.2 3427 11 US-60-453-135-3834  19 19 88.2 3427 11 US-60-453-135-3834  19 19 88.2 3427 11 US-60-453-135-3834  19 19 88.2 3427 11 US-60-453-135-3834  19 19 88.2 3425 11 US-60-453-135-3834  20 19 88.2 3475 11 US-60-453-135-3835  20 19 88.2 3475 11 US-60-453-135-3835  20 19 88.2 3475 11 US-60-453-135-3835  20 19 88.2 3475 11 US-60-453-135-3835  20 19 88.2 3475 11 US-60-453-135-3835  21 18 88.5 30922 7 US-09-949-016-16/00  22 18.4 83.6 598359 7 US-09-947-911-215			æ			SUMMARIES	
No. Score Match Length DB ID   Description	Result		Query				
1 22 100.0 22 5 US-09-270-437D-13 Sequence 326.5 Age 6 US-09-13-99C-326 Sequence 326.5 Age 19.4 88.2 364 6 US-09-13-99C-326 Sequence 326.7 Leg 19.4 88.2 87.1 6 US-09-724-676-8826 Sequence 228701 Sequence 326.7 19.4 88.2 1707 1 PCT-USO2-31857-39 Sequence 39. App 8 19.4 88.2 1707 1 PCT-USO2-31857-39 Sequence 39. App 19.4 88.2 3237 1 US-60-452-136-199 Sequence 512.7 11 19.4 88.2 3237 11 US-60-452-1802 Sequence 612.7 19.4 88.2 3237 11 US-60-453-135-482 Sequence 612.7 19.4 88.2 3237 11 US-60-453-135-482 Sequence 612.7 19.4 88.2 3237 11 US-60-453-135-482 Sequence 8. App 19.4 88.2 3237 11 US-60-453-135-482 Sequence 7.8 19.4 88.2 3237 11 US-60-453-135-482 Sequence 8. App 19.4 88.2 3237 11 US-60-453-135-383 Sequence 3834.7 19.4 88.2 3427 11 US-60-453-135-3834 Sequence 3834.7 19.4 88.2 3427 11 US-60-453-135-3834 Sequence 3237.7 19.4 88.2 3427 11 US-60-453-135-3834 Sequence 3237.7 19.4 88.2 3427 11 US-60-453-135-3834 Sequence 3237.7 19.4 88.2 3427 11 US-60-453-135-3834 Sequence 3237.7 19.4 88.2 3427 11 US-60-453-135-3834 Sequence 3237.7 19.4 88.2 3427 11 US-60-453-135-3834 Sequence 3237.7 19.4 88.2 3427 11 US-60-453-135-3834 Sequence 3237.7 19.4 88.2 3475 11 US-60-453-135-3835 Sequence 3237.7 19.4 88.2 3475 11 US-60-453-135-3835 Sequence 3237.7 19.4 88.2 3475 11 US-60-453-135-3835 Sequence 3235.7 19.4 88.2 3475 11 US-60-453-135-3835 Sequence 3235.7 19.4 88.2 3475 11 US-60-453-135-3835 Sequence 3235.7 19.4 88.5 30922 7 US-09-949-016-16700 Sequence 215.7 App 19.4 88.5 30922 7 US-09-949-016-16700 Sequence 215.7 App 19.4 88.5 30922 7 US-09-947-011-215	No.	Score	Match	Length	98	OI	Description
2 19.4 88.2 364 6 US-09-513-9996-3265 Sequence 226701 88.2 458 6 US-09-724-676A-8826 Sequence 226701 88.2 458 6 US-09-724-676A-8826 Sequence 226701 88.2 19.4 88.2 1707 1 PCT-USOZ-31157-39 Sequence 39. April 19.4 88.2 1707 1 PCT-USOZ-31157-39 Sequence 39. April 19.4 88.2 1707 1 PCT-USOZ-31157-39 Sequence 39. April 19.4 88.2 3237 11 US-0-452-680-612 Sequence 612. April 19.4 88.2 3237 11 US-0-452-680-612 Sequence 612. April 19.4 88.2 3237 11 US-0-452-680-612 Sequence 612. April 19.4 88.2 3237 11 US-0-452-680-612 Sequence 612. April 19.4 88.2 3237 11 US-0-452-680-612 Sequence 612. April 19.4 88.2 3237 11 US-0-452-680-612 Sequence 612. April 19.4 88.2 3427 11 US-0-453-050-882 Sequence 3834, 19.4 88.2 3427 11 US-0-453-135-3834 Sequence 3237, 19.4 88.2 3427 11 US-0-453-135-3834 Sequence 3237, 19.4 88.2 3427 11 US-0-453-135-3834 Sequence 3237, 19.4 88.2 3427 11 US-0-453-135-3834 Sequence 3237, 19.4 88.2 3427 11 US-0-453-135-3834 Sequence 3237, 19.4 88.2 3427 11 US-0-453-135-3835 Sequence 3237, 20. 19.4 88.2 3475 11 US-0-453-135-3835 Sequence 3237, 20. 19.4 88.2 3475 11 US-0-453-135-3835 Sequence 3237, 20. 19.4 88.2 3475 11 US-0-453-050-3834 Sequence 3237, 20. 19.4 88.2 3475 11 US-0-453-050-3834 Sequence 3237, 20. 19.4 88.2 3475 11 US-0-453-050-3835 Sequence 3235, 20. 19.4 88.2 3475 11 US-0-453-050-3835 Sequence 3235, 20. 19.4 88.5 30922 7 US-09-949-016-16700 Sequence 215, April 18.8 85.5 30922 7 US-09-949-016-16700 Sequence 215, April 18.8 85.5 30922 7 US-09-947-911-215	-	22	100.0	22	S	US-09-270-4370-13	
3 19.4 88.2 458 6 US-09-12-291-2820 Sequence 228701 88.2 878 6 US-09-12-293-22801 Sequence 228701 88.2 871 6 US-09-12-293-22801 Sequence 8826, 6 19.4 88.2 1707 1 VG-09-13-139 Sequence 8826, 6 19.4 88.2 1707 1 VG-08-21357-39 Sequence 39.4 Mg 88.2 1707 9 US-10-235-5179 Sequence 39.4 Mg 88.2 3237 8 US-10-235-5179 Sequence 39.4 Mg 88.2 3237 11 US-60-452-680-612 Sequence 612, 11 19.4 88.2 3237 11 US-60-453-135-482 Sequence 612, 11 19.4 88.2 3237 11 US-60-453-135-482 Sequence 612, 11 19.4 88.2 3237 11 US-60-453-135-482 Sequence 612, 11 19.4 88.2 3237 11 US-60-453-135-482 Sequence 612, 11 19.4 88.2 3237 11 US-60-453-135-393 Sequence 61, MpF 19.4 88.2 3427 11 US-60-453-135-3934 Sequence 3834, 11 US-60-453-135-3934 Sequence 3834, 11 US-60-453-135-3934 Sequence 3834, 11 US-60-453-135-3935 Sequence 3835, 21 US-60-453-135-3935 Sequence 3835, 21 US-60-453-135-3935 Sequence 3835, 21 US-60-453-135-3935 Sequence 3835, 21 US-60-453-135-3935 Sequence 3835, 21 US-60-453-135-3935 Sequence 3835, 21 US-60-453-135-3935 Sequence 3835, 21 US-60-453-135-3935 Sequence 3835, 21 US-60-453-135-3935 Sequence 215, Ms 83.5 30922 7 US-09-949-016-16700 Sequence 215, Ms	~	19.4	88.2	164	4	TIG-00-613 0000 1000	Sednence 13, Appl
19.4 88.2   19.4 89.2   19.4	m	4		7 0	٠,	13 00 010 000 11265	
1         1.5.4         88.2         87.1         6 US-09-724-676-8826         Sequence 8826, 56           6         19;4         88.2         1707         1 PCT-USO2-31357-39         Sequence 39, Apg 88.2           7         19.4         88.2         1707         9 US-10-256-445-39         Sequence 39, Apg 89.2           9         19.4         88.2         1707         9 US-10-170-135-5179         Sequence 39, Apg 89.2           10         19.4         88.2         3237         11 US-60-452-680-612         Sequence 612, Sequence 3134, Sequence 3134, Sequence 3134, Sequence 3134, Sequence 3134, Sequence 3134, Sequence 3134, Sequence 3134, Sequence 3134, Sequence 3134, Sequence 3134, Sequence 3135, Sequence 3135, Sequence 3135, Sequence 3135, Sequence 3135, Sequence 3135, Sequence 3135, Sequence 3135, Sequence 3135, Sequence 3135, Sequence 3135, Sequence 3135, Sequence 3135, Sequence 3135, Sequence 3135, Sequence 215, App 7           19.4         88.2         3475         11 US-60-453-135-3835         Sequence 3135, Sequence 3135, Sequence 3135, Sequence 3135, Sequence 3135, Sequence 3135, Sequence 3135, Sequence 3135, Sequence 3135, Sequence 3135, Sequence 3135, Sequence 3135, Sequence 315002, Sequence 315002, Sequence 315002, Sequence 315002, Sequence 315002, S	, <			7	0 1	02-03-312-233-228701	
5         19,4         88.2         87.1         6         US-09-724-676A-8826         Sequence 39.7           7         19,4         88.2         1707         1         FCT-USC2-41357-39         Sequence 39.7         Appleance 39.4           8         19.4         88.2         1707         1         Converse 39.7         Appleance 39.4         Appleance 39.4         Appleance 39.4         Appleance 39.4         Appleance 5179.4         Appleance 5179.4         Sequence 5179.4         Sequence 5179.4         Sequence 612.7         Appleance 612.7         Sequence 612.7         Sequence 612.7         Appleance 612.7         Appleance 612.7         Appleance 612.7         Appleance 612.7         Appleance 612.7         Appleance 612.7         Appleance 612.7         Appleance 612.7         Appleance 612.7         Appleance 612.7         Appleance 612.7         Appleance 612.7         Appleance 612.7         Appleance 612.7<	ر	4. V	88.2	871	9	US-09-724-676-8826	Section of a section S
6 1974 88.2 1707 1 PCT-USO2-31357-39 Sequence 39. Apple 19.4 88.2 1707 9 US-10-562-445-39 Sequence 39. Apple 19.4 88.2 3237 11 US-60-452-680-612 Sequence 519. Apple 19.4 88.2 3237 11 US-60-452-680-612 Sequence 612. Sequence 612. 19.4 88.2 3237 11 US-60-453-052-482 Sequence 612. 19.4 88.2 3237 11 US-60-453-052-482 Sequence 612. 19.4 88.2 3237 12 US-09-270-437D-8 Sequence 8. Apple 19.4 88.2 3427 11 US-60-453-052-1870 Sequence 3834, 17 19.4 88.2 3427 11 US-60-453-052-3834 Sequence 3834, 17 19.4 88.2 3427 11 US-60-453-052-3834 Sequence 3834, 18 19.4 88.2 3427 11 US-60-453-052-3834 Sequence 3834, 19 19.4 88.2 3475 11 US-60-453-052-3835 Sequence 3835, 21 18.4 88.5 30922 7 US-09-949-016-16700 Sequence 3835, 21 18.8 85.5 30922 7 US-09-947-911-215 Sequence 215, A	C)	19.4	88.2	871	ø	US-09-724-676A-8826	Somiones open
7 19.4 88.2 1707 9 US-10-262-445-39 Sequence 39, Ap 9 19.4 88.2 3237 8 US-10-10-125-5179 Sequence 5179, Ap 19.4 88.2 3237 11 US-60-452-680-612 Sequence 5179, Ap 19.4 88.2 3237 11 US-60-453-050-482 Sequence 5179, Ap 19.4 88.2 3237 11 US-60-453-15-482 Sequence 5179, Ap 19.4 88.2 3237 11 US-60-453-15-892 Sequence 482, 13 19.4 88.2 3427 11 US-60-453-15-21870 Sequence 21870, 19.4 88.2 3427 11 US-60-453-135-383 Sequence 3834, 17 19.4 88.2 3427 11 US-60-453-135-383 Sequence 3834, 17 19.4 88.2 3427 11 US-60-453-050-3834 Sequence 3834, 17 19.4 88.2 3427 11 US-60-453-050-3834 Sequence 3287, 18 19.4 88.2 3475 11 US-60-453-135-3835 Sequence 3206, 21 18.8 85.5 30922 7 US-09-949-016-16700 Sequence 215, Ap 18.8 33.6 598359 7 US-09-947-911-215 Sequence 215, Ap 18.8	φ	19.4	88.2	1707	-	PCT-US02-31357-39	Sequence 6626, Ap
8 19.4 88.2 3237 8 US-10-170-235-5179 Sequence 5179, 40 19.4 88.2 3237 11 US-60-452-680-612 Sequence 5179, 10 19.4 88.2 3237 11 US-60-452-680-612 Sequence 612, 11 19.4 88.2 3237 11 US-60-453-050-482 Sequence 482, 11 19.4 88.2 3241 11 US-60-453-050-482 Sequence 612, 19.4 88.2 3412 5 US-09-270-4370-6 Sequence 61, App. 19.4 88.2 3427 11 US-60-453-050-3834 Sequence 3184, 17 19.4 88.2 3427 11 US-60-453-050-3834 Sequence 3184, 18.1 US-60-452-680-3337 Sequence 3184, 19.1 US-60-452-680-3337 Sequence 31834, 19.1 US-60-452-680-3337 Sequence 31834, 21.1 US-60-452-680-3337 Sequence 31835, 21.1 US-60-453-050-3834 Sequence 31835, 21.1 US-60-453-050-3834 Sequence 31835, 21.1 US-60-453-050-3835 Sequence 31835, 21.1 US-60-453-050-3835 Sequence 31835, 21.1 US-60-453-050-3835 Sequence 31835, 21.1 US-60-453-050-3835 Sequence 31835, 21.1 US-60-453-050-3835 Sequence 31835, 21.1 US-60-453-050-3835 Sequence 31835, 21.1 US-60-453-050-3835 Sequence 2155, A.	7	19.4	88.2	1707	σ	115-10-262-445-20	Seduence 39, Appl
9 19.4 88.2 327, 0 CSTO-LTO-LSS-51/9 Sequence 5179, 19.4 88.2 3237 11 US-60-452 680-642 Sequence 612, 11 19.4 88.2 3237 11 US-60-453-050-482 Sequence 612, 12 19.4 88.2 3237 11 US-60-453-050-482 Sequence 482, 13 19.4 88.2 3283 1 US-60-270-437D-8 Sequence 6. Appl 19.4 88.2 3427 11 US-60-453-1050-80-80-80-80-80-80-80-80-80-80-80-80-80	æ	19.4	88.2	2027	١ ۵	DO 104 OF 01 01	Sednence 39, Appl
10 19.4 88.2 32.4 11 US-60-452.680-612 Sequence 612, 32.3 11 US-60-452.680-612 Sequence 612, 32.3 11 US-60-453-135-482 Sequence 612, 32.3 11 US-60-453-135-482 Sequence 482, 32.3 11 US-60-453-050-482 Sequence 482, 32.3 11 US-60-453-050-482 Sequence 8, App. 14 88.2 342.7 11 US-60-452-1870 Sequence 3834, 15 19.4 88.2 342.7 11 US-60-453-135-383 Sequence 3834, 32.3 11 US-60-452-680-323.7 Sequence 3834, 32.3 11 US-60-452-680-323.7 Sequence 3237, 32.3 19.4 88.2 3475 11 US-60-452-680-323.7 Sequence 3237, 32.3 19.4 88.2 3475 11 US-60-452-680-323.7 Sequence 3237, 32.3 19.4 88.2 3475 11 US-60-452-680-323.7 Sequence 3237, 32.3 18.4 88.5 30922 7 US-09-949-016-16700 Sequence 215, A. Sequence	0			1000	,	6/TG-GEZ-0/T-0T-CO	Sequence 5179, Ap
19.4 88.2 3237 11 US-60-453-135-482 Sequence 482, 11 19.4 88.2 3237 11 US-60-453-050-482 Sequence 482, 12 19.4 88.2 3283 5 US-09-270-437-8 Sequence 8, Appl 19.4 88.2 3412 5 US-09-270-4370-6 Sequence 6, Appl 19.4 88.2 3427 8 US-10-170-235-21870 Sequence 318.0, 19.4 88.2 3427 11 US-60-453-050-3834 Sequence 318.0, 19.4 88.2 3427 11 US-60-453-050-3834 Sequence 318.4, 17 19.4 88.2 3427 11 US-60-453-050-3834 Sequence 318.4, 19.4 88.2 3475 11 US-60-453-050-3835 Sequence 318.5, 19.4 88.2 3475 11 US-60-453-050-3835 Sequence 318.5, 20 19.4 88.2 3475 11 US-60-453-050-3835 Sequence 318.5, 21 18.8 85.5 30922 7 US-09-949-016-16700 Sequence 215, Appl 21 US-60-453-050-3835 Sequence 215, Appl 22 18.4 83.6 598359 7 US-09-947-911-215 Sequence 215, Appl 22 18.4 83.6 598359 7 US-09-947-911-215	, (	1	200	3237	7	US-60-452-680-612	Sequence 612. App
11 19.4 88.2 3237 11 US-60-453-050-482 Sequence 482. 12 19.4 88.2 3283 5 US-92-70-437D-8 Sequence 8. App 14 88.2 3422 5 US-92-70-437D-8 Sequence 8. App 15 19.4 88.2 3427 11 US-60-453-185-3834 Sequence 21870. 15 19.4 88.2 3427 11 US-60-453-135-3834 Sequence 3834, 17 19.4 88.2 3427 11 US-60-453-135-3834 Sequence 3834, 18 19.4 88.2 3427 11 US-60-453-135-3834 Sequence 3834, 18 19.4 88.2 3475 11 US-60-452-680-327 Sequence 3206, 20 19.4 88.2 3475 11 US-60-453-135-3835 Sequence 3206, 20 19.4 88.2 3475 11 US-60-453-050-335 Sequence 3335, 20 19.4 88.5 30922 7 US-09-949-016-16700 Sequence 215, A, 18.8 85.5 30922 7 US-09-949-016-16700 Sequence 215, A, Sequence 215, A, Sequence 215, A, Sequence 215, A, Sequence 215, A, Sequence 215, A, Sequence 215, A, Sequence 215, A, Sequence 215, A, Sequence 215, A, A, Sequence 215, A, B, Sequence 215, B, Sequence 215, A, B, Sequence 215, B, B, Sequ	2	19.4	88.2	3237	11	US-60-453-135-482	
12 19.4 88.2 3283 5 US-09-270-437D-8 Sequence 8, App. 19.4 88.2 3412 8 US-09-270-437D-6 Sequence 6, App. 19.4 88.2 3427 11 US-60-453-135-3894 Sequence 3834, 17 19.4 88.2 3427 11 US-60-453-135-3894 Sequence 3834, 17 19.4 88.2 3427 11 US-60-453-135-3894 Sequence 3834, 18 19.4 88.2 3475 11 US-60-452-680-3237 Sequence 3237, 19 19.4 88.2 3475 11 US-60-452-680-3237 Sequence 3835, 20 19.4 88.2 3475 11 US-60-453-135-3835 Sequence 3835, 21 18.8 85.5 30922 7 US-09-949-016-16700 Sequence 215, App. 21 18.4 83.6 598359 7 US-09-947-911-215	1	19.4	88.2	3237	1	US-60-453-050-482	Company to the contract of the
13 19.4 88.2 3412 5 US-09-270-437D-6 14 19.4 88.2 3427 8 US-10-170-335-21870 15 19.4 88.2 3427 11 US-60-453-135-3834 17 19.4 88.2 3427 11 US-60-453-050-3834 18 19.4 88.2 3475 11 US-60-452-680-3237 19 19.4 88.2 3475 11 US-60-452-0866 19 19.4 88.2 3475 11 US-60-453-135-3835 20 19.4 88.2 3475 11 US-60-453-050-3835 21 18.8 85.5 30922 7 US-09-949-016-16700 22 18.4 83.6 598359 7 US-09-947-911-215	12	19.4	88.2	3283	v	US-09-270-4370-8	ddw '20% appac
14 19.4 88.2 3427 8 US-10-170-255-21870 15 19.4 88.2 3427 11 US-60-453-135-9834 17 19.4 88.2 3427 11 US-60-452-050-3834 18 19.4 88.2 3445 11 US-60-452-680-3237 19 19.4 88.2 3475 11 US-60-452-680-3237 20 19.4 88.2 3475 11 US-60-453-135-3835 21 18.8 85.5 30922 7 US-09-949-016-16700 22 18.4 83.6 598359 7 US-09-947-911-215	13	19.4	88.2	3412	ď	3-02-02-01	Sequence 8, Appli
15 19.4 88.2 342.7 8 US-10-170-225-22870 16 19.4 88.2 3427 11 US-60-453-050-3834 17 19.4 88.2 3427 11 US-60-453-050-3834 18 19.4 88.2 3475 11 US-60-452-680-3237 19 19.4 88.2 3475 8 US-10-235-22086 19 19.4 88.2 3475 11 US-60-453-135-3835 20 19.4 88.2 3475 11 US-60-453-050-3835 21 18.8 85.5 30922 7 US-09-949-016-16700 22 18.4 83.6 598359 7 US-09-947-911-215	7.4	0.			•	0-0/5-0/3-00-00	Sequence 6, Appli
15 19.4 88.2 3427 11 US-60-453-135-3834 17 19.4 88.2 3427 11 US-60-453-050-3834 18 19.4 88.2 3445 11 US-60-452-680-3237 19 19.4 88.2 3475 8 US-10.70-235-22086 19 19.4 88.2 3475 11 US-60-453-135-3835 20 19.4 88.2 3475 11 US-60-453-050-3835 21 18.8 85.5 30922 7 US-09-949-016-16700 22 18.4 83.6 598359 7 US-09-947-911-215	7 L	1	7.00	1947	20	US-10-170-235-21870	Seguence 21870. A
15 19.4 88.2 3427 11 US-60-453-050-3834 17 19.4 88.2 3445 11 US-60-452-680-3237 18 19.4 88.2 3475 11 US-60-452-132-22086 19 19.4 88.2 3475 11 US-60-453-135-3835 20 19.4 88.2 3475 11 US-60-453-050-3835 21 18.8 85.5 30922 7 US-09-949-016-16700 22 18.4 83.6 598359 7 US-09-947-911-215	CT.	10	88.2	3427	7.	US-60-453-135-3834	Semience 3834 An
17 19.4 88.2 3445 11 US-60-452-680-3237 18 19.4 88.2 3475 8 US-10-170-235-22086 19 19.4 88.2 3475 11 US-60-453-135-3835 20 19.4 88.2 3475 11 US-60-453-335 21 18.8 85.5 30922 7 US-69-949-016-16700 22 18.4 83.6 598359 7 US-09-947-911-215	16	19.4	88.2	3427	11	US-60-453-050-3834	משיטווטיוטיוטי
18 19.4 88.2 3475 8 US-10-1702-235-22086 19.4 88.2 3475 11 US-60-453-135-3835 20 19.4 88.2 3475 11 US-60-453-050-3835 21 18.8 85.5 30922 7 US-09-949-016-16700 22 18.4 83.6 598359 7 US-09-947-911-215	17	19.4	88.2	3445	-	119-60-452-690	Seducince 1834, Ap
19 19.4 88.2 34.7 9 0.5.10-11,0-255-222886 20 19.4 88.2 3475 11 US-60-453-135-3835 21 18.8 85.5 30922 7 US-09-949-016-16700 22 18.4 83.6 598359 7 US-09-947-911-215	18	19.4	6	3476	1 0	10 10 10 00 00 000	sequence 3237, Ap
20 19.4 88.2 3475 11 US-60-453-135-3835 21 19.8 88.5 30922 7 US-60-453-050-3835 22 18.4 83.6 598359 7 US-09-949-016-16700	0			7 1	0	02-10-1/0-235-22086	Sequence 22086, A
20 19.4 88.2 3475 11 US-60-453-050-3835 .21 18.8 85.5 30922 7 US-09-949-016-16700 22 18.4 83.6 598359 7 US-09-947-911-215	h (		7.89	3475	1	US-60-453-135-3835	Sequence 3835 An
. 21 18.8 85.5 30922 7 US-09-949-016-16700 22 18.4 83.6 598359 7 US-09-947-911-215	7	19.4	88.2	3475	=	US-60-453-050-3835	Company 2025
22 18.4 83.6 598359 7 US-09-947-911-215	c 21	18.8	85.5	30922	7	US-09-949-016700	de regresses and a
CT7-TT6-/16-CO CO	c 55	18.4	83.6	598359	ŗ	11S-09-947-011	Seductice To 100, A
						CT7-TT6-/16-C0 C0	sequence 215, App

		7094	Sequence 70940, A Sequence 18297, A Sequence 153, App	. (1)	Sequence 5301, Ap Sequence 5460, Ap Sequence 5460, Ap	Sequence 52, Appl Sequence 40560, A	
7 US-09-949-016-15816 7 US-09-949-016-12472 7 US-09-949-016-15903		0 US-60-455-444-42575 11 US-60-453-135-70940 11 US-60-453-136-70940	US-09-534-850-18297 US-10-092-900A-153	1 US-10-170-235-32027 1 US-60-441-839-137 1 US-60-452-680-9301	1. US-60-453-135-5460 1. US-60-453-050-5460 US-10-338-044-2260	PCT-US03-05336-52 US-10-170-235-40560 US-09-949-016-152	US-10-170-235-23701 0 US-60-455-444-3409 1 US-60-453-135-6603
84839 9968		202	2580 9	2890 2890 2890	2890 1 2890 1 3560 9	4933 1 4946 8 4985 7	6532 6532 1 6532 1
81.8 80.9 80.9	79.1 79.1 79.1	78.2	78.2	78.2 78.2 78.2	78.2 78.2 78.2	78.2 78.2 78.2	78.2 78.2 78.2
18 17.8 17.8	17.4 17.4 17.4	17.2	17.2	17.2	17.2 17.2 17.2	17.2 17.2 17.2	17.2
. 23 C 24 C 25	26 27 28	c 29 c 30 c 31	0 0 0	0 0 0 4 2 8 8 0 4	ი 338 39	0 0 0 4 4 4 0 1 2	0 0 0 4 4 4 4 5 5 4 4 5 5 6 6 6 6 6 6 6 6 6 6

## ALIGNMENTS

```
APPLICANT: Teang, Solam
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Jockert, Elisabeth
APPLICANT: Jockert, Elisabeth
APPLICANT: Jockert, Elisabeth
APPLICANT: Jockert, Elisabeth
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Antiger
FILE REFERENCE: LUD 5538.1
CURRENT APPLICATION NUMBER: US/09/270,437D
CURRENT APPLICATION NUMBER: 09/061,709
PRIOR PILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 23
LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 100.0%; Score 22; DB 5; Length 22; l Similarity 100.0%; Pred. No. 1.4; 22; Conservative 0; Mismatches 0; Indels
Sequence 13, Application US/09270437D
                                                APPLICANT: Chen, Yao-Tseng
APPLICANT: Gure, Ali
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                        GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-270-437D-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S:
Matches 22
```

1 GCTCTTTGGGGACAGGAGGTC 22 셤

ö

Sequence 3265, Application US/09513999C GENERAL INPORMATION: PAPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Duclert, A. US-09-513-999C-3265

APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C

or

ŏ

ö

```
DAME/KEY: misc feature
LOCATION: (387)...(387)
OTHER INFORMATION: n is equal to a,t,g, or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (380)..(380)
OTHER INFORMATION: n is equal to a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AME/KEY: misc feature
LOCATION: (356)...(357)
DTHER INFORMATION: n is equal to a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (335)..(335)
OTHER INFORMATION: n is equal to a,t,g, or
                                                                 NAME/KEY: misc feature
LOCATION: (87)...(87)
OTHER INFORMATION: n is equal to a,t,g, or
OTHER INFORMATION: n is equal to a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (384)..(384)
OTHER INFORMATION: n is equal to a,t,9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (226)..(226)
OTHER INFORMATION: n is equal to a,t,9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AME/KEY: misc feature
OCATION: (360)..(360)
OTHER INFORMATION: n is equal to a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAWE/KEY: misc_feature
LOCATION: (363)..(363)
OTHER INFORMATION: n is equal to a,t,9,
                                                                                                                                                                                                                                                                                                         NAWE/KEY: misc feature
LOCATION: (204)..(204)
OTHER INFORMATION: n is equal to a,t,9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAME/KEY: misc feature
OCATION: (349)...(349)
OTHER INFORMATION: n is equal to a,t,9,
                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (109)..(110)
OTHER INFORMATION: n is equal to a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAME/KEY: misc feature
LOCATION: (263)
THER INFORMATION: n is equal to a,t,9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc_feature
LOCATION: (352)..(353)
OTHER INFORMATION: n is equal to a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (213)..(214)
OTHER INFORMATION: n is equal to a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAME/KEY: misc feature
OCATION: (222)...(222)
DTHER INFORMATION: n is equal to a,t,9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a,t,g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (369)..(369)
DTHER INFORMATION: n is equal to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (323)..(323)
DTHER INFORMATION: n is equal to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAME/KEY: misc feature
LOCATION: (369)..(369)
                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature LOCATION: (213)..(214)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-912-283-28701, Application US/09912293

Sequence 228701, Application US/09912293

GENERAL INFORMATION: Human Genes, Sequences, and Expression Products 100
FILE REFERENCE: PO-100
CURRENT APPLICATION NUMBER: US/09/912,293
CURRENT PILING DATE: 2001-07-26
PRIOR FILING DATE: 1993-08-09
PRIOR FILING DATE: 1993-08-09
PRIOR FILING DATE: 1993-08-09
PRIOR FILING DATE: 1993-08-09
PRIOR PLILING DATE: 1994-02-12
PRIOR FILING DATE: 1994-02-15
PRIOR APPLICATION NUMBER: 08/104,507
PRIOR APPLICATION NUMBER: 08/104,507
PRIOR PILING DATE: 1994-02-15
PRIOR PILING DATE: 1994-02-15
PRIOR FILING DATE: 1994-02-15
PRIOR FILING DATE: 1994-02-15
PRIOR FILING DATE: 1994-03-31
PRIOR FILING DATE: 1994-03-31
PRIOR FILING DATE: 1994-03-31
PRIOR FILING DATE: 1994-03-31
PRIOR FILING DATE: 1994-03-31
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-13-21
PRIOR FILING DATE: 2000-13-21
PRIOR FILING DATE: 2000-13-21
PRIOR FILING DATE: 2000-13-21
PRIOR FILING DATE: 2000-13-21
PRIOR FILING DATE: 2000-13-21
PRIOR FILING DATE: 2000-13-21
PRIOR FILING DATE: 2000-13-21
PRIOR FILING DATE: 2000-13-21
PRIOR FILING DATE: 2000-13-21
PRIOR FILING DATE: 2000-13-21
PRIOR FILING DATE: 2000-13-21
PRIOR FILING DATE: 2000-13-21
PRIOR FILING DATE: 2000-13-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6; Length 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (52)...(52)
OTHER INFORMATION: n is equal to a,t,g, or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
88.2%; Score.19.4; D
Best Local Similarity 95.2%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches
                         CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: PALENT, PM
SEQ ID NO 3265
LENGTH: 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTCTTTGGGGACAGGAAGGT 21
                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 73..363
FEATURE:
NAME/KEY: misc_feature
LOCATION: 16
OTHER INFORMATION: k=g or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 17 _____; CTHER INFORMATION: k=g or t
US-09-513-999C-3265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature LOCATION: (58)..(58)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                               FEATURE
```

ద ઠ

or

or

ö

```
GENERAL INFORMATION:

JACHISTANT: CURAGEN COEPOTATION;

JACHISTANT: CURAGEN COEPOTATION;

JACHISTANT: CURAGEN COEPOTATION;

JACHISTANT: CURAGEN COEPOTATION;

JACHISTANT: CURAGEN COEPOTATION;

JACHISTANTION: THE SAME

FILE REFERENCE: 21402-462D-601

CURRENT APPLICATION NUMBER: PCT/US02/31357

FRIOR PILING DATE: 2001-10-02

PRIOR PILING DATE: 2001-10-09

PRIOR PILING DATE: 2001-10-09

PRIOR PILING DATE: 2001-10-09

PRIOR PILING DATE: 2001-10-09

PRIOR PILING DATE: 2001-10-09

PRIOR PILING DATE: 2001-10-09

PRIOR PELING DATE: 2001-10-10

PRIOR PELING DATE: 2001-10-10

PRIOR PELING DATE: 2001-10-10

PRIOR PELING DATE: 2001-10-12

PRIOR PELING DATE: 2001-10-13

PRIOR PELING DATE: 2001-10-13

PRIOR PELING DATE: 2001-10-13

PRIOR PELING DATE: 2001-10-13

PRIOR PELING DATE: 2001-10-13

PRIOR PELING DATE: 2001-10-22

PRIOR PELING DATE: 2001-10-22

PRIOR PELING DATE: 2001-10-22

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE: 2001-10-24

PRIOR PELING DATE
                                                                                                                                                                                                                                                                                                                                                                 Gape
                                                                                                                                                                                                                                                                                      Score 19.4; DB 6; Length 871; Pred. No. 33; 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.2%; Score 19.4; C
95.2%; Pred. No. 36;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT-USO2-31357-39
Sequence 39, Application PC/TUS0231357
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-262-445-39; Sequence 39, Application US/10262445; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      374 GCTCTTTGGGGACAGGAAGCT 354
CURRENT FILING DATE: 2000-11-2
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 8826
LENGTH: 871
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 95.2%;
Matches: 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 95.2%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               1 GCTCTTTGGGGACAGGAAGGT
                                                                                                                                                   TYPE: DNA
CORGANISM: Homo sapiens
US-09-724-676A-8826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: (5)..(1669)
PCT-US02-31357-39
                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 95.2%; Pred. No. 31;
Matches 20; Conservative 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
US-09-724-676-8826/C
US-09-724-676-8826/C
Sequence 8826, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION UNMER: US/09/724,676
CURRENT PILING DATE: 2000-11-28
NUMBER: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SEQ ID NO 8826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
US-09-724-676A-8826/c
Sequence 8826, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
ITILE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

88.2%; Score 19:4; DB 6;
Best Local Similarity 95.2%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc feature
LOCATION: (435)...(435)
FEATURE:
NAME/KEY: misc feature
LOCATION: (457)...(457)
LOCATION: (457)...(457)
LOCATION: (457)...(457)
LOCATION: (457)...(457)
USBAINE:
NAME/KEY: misc feature
LOCATION: (457)...(457)
USBAINON: (457)...(457)
      NAME/KEY: misc feature
LOCATION: (403)..(403)
OTHER INFORMATION: n is equal to.a,t,g,
                                                                                                                            NAME/KEY: misc_feature
LOCATION: (410) ... (410)
OTHER INFORMATION: n is equal to a,t,g,
FEATURE:
                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (416)..(416)
OTHER INFORMATION: n is equal to a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (419).
OTHER INFORMATION: n is equal to a,t,g,
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (428). (428)
OTHER INFORMATION: n is equal to a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 GCTCTTTGGGGACAGGT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GCTCTTTGGGGACAGGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  374 GCTCTTTGGGGACAGGAAGCT 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GCTCTTTGGGGACAGGAGGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-8826
```

ઠ

ö

셤

```
Sequence 482, Application US/60453135
Sequence 482, Application US/60453135
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: TAKOUBOVA, Old POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC PLAY MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001456
CURRENT PAPLICATION NUMBER: US/60/453,135
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: PastSEQ for Windows Version 4.0
TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF FILE REFERENCE: CLOOJ380
CURRENT APPLICATION NUMBER: US/10/170,235
CURRENT FILING DATE: 2003-03-17
NUMBER OF EQ ID NOS: 42514
SEQ ID NO 5179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 612, Application US/60452680

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele

APPLICANT: GRUPE, Andrew

TILLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: C1001450

CURRENT APPLICATION NUMBER: US/60/452,680

CURRENT FILING DATE: 2003-03-07

NUMBER OF SEQ ID NOS: 116213

SOFTWARE: FASESEQ for Windows Version 4.0

SEQ ID NO 612

LENGTH: 3237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 3237;
                                                                                                                                                                                                                                                 Length 3237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11;
                                                                                                                                                                                                                                                     DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 19.4; DE; DE; Pred. No. 38; 0; Mismatches
                                                                                                                                                                                                                                                     Score 19.4; DB; Pred. No. 38; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 19.4;
Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GCTCTTTGGGGACAGGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 gciciriogegacagaagci 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 88.2%;
Best Local Similarity 95.2%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 95.2%;
Matches 20; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GCTCTTTGGGGACAGGAAGGT
                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CRGANISM: Homo sapiens
US-60-452-680-612
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 20; Conserva
                                                                                                                                                                        TYPE: DNA ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-60-453-135-482
                                                                                                                                                                                                                 US-10-170-235-5179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-60-453-135-482
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
US-60-452-680-612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5179, Application US/10170235
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OF INVENTION: THE SAME
OF INVENTION: THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 133 SOFTWARE: CuraSeqList version 0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.2%; Score 19.4; DB 9; Length 1707; 95.2%; Pred. No. 36; 1.ve 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/262,445
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: 60/327,454
PRIOR FILING DATE: 2001-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR PILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR PILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR PILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR APPLICATION NUMBER: 60/328,949
PRIOR PILING DATE: 2001-10-12
PRIOR PILING DATE: 2001-10-15
PRIOR PILING DATE: 2001-10-15
PRIOR PILING DATE: 2001-10-15
PRIOR PILING DATE: 2001-10-15
PRIOR PILING DATE: 2001-10-15
PRIOR PILING DATE: 2001-10-15
PRIOR PILING DATE: 2001-10-24
PRIOR PILING DATE: 2001-10-24
PRIOR PILING DATE: 2001-10-24
PRIOR FILING DATE: 2001-10-24
PRIOR FILING DATE: 2001-10-24
PRIOR FILING DATE: 2001-10-24
PRIOR FILING DATE: 2001-10-24
PRIOR FILING DATE: 2001-10-24
                                                                                                                                                                                                                                                                                                                                           Patturajan, Meera
Rieger, Daniel
Spytek, Kimberly
Taupier Jr., Raymond J.
Zerhueen, Bryan
Zhong, Haihong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GCTCTTTGGGGACAGGAAGGT 21
                                      Alsobrook II, John
Burgess, Catherine
Catterton, Elina
Chant, John
Chaudhuri, Amitabha
Edinger, Shlomit
Gerlach, Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 GCTCTTTGGGGACAGGAAGCT
                                                                                                                                                                                                                                                                                                Millet, Isabelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                        Gorman, Linda
Guo, Xiaojia
Kekuda, Ramesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE: 21402-462D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (5)..(1669)
US-10-262-445-39
                                                                                                                                                                                           Giot, Loic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
US-10-170-235-5179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
```

```
APPLICANT: Tasing, Solam

APPLICANT: Tasing, Solam

APPLICANT: Stockert, Elisabeth

APPLICANT: Jager, Elkeabeth

APPLICANT: Jager, Elkeabeth

APPLICANT: Jager, Elkeander

APPLICANT: Old, Lloyd J.

TITLE OF INVENTION: Antigens Per Se, And Uses Thereof

TITLE OF INVENTION: Antigens Per Se, And Uses Thereof

TITLE OF INVENTION: Antigens Per Se, And Uses Thereof

TITLE OF INVENTION: Antigens Per Se, And Uses Thereof

CURRENT APPLICATION NUMBER: US/09/70,437D

CURRENT APPLICATION NUMBER: 09/061,709

PRIOR APPLICATION NUMBER: 09/061,709

PRIOR FILING DATE: 1998-04-17

NUMBER OF SEQ ID NOS: 23

LENGTH: 3412

TYPE: DNA

PRANCKE: CDS

NAME/KEY: CDS

NAME/KEY: CDS

COCATION: 3372

NAME/KEY: CDS

US-09-270-437D-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14

US-10-170-235-21870

SEQUENCE 21870, APPLICATION US/10170235

SEQUENCE 21870, APPLICANT: VENTER, J. Craig

TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HI
TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
CURRENT PILING DATE: 2003-03-17
NUMBER OF SEQ ID NOS: 42514
SEQ ID NO 21870
LENGHR: 3427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-60-453-135-3834
; Sequence 3834, Application US/60453135
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olga
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01456
; CURRENT APPLICATION NUMBER: US/60/453,135
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5; Length 3412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88.2%; Score 19.4; DB 8; ilarity 95.2%; Pred. No. 39; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.2%; Score 19.4; Diarity 95.2%; Pred. No. 39; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 GCTCTTTGGGGACAGGATGCT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 dererredegacacaacer 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GCTCTTTGGGGACAGGAGGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GCTCTTTGGGGACAGGAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 20, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-170-235-21870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gire, All APPLICANT: Gire, All APPLICANT: Teang, Solam APPLICANT: Teang, Solam APPLICANT: Teang, Solam APPLICANT: Stockert, Elisabeth APPLICANT: Stockert, Elisabeth APPLICANT: Stockert, Elisabeth APPLICANT: Stockert, Elisabeth APPLICANT: Muth, Alexander APPLICANT: Muth, Alexander APPLICANT: Muth, Alexander TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Antige TITLE OF INVENTION: AND 538 1 CURRENT PRING DATE: 1999-03-16 CURRENT FILING DATE: 1999-03-16 PRIOR APPLICATION NUMBER: 09/061,709 PRIOR PRING DATE: 1998-04-17 NUMBER OF SEQ ID NOS: 23 SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                       US-60-453-050-482

| Sequence 482, Application US/60453050
| Sequence 482, Application US/60453050
| GENERAL INFORMATION:
| APPLICANT: CARGILL, Michele
| APPLICANT: LUKE, May
| TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
| TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
| CURRENT FILING DATE: 2003-03-10
| CURRENT FILING DATE: 2003-03-10
| NUMBER OF SEQ ID NOS: 82762
| SEQ ID NO 482
| SEQ ID NO 482
| LENGTH: 3237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11; Length 3237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 5; Length 3283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.2%; Score 19.4; D
95.2%; Pred. No. 38;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 19.4; DB; Pred. No. 38; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOCATION: 3243
COTHER INFORMATION: unsure of nucleotide US-09-270-437D-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 8, Application US/09270437D ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/09270437D GENERAL INFORMATION:
  76 GCTCTTTGGGGACAGGAAGCT 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GCTCTTTGGGGACAGGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 GCTCTTTGGGGACAGGT 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 GCTCTTTGGGGACAGGAGCT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 95.2%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GCTCTTTGGGGACAGGAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 95.2
Matches 20, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA

ORGANISM: Homo sapiens
US-60-453-050-482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
US-09-270-437D-6
ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

.; 0

Gaps

5 4578 1 Ltd.	Search time 766 Seconds (without alignments) 465.145 Million cell updates/sec				32308132	
GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd. OM nucleic - nucleic search, using sw model	Run on: April 18, 2003, 04:47:40 ; Search time 766 Seconds (without alignments) 465.145 Million cell upo	Title: US-09-270-437D-13 Perfect score: 22 Sequence: 1 gctctttggggacaggaaggtc 22	Scoring table: IDENTITY NUC Gapext 1.0	Searched: 16154066 seqs, 8097743376 residues	Total number of hits satisfying chosen parameters:	Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

1: em\_estba:\*
2: em\_esthum:\*
3: em\_esthum:\*
4: em\_esthum:\*
5: em\_estpo:\*
6: em\_estpo:\*
7: em\_estro:\*
8: em\_estro:\*
10: gb\_est:\*
11: gb\_htc:\*
11: gb\_htc:\*
12: gb\_est2:\*
13: gb\_est2:\*
14: gb\_est2:\*
15: em\_estfun:\*
16: em\_estfun:\*
17: gb\_est2:\*
18: em\_estfun:\*
19: em\_gss\_hum:\*
17: gb\_gs:\*
18: em\_gss\_hum:\*
19: em\_gss\_hum:\*
10: em\_gss\_hum:\*
20: em\_gss\_hum:\*
21: em\_gss\_hum:\*
22: em\_gss\_hum:\*
23: em\_gss\_hum:\*
24: em\_gss\_hum:\*
25: em\_gss\_hum:\*
26: em\_gss\_hus:\*
26: em\_gss\_hus:\*
27: em\_gss\_no:\*
26: em\_gss\_no:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	AA226813 zr18f09.r AL121466 DKRZD762L BG007027 RC1-GN023 H66879 yul7a11.r1 BF014566 LI3-UT011 BQ211568 AGENCOURT
SUMMARIES	DB ID	9 AA226813 9 AL121466 12 BG0707027 14 H65979 12 BF914566 14 BQ221568
	08	
	Query Match Length DB ID	330 453 478 479 620 851
*	Ouery Match	888.22 888.22 888.22 888.23
	esult No. Score	011 011 010 010 010 010 010 010 010 010
	Result No.	Ω ። α ω 4 τυ Λο

81336 60252	3346 60270	125 60339	1358 53819	BF189397 234957 Ma	3653 FR22en	4261805 CH230-	38064 PDCT-24-	1515 602529E	20	24.6	BO706255 ACENCOIDE	621	v	BB872349 BB872349	Z84036 SSZ84036 Po	BB863724 BB863724	BB852457 BB852457	'n	BB852318 BB852318	BB853640 BB853640	BB855310 BB855310	BM107521 511770 MA	BO770242 III-M-FID-	B0235601 hd83c10 a	BB660288	4	BB618315	3944 6027	70	3088 6033	1345 AGEN	21716 hrsaho4	669	91260 RR19126	1002	1000	050750 0057000	B51576	
BG481336			BM484358	8939	AI623653	BH261805	BH098064	BG480515	BC015720	PT022C03U	BQ706255	AK015621	AL597676	BB872349	284036	BB863724	BB852457	BM253624	BB852318	BB853640	BB855310	BM107521	BQ770242	BQ235601			BB618315		4297	9808	5434	E221	BB163693	9126	<b>B363</b>	B438	757	851	
12	-	-	-	H	σ	-	-	Н	-	11	14	11	σ	10	7	2	10	13	10	10	2	13	_	_	_	-	_	-	-	-	-	4	Н	-	ч	10	-		
874	9 9	264	309	373	471	266	680	856	2768	738	861	1742	299	368	429	434	448	449	458	469	489	528	541	582	617	649	668	673	715	812	1146	140	150	150	152	154	154	155	
88.2	7.00	85.5	85.5	85.5	85.5	83.6	83.6	83.6	83.6	81.8	81.8	81.8	80.9	80.9	80.9	80.9	80.9	80.9	80.9	80.9	80.9	80.9	80.9	80.9	80.9	80.9	80.0	60.08	80.9	60.0	80.9	79.1	79.1	79.1	79.1	79.1	79.1	79.1	
9.0	h c		Ď,	18.8		œ.	∞ .	œ	മ	18	18	٠.,	17.8	<b>~</b> 1	٠,	_	<u>,                                     </u>	_	17.8	ŗ.	Ľ.	17.8	Ċ	٠.		ç,	· .	٠,	٠,	٠,	٠,	٠.	ζ.	۲.	ζ.	17.4	17.4	17.4	
r a	0 0	, c	7	7	7.7	<u>۳</u>	14	12	16	11	18	5 6	0 7	7.0	7 (	5.5	24	5.5	56	27	28	5 6	0 .	31	32		ى ر 4 ت	n (	ם ני ני	` (	D 0	ر بر	0 .	41	42	43	44	45	
	(	י כ	י	υ		U			υ		O			,	C																		U	υ	υ	υ	υ	ט	

## ALIGNMENTS

RESULT 1

			•
AA226813 ZI18f09.rl Stratagene NT2 neuronal precursor 937230 Homo aapiens CDNA clone IMAGE:663785 5', mRNA sequence. AA226813.1 GI:1848349 EST.	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Hominidae; Homo.  1 (bases 1 to 330) Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Kucaba,T., Lacy,M., Le,M., Le,M., Mardis,E. Moore	,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,W.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M. Generation and analysis of 280,000 human expressed sequence tags 97044478  Contact: Wilson RK	.108 contact the
linear Bor 937230	Chordata; Craniata; Vertebrata; Eutele Primates; Catarrhini; Hominidae; Homo. :, Becker,M., Bonaldo,M.F., Chiapelli, ',N., DuBuque,T., Favello,A., Gish,M., 'aba,T., Lacy,M., Le,M., Le,N., Marchis,	fkin,L., Reerry-Meg,J. Wilson,R. expressed e	ouis, MO 63 agh LLNL ,
mRNA nal precur A sequence	raniata; V atarrhini; , Bonaldo e,T., Fave	nge,C., Ri in,F., Thi irston,R., 000 human (	Medicine 101, St. Lo free throu
330 bp NT2 neuro 15 5', mRN	ordata; C: imates; C: Becker,M. ., DuBuque	B,J., Prar B,M.B., Ta n,P., Wate s of 280,0 -828 (1996	School of ay, Box 85 1.edu royalty-
330 bp mRNA Stratagene NT2 neuronal precurs IMAGE:663785 5', mRNA sequence. GI:1848349	fetazoa, Ch ttheria, Pr to 330) Lennon,G., Dietrich,N	M., Parson , K., Soare , Wohldman nd analysi 6 (9), 807	niversity Park Parkw 1800 1810 atson.wust atsonse
AA226813 zr18f09.r1 cDNA clone AA226813 AA226813.1 EST. human.	Homo sapiens Eukaryota, Metazoa, Mammalia, Eutheria, 1 (bases 1 to 330) Hillier,L., Lennon,G. Chissoe,S., Dietrich M., Hultman,M., Kuo	'B., Morris, M., Parsons, J., Prang Schellenberg, K., Soares, M.B., Tan Underwood, K., Wohldmann, P., Water Genoration and analysis of 280,00 Genome Res. 6 (9), 807-828 (1996) 97044478	washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the
AA226813 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE	ORGANISM REFERENCE AUTHORS	TITLE JOURNAL MEDLINE COMMENT	

```
Similarity
                                                                                                                                                                                                                                                                      human.
Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                            BG007027/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              474
                                                                                                                                                                                                 DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                    ORGANISM
                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                        VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
H66979
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                      SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                     ò
                                                                                                   셤
                                                                                                                                                                                                                      This is the 5' sequence of the clone insert clone from S. Wiemann, Molecular Genome Analysis, German Cancer Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Clone from S. Wiemann, Molecular Genome Analysis, center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Madidenomix (Martinsried/Germany) within the CDNA sequencing consortium of the German Genome Project. No sl sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 25-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                             ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

1 (Dases 1 to 453)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone (DKFZg762L097) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin. Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
 IMAGE Consortium (info@image.llnl.gov) for further information.
Seg primer: -28ml3 revl ET from Amersham
High quality sequence stop: 321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
                                                                                                        /db_xref="cdD8:5589715"
/db_xref="cdD8:5589715"
/db_xref="taxon:9606"
/clone="INAGE:663785"
/clone=lib="Stratagene NT2 neuronal precursor 937230"
/rissue_type="neuroepithelial cells"
/rissue_type="neuroepithelial cells"
/lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   453 bp mRNA linear EST 25-Fi
DKFZp762L097 r1 762 (synonym: hmel2) Homo sapiens cDNA clone
DKFZp762L097 s', mRNA sequence.
AL121466
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                           88.2%; Score 19.4; DB 9; Length 330; 95.2%; Pred. No. 1.8e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db xref="taxon:9606"
/db xref="taxon:9606"
/clone="DKPZp762L097"
/clone=lib="762 (synonym: hmel2)"
/tissue_type="melanoma (MeWo cell line)"
                                                                                                 /organism="Homo_sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="adult"
/lab_host="DH10B"
                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST (Ottenwaelder, et al.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Ottenwaelder B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 GCTCTTTGGGGACAGGAAGCT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                       21
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GCTCTTTGGGGACAGGAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wiemann, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human.
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL121466
                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
```

ઠ

```
/mote-forgan: placenta normal; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse Ranscription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Par: +55-11-2704922

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
Magalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
Diass 1 to 478;
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagali, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Mataukuma, A., Baria, G.S., Simpson, D.H., Goldman, G.H., Garvalho, A.F., Mataukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              478 bp mRNA linear EST 24-JAN-200
RCL-GN0235-271100-021-a10 GN0235 Homo sapiens cDNA, mRNA sequence.
BG007027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 478;
                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
Score 19.4; DB 9; Length 453;.
Pred. No. 1.88+02;
); Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.2%; Score 19.4; DB 12;
95.2%; Pred. No. 1.8e+02;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/clone lib="GN0235"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21
                                                                                                                            ö
                                                                                                                                                                                                                                                                                                               118 gererregggacagaager 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BG007027.1 GI:12450789
                                                                                                                                                                                                                                21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GCTCTTTGGGGACAGGAAGGT
                                  88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             deretringegacacagaagen
                                                                                                                                                                                                                      1 GCTCTTTGGGGACAGGAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                            20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence tags
```

```
/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone lth="HT0114"

/dev_stage="Adult"

/dev_stage="Adult"

/noce="Organ: uterus tumor; Vector: puc18; Site_1: SmaI;

Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES POR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research
profiles into the DUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 620)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matcukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-UT0114-
011200-362-E06&t5=2000-12-01&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                851 bp mRNA linear EST 02-MAY-2002
                                                                                                                                                                                                  Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                       Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 851)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Conteact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata, Craniata, Vertebrata, Buteleostomi,
Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                   Peroc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 19.4; DB 12; Length 620;
Pred. No. 1.8e+02;
0; Mismatches 1; Indels 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seg primer: puc 18 forward
High quality sequence stop: 619.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BQ221568.1 GI:20402968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 88.2%;
1 Similarity 95.2%;
20; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                       Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GCTCTTTGGGGACAGGAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BQ221568
AGENCOURT 7559207 N
5', mRNA Sequence.
BQ221568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .620
                                                                                                                                                                               Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local
Matches 2
                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BQ221568
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                      MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo maplens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 479)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston The WashU-Marck EST Project
Unpublished (1995)
Contact: Wilson RK
                EST 18-OCT-1995
H66979 479 bp mRNA linear EST 18-OCT-1995
yulall.rl Soares fetal liver spleen lNFLS Homo sapiens CDNA clone
IMAGE:234044 5' similar to contains Alu repetitive element;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   620 bp mRNA linear EST 18-JAN-2001
BF914566
BF914566.1 GI:12306024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Source: IMAGE Consortium, Linn.
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1511
High quality sequence stops: 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

88.2%; Score 19.4; DB 14; Length 479;
Best Local Similarity 95.2%; Pred. No. 1.88+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:234044"
/clone_lib="Soares fetal liver spleen INFLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="GDB:3787221"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seg primer: M13RP1
High quality sequence stop: 401.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 GCTCTTTGGGGACAGGAAGCT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GCTCTTTGGGGACAGGAAGGT 21
                                                                                         Н66979
Н66979.1 GI:1025719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human.
LOCUS
DEFINITION
                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
COMMENT
                                                                                                         VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
BF914566
LOCUS
```

ઠ 셤

ô

ö

Gaps

ö

Length 874; Indels

```
Score 19.4; DB 12;
Pred. No. 1.9e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BI871125.1 GI:16044798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GCTCTTTGGGGACAGGAAGGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gcrcrrrdeedacaedaagcr 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG748346.1 GI:14058999
                                                                                                                                                                                                                   116 GCTCTTTGGGGACAGGAAGCT 136
                                                                                                                                                                           1 GCTCTTTGGGGACAGGAAGGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 88.2%;
Best Local Similarity 95.2%;
Matches 20; Conservative
                                                    88.2%;
                                                                                                                   20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
                                                           Query Match
Best Local Similarity
Matches 20, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG74834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BI871125/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
                                                                                                                                                                                                                                                                                                                                                RESULT 8
BG748346
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organia="Homo sapiens"
/dp xref="Homo sapiens"
/db xref="traxon:9606"
/clone="IRAGE:4652395"
/clone="IRAGE:4652395"
/clone="IRAGE:4652395"
/clone="IRAGE:4652395"
/clone="IRAGE:4652395"
/lab host="MIH_MGC_21"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lab xereage-nessistant)
/lab host="DH10B (phage-resistant)"
/lab xereage-nessistant)
/lab xereage-nessistant)
/lab xereage-nessistant
/lab xereage-nessistant)
/lab xereage-nessistant
/lab xereage-nessistant
/lab xereage-nessistant
/lab xereage-nessistant
/lab xereage-nessistant
/lab xereage-nessistant
/lab xereage-nessistant
/lab xereage-nessistant
/lab xereage-nessistant
/lab xereage-nessistant
/lab xereage-nessistant
/lab xereage-nessistant
/lab xereage-nessistant
/lab xereage-nessistant
/lab xereage-nessistant
/lab xereage-nessistant
/lab xereage-nessistant
/lab xereage-nessistant
/lab xereage-nessistant
/lab xereage-nessistant
/lab xereage-nessistant
/lab xereage-nessistant
/lab xereage-nessistant
/lab xereage-nessistant
/lab xereage-nessistant
/lab xereage-nessistant
/lab xereage-nessistant
/lab xereage-nessista
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Experience Sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 874)

1 (bases 1 to 874)

S NIH-MGC http://mgc.nci.nih.gov/

I Unpublished (1999)

L Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:

http://image.lln.gov

Plate: LLCM136 row

Location/Qualifiers

S High quality sequence erop: 688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG481336 874 bp mRNA linear EST 21-MAR-2001
602528680F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4652395 5',
mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                      /organism="Homo sapiens"
/db zref="taxon:9606"
/db zref="taxon:9606"
/clone=lib="NHMGE:6046477"
/clone=lib="NHMGE"
/tab host="DHIOB. (phage-resistant)"
/hote="Organ: Skin; Vector: pGNV-SPORT6; Site 1: NotI;
Site 2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Aperage insert size 2 kb. Library constructed by Life
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Flate: LLAM13292 row: f column: 14 High quality sequence stop: 637.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.2%; Score 19.4; DB 14; Length 851; 95.2%; Pred. No. 1.9e+02; ive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 g 157 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Technologies."
234 c 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG481336
BG481336.1 GI:13413615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GCTCTTTGGGGACAGGAAGGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                numan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG481336
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

```
Contact: Kobert Strausberg, Pn.D.

Email: Gapba-rémail.nih.gov

Tissue Procurement: Arcayed

Tissue Procurement: Arcayed by: The I.M.A.G.B. Consortium (LINL)

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.B. Consortium/LiNL at:

Clone distribution: MGC column: 02

High quality sequence stop: 773.

High quality sequence stop: 773.

High quality sequence stop: 773.

Account throw of throw of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie of the incompanie 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BI871125
603395008F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5405040 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
BG748346 889 bp mRNA linear EST 15-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.
1 (hases 1 to 889)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 19.4; DB 12; Length 889;
Pred. No. 1.9e+02;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ...
```

S

ô

Gaps

°,

EST 02-NOV-2000

```
Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pig.

Sus scrofa

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.

(Dases 1 to 373)

Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.

Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A.; Laegraid, W.W.

Bosign and use of two pooled tissue normalized cDNA libraries for Chipublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db xref="texton:0823"
/clone_lib="MARC_2PIG"
/tissue_type="pooled"
/lab_hoft="DH10B"
/lab_hoft="DH10B"
/note="Vector: pGMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled tissue From testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."

100 c 106 g 76 t
                                                                                                                                                                                                                                                                                                                                                                                                              85.5%; Score 18.8; DB 13; Length 309; 90.9%; Pred. No. 3.2e+02; Live 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  373 bp mRNA linear
234957 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
BF189397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TPL: 402 762 4330
Ex: 402 762 4390
Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plate: 57 row: A column: 18
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR PRIMERS
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GCTCTTTGGGGACAGGACGTC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF189397.1 GI:11072766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 GCTCTTTGAGGACTGGAAGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .373
                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
es 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
BF189397/c
LOCUS
                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
1 (bases 1 to 309)
Stone, X. T., Heaton, M.P., Rohrer, G.A., Smith, T.P.L., Casas, E., and Keele, J.W.
Design and use of two pooled tissue normalized cDNA libraries for Unpublished (2000)
Contact: Smith TPL
Do Box 16, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4366
Fax: 402 762 4399
                                                        Lukaryote; Metazoa; Chordata; Craniata; Vertebrata; Eutelecetomi;
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Eutelecetomi;
E 1 (bases 1 to 264)
I (bases 1 to 264)
I (bases 1 to 264)
I Unpublished (1999)
Contact: Robert Strausbeag, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be http://image.llnl.gov
Round through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAM12032 row: p column: 01
High quality sequence start: 9
High quality sequence stop: 264.
Incoation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo saplens"

/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:5465040"
/clone="Ib="NIH MGC 90"
/tissue_type="adenocarcinoma, cell line"
/lab_nost="DH108 (phage-resistant)"
/lab_nost="DH108 (phage-resistant)"
/loce="Organ: liver; Vector: pCMv.SpORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average innert size_17 kb. Library enriched for Average inners and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 05-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 85.5%; Score 18.8; DB 13; Length 264; 1 Similarity 90.9%; Pred. No. 3.28+02; 20; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BM484358 309 bp mRNA linear 538191 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence. BM484358.1 GI:18534686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 GCTCTGTGGGGCAGGAGGTC 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GCTCTTTGGGGACAGGTC 22
                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                     REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
BM484358/c
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
```

ò

85.5%; Score 18.8; DB 12; Length 373;

TITLE

ð

```
Enkaryora, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryora; Metazoa; Chordata; Sciurognathi; Muridae; Musinae; Musmalla; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. B. 1 (bases 1 to 680)

25 I (bases 1 to 680)

26 Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M., Tsegaye,G., Geer,K., Krol,W., Shvattsbeyn,A., Gebregeorgis,E., Russell,D., de Jong,P. and Fraser,C.M.
Russell,D., de Jong,P. and Fraser,C.M.
Russell,D., de Jong,P. and Fraser,C.M.
Unpublished (1999)

Other GSSS: RPCI-24-271L15.TV

Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Frax: 301 838 0208
Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BH098064 680 bp DNA linear GSS 19-JUL-2001
RPCI-24-271L15.TJ RPCI-24 Mus musculus genomic clone RPCI-24-271L15
                                                                                                                                                                                                                                                                                                       Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Blate: 185 row: B column: 17
Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., d Jong,P. and Fraser,C.M. art BAC End Sequences from Library CHORI-230 ECORI segment Umpublished (1999)
Other GSSS: CH230-185B17.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Female"
/cell_type="Brain"
/cell_type="Vector: pTARBAC2.1; Site_1: BcoRI; Site_2: BcoRI;
/note="Wector: pTARBAC4MCW) BAC library produced by
CHORI-230 Rat (BN/SeNH8d/MCW) BAC library produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 83.6%; Score 18.4; DB 17; Length 566; Best Local Similarity 95.0%; Pred. No. 5.1e+02; Matches 19; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                 Contact: Shaying Zhao
Department of Bukaryotic Genomics
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    db xref="taxon:10116"
/clone="CH230-185B17"
/clone lib="CHORI-230 Segment 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Rattus norvegicus"
/strain="BN/SsNHsd/MCW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pieter de Jong"
121 c 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BH098064.1 GI:14919489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             484 rcrrrddddacagragarc 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 TCTTTGGGGACAGGAGGTC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , DNA sequence.
BH098064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
BH098064
                                                                                               TITLE
JOURNAL
COMMENT
       REFERENCE
                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         566 bp DNA linear GSS 30-NOV-2001 CH230-185B17.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone CH230-185B17, DNA sequence.
BH261805
BH261805.1 GI:17167720
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
Life Technologies catalog #: 11548-013
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
DNA Sequencing by: Washington University Genome information can be
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Lienghi: 144 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 421
POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B"
//note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: Sall;
Site 2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                             A1623653 A1 CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2229344 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 471)
NCT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 85.5%; Score 18.8; DB 9; Length 471; Best Local Similarity 90.9%; Pred. No. 3.3e+02; Matches 20; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 others
               Pred. No. 3.3e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:2229344"
/clone lib="MCI CGAP Panl"
/tissue_type="adenocarcinoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTCTTTGGGGACAGGAGGTC 22
                                                                                            1 GCTCTTTGGGGACAGGAAGGTC 22
                                                                                                                             87 GCTCTTTGAGGACTGGAAGGTC 66
                                                                                                                                                                                                                                                                                                                                            AI623653
AI623653.1 GI:4648584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 GCTCTGTGGGGGGCAGGAAGGTC
                         Best Local Similarity 90.9%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93 C
                                                                                                                                                                                                                                                                                                              mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Norway rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus.
                                                                                                                                                                                                                                                                    AI623653
                                                                                                                                                                                                                                                                                                                                                                                                                uman.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
BH261805/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                       RESULT 12
AI623653
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                            ACCESSION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
```

ORIGIN

g ઠ

COMMENT

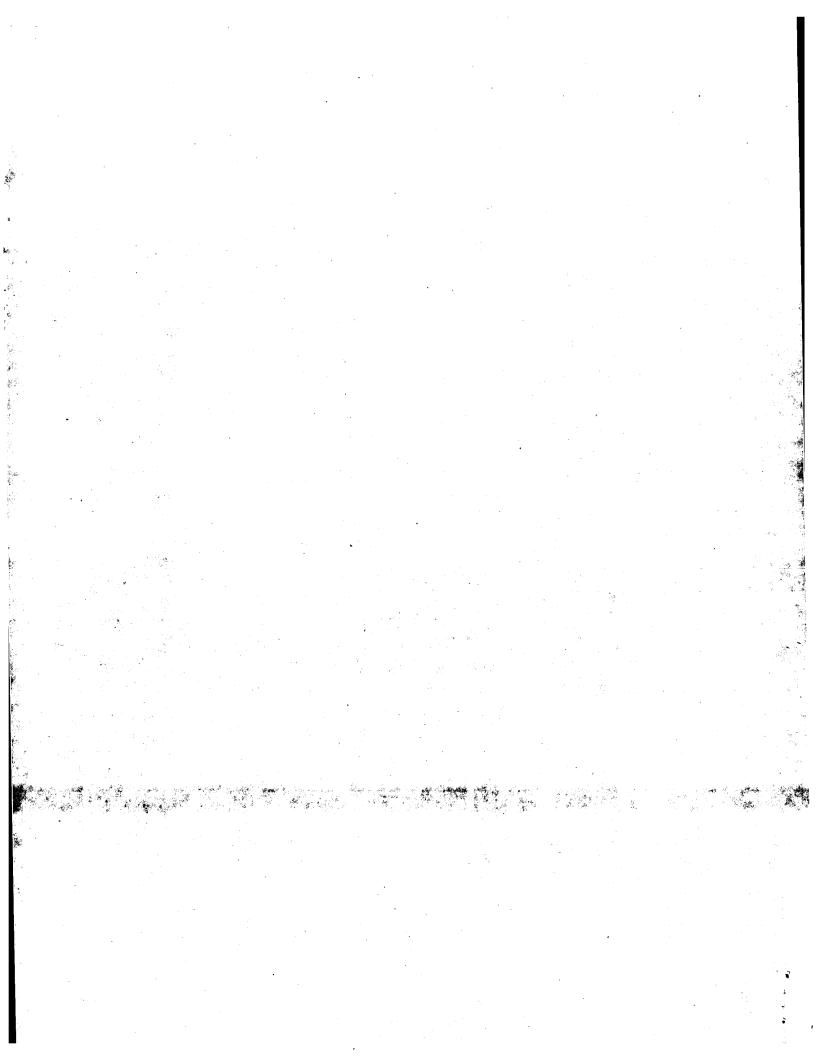
```
1. .856
/organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:465291"
/clone="IMAGE:465291"
/clone="type="choriocarcinoma"
/tissue_type="choriocarcinoma"
/tissue_type="choriocarcinoma"
/lab_hose="DH108" (phage=resistant)"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: BcoRI; DNA made by oligo-dr priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG (G). Size-selected >500bp
Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejongémeil.cho.org). Clones may be purchased from BACPAC Resources (http://www.clori.org/bacpac/orderingframe.htm). BAC end plate: 271 row. L column: 15 Seg primer: SP6 Column: 15 Seg primer: SP6 Column: 15 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG480515
602529520F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4652981 5',
                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Wector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCT-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using Mbol partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1:0.956)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbe-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue Procurement, ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.
Plate: LLCM438 row: h column: 06
High quality sequence stop: 661.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83.6%; Score 18.4; DB 17; Length 680; 95.0%; Pred. No. 5.1e+02; Live 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 t
                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-271LIS"
/clone lib="RPCI-24"
                                                                                                                                                                                                  Location/Qualifiers
1. .680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG480515.1 GI:13412705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 CTCTTTGGGGACAGGAGGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 crcrrregegacacadader 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 95.0
hes 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Si
Matches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS
DEPINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG480515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ద
```

```
for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." ORIGIN
```

Query Match
Best Local Similarity 95.0%; Pred. No. 5.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps

ö

Search completed: April 18, 2003, 07:32:01 Job time : 770.167 secs



```
GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
```

OM nucleic - nu	OM nucleic - nucleic search, using sw model	
Run on:	April 18, 2003, 04:46:26 ; Search time 292 Seconds (Without alignments) 2192.677 Million cell updates/sec	
Title: Perfect score:	US-09-270-437D-14	
Sequence:		
Scoring table:	IDENTITY NUC Gapop 10.0 , Gapext 1.0	
Searched:	2054640 seqs, 14551402878 residues	

Total number of hits satisfying chosen parameters: 4109280
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :		GenEmbl:*
	ä	
		gb_htg:*
		gp_in: *
		ab_om:*
		3p ov:*
		gb_pat:*
		tud qb
		gb_p1:*
		dp pr:*
	ä	gb ro: *
	ä	gb_sts:*
	~:	
	<u></u>	gp_nu: *
	::	gb_v1:*
	.:.	em_ba:*
		em_fun:*
	17:	em_hum: *
	18:	em_in:*
	19:	em_mu:*
	20:	em om:•
	21:	em or:*
	22:	em_ov:*
	23:	em_pat:*
	24:	em ph: *
	25:	em_p1:*
	26:	em_ro:*
	27:	em sts:*
	28:	em_un: *
	ć	

28: em un::
29: em vi:\*
30: em vi:\*
31: em htg\_thum:\*
31: em htg\_other:\*
33: em htg\_other:\*
35: em htg\_other:\*
36: em htg\_rod:\*
37: em htg\_rod:\*
36: em htg\_rod:\*
37: em htg\_rod:\*
39: em htg\_other:\*
41: em htgo\_omus:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ch Length DB  2010 9  3012 9  3010 9  3412 6  0 3412 6  0 3412 6  0 3642 9  0 50320 2  0 124649 9  0 1024 1  1 1259 1  1 1259 1  1 1959 1  2 11521 1  2 1249 1  2 1249 1  2 12538 8  2 1152 9  1 1402 1  2 1294 1  2 2 1294 1  2 2 1294 1  2 2 1294 1  2 2 1294 8  2 11320 1  2 2 1294 8  2 11320 1  2 2 1294 8  2 1294 8  2 1294 8  2 1294 8  2 1294 8  2 12955 4  2 12955 4  2 12955 4  3 1350 1  3 1350 1  3 1350 1  3 1350 1  3 1350 1  3 1350 1  3 1350 1  3 1350 1  3 1350 1  3 1350 1  3 1350 1  3 1350 1  3 1350 1  3 1350 1  3 1350 1  3 1350 1  3 1350 1  3 1350 1  3 1350 1  3 1555 1  3 1555 4	C02564 C02564 C02099 C01009 C00862
Length 2010 3283 3412 3412 3412 3642 3642 3642 3642 3642 11099 11109 1109 1109	
A Manage 110000110000110000110000110000110000110000	.2 148824 .2 151343 .2 159462 .2 160930 .2 183455
Benilt No. No. No. No. No. No. No. No. No. No.	11 11 11 11 11

RESULT 1

AF117107

LOCUS

DEFINITION Home sapiens IGF-II mRNA-binding protein 2 (IMP-2) mRNA, complete complet

ALIGNMENTS

Length 3283;

9

```
/ LTAIL ALL OF THE TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAT 17-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unknown.
Unknown.
Unclassified.
Unclassified.
(L bases I to 3283)
Chen, Y.-T., Gure, A., Tsang, S., Stockert, E., Jager, E., Alexander, K. and Old, L.J.
and Old, L.J.
Isolated mucleic acid molecule encoding cancer associated antigen, Isolated nucleic, and uses thereof the antigen itself, and uses thereof Patent: US 6297364-A 8 02-OCT-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                            '(bases 1 to 2010)
Nielsen,J., Christiansen,J., Lykke-Andersen,J., Johnsen,A.H.,
Nielsen,J., and Nielsen,F.C.
Direct Submission
Submitseld 30-DEC-1998) Institute of Molecular Biology, University
of Copenhagen, Soelvgade 83H, Copenhagen DK-1307, Denmark
Location/Qualifiers
A family of insulin-like growth factor II mRNA-binding proteins represses translation in late development Mol. Cell. Biol. 19 (2), 1262-1270 (1999) 99108099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="alternative start-codon gives an additional
N-terminal methionine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="IMP-2"
/note="binds multiple sites in IGF-II mRNA 5/UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 22; DB 9; Length 2010;
Pred. No. 10;
; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="IGF-II mRNA-binding protein 2"
/protein_id="AAD09827.1"
/db_xref="GI:4191610".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3283 bp
Sequence 8 from patent US 6297364.
AR171867
AR171867.1 GI:17910817
                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
1. _2010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="unknown"
833 c 779 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 GACGTTGACAACGGCGGTTTCT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; St. Best Local Similarity 100.0%; P. Matches 22; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GACGITGACAACGGCGGTITCT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="IMP-2"
47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="IMP-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          945 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
AR171867/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
                                                                                                                                                         PUBMED
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                         PEATURES
                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
```

```
Web site: http://www.nisc.nih.gov/
Neb site: http://www.nisc.nih.gov
Contact: nisc.gognhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BC021290
3642 bp mRNA linear PRI 22-JAN-2002 Homo sapiens, IGF-II mRNA-binding protein 2, clone MGC:29539 INAGE:5090334, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bamanlai; Butheria; Primates; Catarrhini; Hominidae; Homo. (Cases 1 to 3642)
                                                                                                                                                                                    PAT 17-DEC-2001
                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 3412)
Chen Y.-T., Gure,A., Tsang,S., Stockert,E., Jager,E., Alexander,K.
and Old,L.J.
                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acid molecule encoding cancer associated antigen, the antigen itself, and uses thereof patent: US 6297364-A 6 02-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (14.5AN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaitheraburg, Maryland;
Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                           linear
                                    Indels
                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
Score 22; DB 6;
Pred. No. 9.6;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch
1 Similarity 100.0%; Pred. No. 9.6;
22; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             750
                                                                                                                                                                                           AR171865
Sequence 6 from patent US 6297364.
AR171865
AR171865.1 GI:17910815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="unknown"
887 c 804 g
                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BC021290.1 GI:18204200
                                                                                                         444 GACGTTGACAACGGCGGTTTCT 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22
                                        ö
                                                                         22
     Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 22; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GACGITGACAACGGCGGTITCT
                                                                         1 GACGITGACAACGGCGGITTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                            Unknown.
Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 22; Conserve
                                                                                                                                                                                                                                                                                         Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
BC021290/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
TITLE
                                                                                                                                                                    RESULT 3
AR171865/c
LOCUS
                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                           SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REMARK
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                          VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                  8
```

```
Birren, B., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Bairren, B., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Bairren, B., Nusbaum, C., Lander, E., Boushigalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Dazellano, K., Dewar, K., Diaz, J. S., Dodge, S., Farceira, P., FitzGerald, M., Gage, D., Galagan, J., Farco, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Honne, L., Milme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad, Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., Machen, C., Machonald, P., Major, J., Mathews, C., Machen, J., Moly, C., Norman, C., Norbu, C., Norbu, C., Norbu, C., Norbu, C., Norbu, C., Norbu, C., Norbu, C., Norbu, C., Norbu, C., Norbu, C., Norbu, C., Norbu, C., Norbu, C., Senter, P., Phurkhang, P., Plerre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Submitted (105-JUL-2002) Whitchead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / LTAIRLAGOULLKSGYAPVDADDLRQLFGDRKLPLAGQVLLKSGYAPVD
YPDQNWAIRAIETLSGKVELHGKIMEVDYSVSKKLRSRKIQIRNIPPHLQWEVLLGGLL
AGYGTVERVRYDYDTETRAVVNYTYATREBALTAMEKLSGHOFENYSFKISYIPDEEV
SSPSPPCRAQRGDHSSREQGHAPGGTSQARQIDFPLRILVPTQFVGAIIGKEGLTIKN
ITKQTQSRVDIHRKENSGAABKRVTIHATPEGTSEACRMILEIMQKRADETKLAEIF
LKILAHNGLVGRLIGKEGRNIKKIEHETGTKLITISSLQDLSIYNPERTITVKGTVEAC
ASAEIEIMKKLREAFENDMLAVNTHSQYFSSLYFHHQFOPPHHSYPEQEIVULFIP
TQAVQAIIGKKGAAIIKALRAFASSIKIAPBAGPDVSERWVIITGPPEAQGRIF
GKLKEENFFNPKEEVKLEAHIRVPSSTAGRVIGKGGKTVNBLQNITSBAVIVPROQTE
DRUEEVIVRLIGHFFAGGRIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 50320)

Birren, B., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 18, clone CTD-2307113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                /product="hepatocellular carcinoma autoantigen"
/protein_id="AAD31596.1"
/db_xref="GI:4883681"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 22; DB 9; Length 3667;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 22; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                    /gene="p62"
436 .2106
/gene="p62"
/note="RNA-binding protein"

    .3667
    /organism="Homo sapiens"
    /db_xref="taxon:9606"

                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                846 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  810 GACGTTGACAACGGCGGTTTCT 789
                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC126373.1 GI:21699324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GACGITGACAACGCCGGITICI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 50320)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      882 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG; HTGS_PHASEO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human.
                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
AC126373/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                   FEATURES
                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / (' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' ...'' |
// ' 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3667 bp mRNA linear PRI 23-MAY-1999
Homo sapiens hepatocellular carcinoma autoantigen (p62) mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J., Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Zhang,L.-H. and Green,B.D.
                                                                                                                                                                Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 39 Row: o Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5729883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. (1 (bases 1 to 3667)
Zhang, J.Y., Chan, E.K., Peng, X.X. and Tan, E.M.
A novel cycoplasmic protein with RNA-binding motifs is an autoantigen in human hepatocellular carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (03-APR-1998) Molecular & Experimental Medicine, The
Scripps Research Institute, 10550 N. Torrey Pines Road, La Jolla,
CA 92037, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                     1. 3642

/ Organism="Homo sapiens"

/db_xref="LocusID:10644"

/db_xref="caxon:9606"

/clone="MGC:28539 IMAGE:5090334"

/tismue type="Pancreas, epithelioid carcinoma"

/clone_lib="NIH MGC 42"

/lab_host="DH10E-R"

/note="Nector: pOTB7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 22; DB 9; Length 3642; 100.0%; Pred. No. 9.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 3667)
Zhang,J.Y., Chan,E.K.L., Peng,X.X. and Tan,E.M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             448 GACGTTGACAACGGCGGTTTCT 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GACGITGACAACGGCGGTTTCT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF057352
AF057352.1 GI:4883680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1077 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10190901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
AF057352/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCUS
                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PUBMED
```

ઠે 유

```
COMMENT
```

```
an contig of 778 bp in length 100 bp in contig of 778 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp 
                                                                                                                                                                          253/1: contig of 768 bp in length 26239: contig of 768 bp in length 6399; gap of 100 bp 27090: contig of 751 bp in length 7790: gap of 100 bp 28646: contig of 765 bp in length 8806; gap of 100 bp 2669: contig of 761 bp in length 89769; gap of 100 bp 2669: contig of 761 bp in length 89769; gap of 100 bp 36550: contig of 761 bp in length 89769: gap of 100 bp 36550: contig of 771 bp in length 31423: contig of 773 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        737 bp ---
100 bp
770 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 bp

f 750 bp in length

100 bp in length

100 bp in length

100 bp in length

1744 bp in length

100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 bp
F 772 bp in length
100 bp
F 789 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 bp
f 778 bp in length
100 bp
f 749 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14: 917: Control of 100 bp 45158: control of 744 bp in length 45158: gap of 100 bp 158: gap of 782 bp in length 40: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46894: contig of 754 bp in length
46994: gap of 100 bp
47754: contig of 760 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96: gap of 100 bp 49446: contig of 774 bp in length 46: gap of 100 bp 50320: contig of 774 bp in length.
                                                                                                                   in length
                                                                                                                                                           in length
in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 bp
100 bp
100 bp
                                                                                                ap of 100 bp : contig of 716 bp i ap of 100 bp : contig of 746 bp i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 bp
756 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="18"
/map="18"
                                                             46: gap of 100 b
23709: contig of 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45: gap of
43454: contig of 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             523: gap of 10
32279: contig of 7
379: gap of 10
33129: contig of 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73: gap of
10051: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51: gap of 1
10900: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7413 37512: gap of 1
7513 38284: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34928: gap of 1
35665: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49447 49546: gap of
49547 50320: contig o
Location/Qualifiers
                                         contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41000: gap of
41778: con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45258: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35765: gap of 36535: con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8285 38384: qap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34084: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap of
                                                                                                      23809: gap of
                                                                                                                                              24625: gap of
25371: con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48596:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37412:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33984:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34828:
                                                                                                                            24525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42745:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43554:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44414:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46140:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47854:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41878:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36635:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39273:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31523:
                                                                                                                                                                                                                                                                      27190:
                                                                                                                                                                                                                                 26339:
                                                                                                                                                                                                                                                                                                                                                                                            29769:
                                                                                                                                                                                       25471:
                                                               22946:
                                                                                                                                                                                                                                                                                                                28046:
                                                                                                                                                                                                                                                                                                                                                                                                                                      30650:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3130 33229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40151
                                                                                                                                                                                                                                                                                                                                                       28908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                Research
                                                                                                    for Genome
                                                                                                                                                                                                                                                                                                                                            arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                 All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                               NOTE: This record contains 59 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5303: gap of 100 bp 16010: contig of 707 bp in length 16872: gap of 100 bp 1762 bp in length 17715: contig of 743 bp in length 18587: contig of 743 bp in length 18587: contig of 772 bp in length 18587: contig of 772 bp in length 19887: contig of 772 bp in length 19464: contig of 777 bp in length 19464: contig of 777 bp in length
                                                                                                                                                           Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L27661
Center clone name: 2307_1_13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 bp
of 741 bp in length
100 bp
of 714 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87: gap of 100 pp
12655: contig of 768 bp in length
55: gap of 100 bp
1742 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig of 739 bp in length
p of 100 bp
contig of 732 bp in length
p of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 bp
768 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4366 14465: gap of 100 bp
4466 15203: contig of 738 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 bp
f 795 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bp
49 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 bp
E 755 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11787; contig of 720 bp in length
87; gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 bp
f 738 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 bp
f 782 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 bp
f 765 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                767 866: gap of 100 bp
867 1574: contig of 708 bp in length
575 1674: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 bp
[ 771 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               766 bp in length
                                                                                   Center: Whitehead Institute/ MIT Center
                                                                                                                                           Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dq 00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of 100 b
57: contig of 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21235: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l: gap of 10
10136: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     766: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20303: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3498 13597; gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16110: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21135:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        413 2512; gap of 3283; co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2513
3284 3383: gap c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: gap (
5820: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , 6785; 9c.
7580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9281:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . gap
6685:
                                                                                                                                 Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2412:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8432:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10967:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4938:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20403:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16972:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17815:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19564:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.
4939 5038: 9
5039 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18687:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3137 10236:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0968 11067:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11887:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2656 12755:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9381:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5204 15303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4224:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5920:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7680:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8532:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              821
```

ORIGIN

ò

```
Center project name: RP11-394021

Center clone name: RP11-394021

Center clone name: RP11-394021

Sequencing vector: M12

Chemistry: Dye-primer Bodipy: 2% of reads
Chemistry: Dye-terminacor Big Dye: 9% of reads
Chemistry: Dye-terminacor Big Dye: 9% of reads
Assembly program: Phrap; version 0.990329

Consensus quality: 200560 bases at least Q40

Consensus quality: 200562 bases at least Q30

Consensus quality: 200621 bases at least Q30

Consensus quality: 200621 bases at least Q30

Consensus quality: 200621 bases at least Q30

Consensus quality: 200621 bases; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tunc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as Tuns of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                       Worley, K.C.
Direct Submission

Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, IX 77030, USA
On Jul 19, 2002 this sequence version replaced gi:21539678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC094924 124849 bp DNA linear HTG 10-JUL-2002
Rattus norvegicus clone CH230-3M13, *** SEQUENCING IN PROGRESS ***,
                                    Baylor College of Medicine, One USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 22; DB 2; Length 200947; llarity 100.0%; Pred. No. 6.9; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 13815: contig of 13815 bp in length 13816 13915: gap of unknown length 13916 200947: contig of 187032 bp in length.
                                                                                                                                                                                                                                                                                    Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Drafting Center Code: BCM
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="teaxon:9606"
/chromosome="3"
/clone="RP11-394021"
59914 a 43317 c 42497 g 55118 t
                           Molecular and Human Genetics,
flor Plaza, Houston, TX 77030,
(bases 1 to 200947)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 75177 GACGTTGACAACGGCGGTTTCT 75198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GACGITGACAACGGCGGITICI 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC094924.3 GI:21716147
HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 unordered pieces.
AC094924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
AC094924/c
LOCUS
DEFINITION
                                                                               REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                         COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homes raptens appears to the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control
                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACUIS961 . 200947 bp DNA linear HTG 24-JUL-2002
Homo sapiens chromosome 3 clone RP11-394J21, WORKING DRAFT
SCOURNCE, 2 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (09-DEC-1999) Human Genome Sequencing Center, Department
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACO16961.27 GI:21908412
HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN.
Homo sapiens.
                                                                                                                                                                                                                    ö
                                                                                                                                           Query Match
100.0%; Score 22; DB 2; Length 50320;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0
                                                                  6113 others
                                                                                                                                                                                                              0; Indels
/clone="CTD-2307113"
/clone_lib="CITD1 Human BAC"
9574 c 10122 g 12507 t
                                                                                                                                                                                                                                                                                          567 GACGTTGACAACGGCGGTTTCT 546
                                                                                                                                                                                                                                                                  22
                                                                                                                                                                                                                                                            1 GACGTTGACAACGGCGGTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 200947)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                         12004 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC016961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Worley, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
ORGANISM
                                                      BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                AC016961
```

ô

```
ANTHONE IN theses I to 12489, A Mile Josean, F.R., Milen, C., Marthunge, M.C., Kern, N. Manner, R. Banken, C., Mado-Odkola, B., Mil-Josean, F.R., Milen, C., Marthunge, M.C., Kern, N. Manner, R., Banken, C., Mado-Odkola, B., Milen, C., Marthunge, M.C., Kern, N. Manner, R., Banken, C., Carrot, T. E., Carrot, F. C., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot, T. E., Carrot
```

```
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently consists of 48 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                op ...
length
'n length
                                                                                                           f unknown length
g of 1589 bp in length
f unknown length
g of 1346 bp in length
f unknown length
q of 1091 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bp in length
                                                                                                                                                                                                                                                                                           of 1389 bp in length
                                                                                                                                                                                                                                                                                                              bp.in length
                                                                                                                                                                                                                                                                                                                                                                       of 1051 bp in length
unknown length
of 1378 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                            bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                               bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bp in length
                                                                                                                                                                                    length
bp in length
                                                                                                                                                                                                      known length
1030 bp in length
                                                                                                                                                                                                                                                       of 1281 bp in length
                                                                                                                                                                                                                                    of 1351 bp in length
                                                                                                                                                                            bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ength
                                                                                                                                                                                                                                                                                                                                                             ength
                                                                                                                                                                                                                                                                                                                                                                                                                    ength
                                                                                                                                                                                                                                                                                                                                                                                                                                       ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ength
                                                                                                                                                                                                                                                                                                                                         length
                                                                                                                                                                                                                                                                                                                                                                                                  ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ength
                                                                                                                                                                                                                           length
                                                                                                                                                                                                                                                                                                                        length
                                                                                                                                                                                                                                                                 length
                                                                                                                                                                                                                                                                                    length
                                                                                                                                                                                                                                                                                                     length
                                                                                                                                                                    length
                                                                                                                                                                                                                                               length
                                                                                                                                                                                                                                                                                                                                                                                                                                                   pp in
                                                                                                                                                                                                                                                                                                                        unknown len
of 1712 bp
                                                                                                                                                                                                                                                                         contig of 1724 bp
gap of unknown ler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig of 2992 k
gap of unknown l
contig of 1420 b
gap of unknown l
contig of 1105 b
gap of unknown l
                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig of 1923 b
gap of unknown l
contig of unknown l
gap of unknown l
gap of unknown l
contig of 2337 b
gap of unknown l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of 1098 lunknown
                                                                                                                                                                                                                                                                                                     unknown of 1283 h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                                                                                                                                                                            2381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2759
                                                                                                                                                                                                                                                                                                                                           unknown
                                                                                                                                                                                                                                                                                                                                                     1605
                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                1336
                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
                                                                                                                                                           contig of 1091
gap of unknown
                                                                                                                                                                                                of 1138
                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig of
gap of unk
contig of
gap of unk
contig of
                                                                                                                                                                                                                                                                                                                                                                                                                              oĘ
                                                                                                                                                                             contig of J
                                                                                                                                                                                                                                                                                                                                                                                                              of
                                                                                                                                                                                                                                                                                                                                                       ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig
gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of
                                                                                                                                                                                                                                                                                                                                            gap of
contig
                                                                                                                                                                                                                                                                                                                                                                        contig
gap of
                                                                                                   contig gap of contig gap of contig contig
                                                                                                                                                                                                                                                                                              contig
                                                                                                                                                                                                                                                                                                                       gap of
                                                                                                                                                                                                                                                                                                                                   contig
                                                                                                                                                                                                                                                                                                                                                                                           contig
                                                                                                                                                                                                                                                                                                                                                                                                              contig
                                                                                                                                                                                                                                                                                                                                                                                                                                 contig
                                                                                                                                                                                                                                                                                                                                                                                                                     gap of
                                                                                                                                                                                                                                                         contig
                                                                                                                                                                                                                                                                                                                 contig
                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of
                                                                                                                                                  gap oế
                                                                                                                                                                                                                     contig
                                                                                                                                                                                                                                       contig
                                                                                                                                                                                                                                                                                                        gap of
                                                                                                                                                                                                                                                                                                                                                                                                   gap of
                                                                                                                                                                                                         gap of
                                                                                                                                                                                                                              gap of
                                                                                                                                                                                                                                                 gap of
                                                                                                                                                                                                                                                                 gap of
                                                                                                                                                                                                                                                                                     gap of
                                                                                                                                                                                                                                                                                                                                                                gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50676:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54385:
                                                                                                                                                                                                                                                                                              4980:
                                                                                                                                                                                                                                                                                                                                                        9880:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6968:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44117:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45537:
                                                                                                                                          4159:
4259:
5350:
5450:
                                                                                                                                                                                                                                                                            3491:
                                                                                                                                                                                                                                                                                                         5080:
                                                                                                                                                                                                                                                                                                                           6463:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    8449:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52607
                                                                                                                                                                                                                                       10286:
                                                                                                                                                                               6467:
                                                                                                                                                                                                            7805:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44017
                                                                                                                                                                                                                                                         11667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44118
45538
45638
46743
46843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48413
50677
50777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52608
52708
54386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36969
39728
39828
40926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41026
                                                                                                                                                                                                                                                                                                                                                                                                                                                             28450
28550
30855
30955
32875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35422
                                                                                                                                                                                                                                                                                                                                   16464
18176
18276
                                                                                                                                                                                                                                                                                                                                                                                           21132
                                                                                                                                                                                                                                                                                                                                                                                                              22610
24991
                                                                                                                                                                                                                                                                                                                                                                                                                                                     26527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32975
                                                                                                                                                                                                                                                         10387
11668
11768
13492
13592
14981
15081
                                                                                                                                                                                                                                                                                                                           6364
                                                                                                                                                                                                                                                                                                                                                                19861
                                                                                                                                                                                                                                                                                                                                                                          19981
                                                                                                                                                                                                                                                                                                                                                                                   1032
                                                                                                                                                                                                                                                                                                                                                                                                                                  5091
                                                                                                                                                                                                                                                                                                                                                                                                                                          26427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35322
                                                                                                                                                                                                                                                 10287
                                                                                                               1025
```

```
Barnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Gabis, A., Garot, J., Foster, P., Frantz, P., Gabis, A., Garota, J., Garner, T., Garza, N., Gill, R., Gortell, J. Ha., Guevara, W., Gunaratne, P., Hales, Hawes, A., Harnandez, J. Hartis, C., Hartis, C., Hartis, C., Hartis, C., Hartis, C., Hartis, C., Hartis, C., Hartis, C., Hartis, C., Hartis, C., Hartis, C., Hartis, C., Hartis, C., Hartis, C., Hartis, C., Hartis, C., Hullyk, S., Hume, J., Jackson, L. E., Jacobson, B., Mallyk, S., Hume, J., Joudah, S., Karlsson, E., Johnson, R., Johlson, R., Johlson, R., Johlson, R., Johlson, R., Johlson, R., Johlson, C., Lewis, L., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Li, W., Loulesged, H., Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Martinar, Mart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 62 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (06-UUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Bylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 161691)
Worley, K. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: GFBU
Center clone name: CH230-43M20
Center clone name: CH230-43M20
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329
Consensus quality: 112006 bases at least Q40
Consensus quality: 118246 bases at least Q20
Consensus quality: 122772 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g of 1016 bp in length
f unknown length
g of 1170 bp in length
f unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1016: contig c
1116: gap of v
2286: contig c
2386: gap of v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 161691)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .1017
1117
2287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161691 bp DNA linear HTG 11-JUL-2002
Rattus norvegicus clone CH230-43M20, *** SEQUENCING IN PROGRESS
***, 62 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Buvck, J., Bowie, S., Brieva, M., Brown, B., Brown, M., Bryant, N.D., Buvck, J., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chack, J., Chavez, D., Chen, G., Coyle, M.D., Dathorne, S.R., David, R., Delaney, K.R., Delgado, O., Denn, A.L., Dink, H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
92.7%; Score 20.4; DB 2; Length 124849;
Best Local Similarity 95.5%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98740: Contig of 3404 bp in length 98640: gap of unknown length 102540: contig of 3706 bp in length 105640: gap of unknown length 10957: contig of 6817 bp in length 11562: contig of 8105 bp in length 117762: gap of unknown length 117762: gap of unknown length 117762: gap of unknown length 114449; contig of 7087 bp in length
                                                                                                                                                                                                                                                                                                                                           Jp ...
length
'n length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9902 others
                                                                                                                             length
bp in length
                                                                                                                                                                                                                                                                                    length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                               length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 length
bp in length
                                                                                                                                                                                                             length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     length
                                                                                                                                                                                                                                                                                                                                                                                                                  pp in
contig of 3774 by gap of unknown logged of unknown logged of contig of 2701 by gap of unknown logged of 2843 by gap of unknown logged of 4459 by gap of unknown logged of 4459 by gap of unknown logged of 4459 by gap of unknown logged of 4459 by gap of unknown logged of 4459 by gap of unknown logged of 4371 by gap of unknown logged of 3371 by gap of unknown logged of 3770 by gap of unknown logged of 3770 by gap of unknown logged of 3770 by gap of unknown logged of 3770 by gap of unknown logged of 3770 by gap of unknown logged of 3770 by gap of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unknown logged of unkn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31267 a 26760 c 26699 g 30221 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \text{\columbia.cm.10116"}
\text{\columbia.cm.1013"}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 36120 GACGTTGACAACGGCTGTTTCT 36099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GACGTTGACAACGGCGGTTTCT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC126477.1 GI:21700419
HTG; HTGS PHASE1.
Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86895:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91366:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91466:
                                                                                                            61229
64030
64130
64130
67246
67246
770189
770189
770189
770189
770189
78696
86896
86896
86996
86996
86996
86996
86996
86996
86996
86996
86996
86996
86996
86996
86996
86996
86996
86996
86996
86996
86996
86996
86996
86996
86996
86996
86996
86996
86996
86996
86996
86996
86996
86996
86996
86996
86996
86996
86996
86996
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
86999
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109458
109558
117663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
AC126477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
```

ORIGIN

δ

```
op ...
length
'n length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length
bp in length
length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bp in length
length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length
bp in length
length
bp in length
length
length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length
bp in length
length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length
bp in length
                                                                                                                                                                                                                                                                                                                                                                          /p --
length
in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length
bp in length
length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ength
op in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length
op in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       known length
1640 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length
bo in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown length
of 1431 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                        length
bp in length
                                                                                                                                                                                                                                                                                            in length
                                                                                                                                                                                                                                                                                                                                   length
bp in length
                                                                                       length
bp in length
                                                                                                                                                                                                        length
bp in length
                                                                                                                                                                              bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length
                                                                                                                                                                                                                                                                      length
                                                                                                                                                 ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig of 2858 bp i
gap of unknown leng
contig of 1985 bp i
gap of unknown leng
contig of 1433 bp i
gap of unknown leng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig of 1957 b
gap of unknown l
contig of 1239 b
gap of unknown l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig of 2565 b
gap of unknown l
contig of 1196 b
gap of unknown l
contig of 1669 b
gap of unknown l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown l
of 1816 k
unknown l
of 2565 k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
of 1947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown ]
of 2006 h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of 1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of 2269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of 1958 Junknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of 1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of 1370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of 1955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of 1932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                                              of 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
                                                                                                                       of 1579
                                                                                                                                                                              of 1252
                                                                                                                                                                                                                                            of 1547
                                                                                                                                                                                                                                                                                                         of 1464
                                                                                                                                                                                                                                                                                                                                      unknown
                                                                                                                                                                                                                                                                                                                                                                    of 1219
                                                                                          unknown
                                                                                                                                                                                                                                                                         unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap of contig contig contig contig contig conting conting conting conting conting conting conting conting conting conting conting conting conting conting conting conting conting conting conting conting conting conting conting conting conting conting continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue continue conti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gap of
contig contig contig contig contig contig contig contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig contig gap of contig contig contig gap of contig contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55866:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1064:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17457:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17557:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19515:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19615:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21085:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23040:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51126
51226
54460
54560
56016
56116
59018
59118
61065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68116
68216
70970
71070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63534
65767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46061
47730
47830
49787
                                                                                                                                                                                                                                                                                                                10507
111971
113290
113390
113390
114578
11558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
117558
1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7978
8078
0084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2100
4665
4765
5961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6884
```

```
Clark.S.
Direct Submission

Direct Submission

No. Submission

No. Submission

No. Submission

CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone

CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone

requests: clonerequest@sanger.ac.uk

On Sep 11, 2001 this sequence version replaced gi:15022347.

On Sep 11, 2001 this sequence version replaced gi:15022347.

Nhere differences are found these are annotated as variations

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

corresponding to the overlapping clone name. Note that the

variation annotation may not be found in the sequences submission

variation annotation may not be found in the sequences with

only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all

regions were either double-stranded or sequenced with an alternate

chemistry or covered by high quality data (1.e., phred quality >=

chemistry or covered by high quality data (1.e., phred quality >=

chemistry or covered by high quality data (1.e., phred quality >=

chemistry or covered by high quality data (1.e., phred quality >=

chemistry or covered by high quality abort covered by at least

one plasmid subclone or more than one M13 subclone; and the

assembly was confirmed by restriction digest. The following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL596177 91084 bp DNA linear PRI 08-SEP-2001
Human DNA sequence from clone RP11-325P15 on chromosome 1, complete
sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 91084)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 161691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig of asset by in temperature of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a second of a sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length
bp in length
length
bp in length
                                                                                               bp in length
length
bp in length
                                                                                                                                                                                                                                                                                          length
bp in length
length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                yap or unknown length
contig of 2463 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bp in length
                       bp in length
length
                                                                                                                                                                                                               length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                          length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig of 4073 bp in J
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 20.4; DE
Pred. No. 41;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
of 3511 h
                                                                                                                                               unknown l
of 3228 b
unknown l
of 3429 b
                                                                                                                                                                                                                                                                                                                                                                                                      of 2173 b
unknown of 2802 b
                                                                                                                                                                                                                                                                                                  unknown
of 2228
                                                                       unknown
of 2535 l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of 2858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
unknown
                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                       Gontigo e gap of ve contigo e gap of ve contigo e gap of ve contigo e gap of ve contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contigo e contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 148271 GACGTIGACAACGGCIGITICT 148292
                                   contig
gap of 1
contig
gap of 1
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL596177
AL596177.4 GI:15552942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GACGTTGACAACGGCGGTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122298:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115562:
115662:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107915:
                                                                                                                                                                                                                                                                                                                                          88411:
88511:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103949:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107815:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113093:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103849:
                                                                                                                                                                                                                                                               86083:
                                                                                                                                                                                                                                                                                                          86183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          90784:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97197:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97297:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .00255:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 95.5
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113094
115563
115663
118126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107816
107916
112994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100156
100256
103850
103950
   73345
73445
76692
76692
79227
79327
79327
82555
82655
86084
86184
                                                                                                                                                                                                                                                                                                                                                                                                                      88512
90685
90785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93587
93687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97198
97298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
AL596177/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE.
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
```

```
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "S Tobases I to 11259)

Saltren, B. Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Baldwin, J., Barna, N., Bastien, V., Beda, F., Campoplano, A., Castle, A., Chospel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Grand-Plerre, N., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Janders, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheerers, R., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Pleani, C., Pollara, V., Raymond, C., Riley, R., Pierre, N., Pleani, C., Pollara, V., Raymond, C., Riley, R., Spencer, B., Roy, A., Santos, R., Santos, R., Schauer, S., Severy, P., Spencer, B.,
abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL, Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                  http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping http://www.sanger.ac.uk/HGP/Chrl RP11-235p15 is from the library RPCI-11.2 constructed by the group http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens chromosome 15 clone RP11-76D16 map 15, LOW-PASS SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                      IMPORTANT: This sequence is not the entire insert of clone RP11-325P1S It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true left end of clone RP11-325P1S is at 1 in this sequence. The true left end of clone RP11-335P1S is at 1 in this sequence. The true right end of clone RP11-337C18 is at 8908S in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.5%; Score 18.8; DB 9; Length 91084; 90.9%; Pred. No. 2.5e+02; 1ve 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 112259)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 15, clone RP11-76D16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RPCI-11.2"
19586 c 19377 g 25047 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/clone="RP11-325P15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 1. .91084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9827 GACGTTGACAACAGTGGTTTCT 9806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC026579
AC026579.2 GI:17048293
HTG; HTGS PHASE0.
HOmo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GACGITGACAACGGCGGTITCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 20, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27074 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC026579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGIN
```

ò

```
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Trefafaye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J., Vassillav, H., Viel, R., Vo., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M., Wilson, D., Ye, W.J., Subricts Subrission, Submitted (2-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 03141, USA On Nov 22, 2001 this sequence version replaced gi:7284066. Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                              Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                       * NOTE: This record contains 139 individual
* Sequencing reads that have not been assembled into
* contiger. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will
                                                                                                                                                                                                                                                                                         Center code: WIBR
Web atte: http://www.seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10356 10455; gap of eveb bp in length 10456 11162: contig of 707 bp in length 11163 11262; gap of 100 bp in length 11263 1262; gap of 100 bp in length 11263 12062; contig of 700 bp in length 11263 12062; gap of 100 bp in length 12760 12859; gap of 100 bp in length 12534 13633; gap of 100 bp in length 13534 13633; gap of 100 bp in length 1354 13635; contig of 674 bp in length 14356 14455; contig of 705 bp in length 14356 15160; contig of 705 bp in length 15161 15260; gap of 100 bp in length 15261 15579; contig of 705 bp in length 15261 15373; contig of 705 bp in length 16773 16778; contig of 706 bp in length 16779 16878; gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 bp
of 696 bp in length
100 bp
of 723 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 714: contig of 714 bp in length 15 814: gap of 100 bp 15 1541: contig of 727 bp in length 1542 1641: gap of 100 bp 2329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2320 2329: contig of 688 bp in length 2330 2429: gap of 100 bp 1144 324.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3144 3243; gap of 100 bp 10 length 3244 3955; contig of 714 bp in length 3244 3955; contig of 719 bp 3955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 bp
f 671 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 bp
f 707 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 bp
E 726 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 bp
f 694 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 bp
if 698 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 bp
f 685 bp in length
                                                                                                                                                                                                                                                                                                                                                                           Center project name: 18359
Center clone name: 76_D_16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5633: gap of
6329: con
6429: gap of
7152: con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0: gap of
10355: con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7252: gap of
7978: co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8078: gap of
8772: cor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8872: gap of
9570: co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5533: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4826:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5633:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9670:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9671
```

```
17647 17653; contig of 685 bp in length 17648 17653; gap of 100 bp 116819; contig of 709 bp in length 18713 18712 gap of 6 100 bp 116819; contig of 709 bp in length 18713 18712 gap of 6 100 bp in length 19268 20778; contig of 695 bp in length 20789; gap of 100 bp in length 20793 20778; gap of 100 bp in length 20793 20778; gap of 100 bp in length 20793 20779; gap of 100 bp in length 20793 20779; gap of 100 bp in length 20793 20779; gap of 100 bp in length 20793 20779; gap of 100 bp in length 20793 20779; gap of 100 bp in length 20793 20779; gap of 100 bp in length 20793 20779; gap of 100 bp in length 20793 20793; gap of 100 bp in length 20793 20793; gap of 100 bp in length 20794 2075; gap of 100 bp in length 20794 2075; gap of 100 bp in length 20794 2075; gap of 100 bp in length 20794 2075; gap of 100 bp in length 20794 2075; gap of 100 bp in length 20794 2075; gap of 100 bp in length 20794 2075; gap of 100 bp in length 20794 2075; gap of 100 bp in length 20794 2075; gap of 100 bp in length 20794 20794; contig of 705 bp in length 20794 20794; contig of 705 bp in length 20794 20794; contig of 705 bp in length 20794 20794; contig of 705 bp in length 20794 20794; contig of 705 bp in length 20794 20794; contig of 705 bp in length 20794 20794; contig of 705 bp in length 20794 20794; contig of 705 bp in length 20794 20794; contig of 705 bp in length 20794 20794; contig of 705 bp in length 20794 20794; contig of 705 bp in length 20794 20794; contig of 705 bp in length 20794 20794; contig of 705 bp in length 20794 20794; contig of 705 bp in length 20794 20794; contig of 705 bp in length 20794 20794; gap of 100 bp in length 20794 20794; gap of 100 bp in length 20794 20794; gap of 100 bp in length 20794 20794; gap of 100 bp in length 20794 20794; gap of 100 bp in length 20794 20794; gap of 100 bp in length 20794 20794; gap of 100 bp in length 20794 20794; gap of 100 bp in length 20794 20794; gap of 100 bp in length 20794 20794; gap of 100 bp in length 20794 20794; gap of 100 bp in length 20794 20794; gap of 100 bp in leng
```

```
Homo saplens
Ebkarycota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukarycota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 142971)

Bodota, B., Bouck, J., Bailey, M., Barbaria, J., Blankenburg, K.,
Bukett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C.,
Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C.,
Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C.,
Burkett, C., Deshazo, D., Ding, Y., Domah-Rashid, N.,
David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N.,
Forcum-Tansey, J., Frantz, P., Ganesh, R., Gorrell, J.H., Gorrell, L.L.,
Forcum-Tansey, J., Frantz, P., Lischarge, J., Hogues, M., Tones, M., Kelly, S., Kneitz, S., Kondejewski, N., Kong, Y., Kovar, C.,
Jones, M., Kelly, S., Kneitz, S., Kondejewski, N., Kong, Y., Kovar, C.,
Lau, S., Leal, B., Lee, E., Li, Z., Lichtarge, O., Liu, J., Liu, M.,
Martinez, C., McLeod, M.P., Mel, G., Merscher, S., Miller, A.,
Martinez, C., McLeod, M.P., Mel, G., Merscher, S., Miller, A.,
Martinez, C., McLeod, M.P., Mel, G., Merscher, S., Melne, Payton, B.,
Payton, B., Perez, L., Pu, E.L., Quiles, M., Reiter, D., Rives, M.,
Payton, B., Perez, L., Pu, E.L., Quiles, M., Reiter, D., Rives, M.,
Samuel, S., Say, J., Scherer, S., Sheh, E., Sheh, H., Shim, C.,
Vinson, R., Vo, O., Wahbah, M., Watlington, S., Weinstock, I. R., Williamson, A., Worley, K., Wren, J., Wrensford, G., Whang, A., Wolley, K., Wren, J., Welson, D. and
Gibbs P. Williamson, A., Worley, K., Wren, J., Welson, D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Worley, K.C.
Direct Submission
Submitted (07-JAN-2000) Human Genome Sequencing Center, Department
Submitted (07-JAN 2000) Human Genetics, Baylor College of Medicine, One
of Molecular and Human Genetics, Baylor College of Medicine, One
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC020629 142971 bp DNA linear PRI 07-MAR-2002
Homo sapiens 12q BAC RP11-76E16 (Roswell Park Cancer Institute
Human BAC Library) complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 112259;
46404 46503: gap of 100 bp 47207 47206: contig of 703 bp in length 47207 47306: gap of 100 bp 47307 47306: gap of 689 bp in length 47307 47306: gap of 689 bp in length 47307 47395: contig of 689 bp in length 48096 48039: gap of 100 bp 48094 4963: contig of 570 bp in length 49464 49563: gap of 100 bp in length 49564 49563: gap of 100 bp in length 50251 5050: gap of 100 bp 50351 51992 51993: contig of 741 bp in length 51910 52009: gap of 100 bp 51910 52009: gap of 100 bp 51910 52009: gap of 100 bp 52010 52010 52714 52813: gap of 100 bp 52010 52714 52813: gap of 100 bp 52814 52813: gap of 100 bp 52814 52813: gap of 100 bp 52814 52814 52813: gap of 100 bp 52814 52813: gap of 100 bp 52814 52813: gap of 100 bp 52814 52813: gap of 100 bp 52814 52813: gap of 100 bp 52814 52813: gap of 100 bp 52814 52813: gap of 100 bp 52814 52813: gap of 100 bp 52814 52813: gap of 100 bp 52814 52813: gap of 100 bp 52814 52813: gap of 100 bp 52814 52813: gap of 100 bp 52814 52813: gap of 100 bp 52814 52813: gap of 100 bp 52814 52814 52813: gap of 100 bp 52814 52813 54437: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54437: gap of 100 bp 55155: contig of 718 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.5%; Score 18.8; DB 2; 90.9%; Pred. No. 2.4e+02; ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 77471 GACGTTGACAACAGCGGTCTCT 77492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 142971)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC020629
AC020629.6 GI:7656675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GACGITGACAACGGCGGITICI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53627
54338
54438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Simi
Matches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
AC020629/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

us-09-270-437d-14.rge

REFERENCE AUTHORS TITLE JOURNAL

REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

COMMENT

	(n) angaactett (n) gaactettec (n) gagcacctet (n) gagcacctet (n) aatatggtat (n) gataccaca	* * *	100	1.01 qxfo. Location/Qualifiers 114297 	14'236 258anily="A-rich" 258378 /rpt_family="Aluyb" /rpt_family="Alusx" /rpt_family="Alusx" /rpt_family="Alusx" /rpt_family="Alusx" /rpt_family="Alusx" /rpt_family="Aliger2a" /rpt_family="MSTD" 3283502 /standard_name="G05956" /standard_name="G05956" /standard_name="Cda0yb04"
16604 18385 218879 21881 221806 221906 38915 38915 55675 57675 94121 95230 95231 10168	120978 120980 139508 139508 139698 140104	# P P P P P P P P P P P P P P P P P P P	•	Version:	repeat_region repeat_region repeat_region repeat_region STS
Baylor Plaza, Houston, TX 77030, USA  S (bases 1 to 142971)  S Worley, K.C.  Direct Submission  L Submitted (27-APR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  R (bases 1 to 142971)  S Worley, K.C.  Direct Submission  L Submitted (28-APR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  S (bases 1 to 142971)  Morley, K.C.  Direct Submission  S (bases 1 to 142971)  Morley, K.C.  Direct Submission  S (bases 1 to 142971)  Morley, K.C.  Submitted (07-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Of Molecular and Human Genetics, Baylor College of Medicine, One Of Molecular and Human Genetics, Baylor College of Medicine, One Of Molecular and Human Genetics, College of Medicine, One On Apr 27, 2000 this sequence version replaced gi:7025656.  INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email	~ ~ ~ ~ ~	Total mapping efforts.  Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.  Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 18-34) to the EST and CDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.	SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.	QUALLIY OF INIVIDIAL BASES: This sequence meets stringent quality atandards - estimated error rate less than 1 per 10;000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.  QUALSTAT-REPORT	Contig length  Contig length  Phrap values in estimate:  Average error rate (BCM-Phrap estimate):  Praction of Phrap values lees than 40:  Number of Consensus changing edits:  Number of N's in consensus:  Number of N's in consensus changing edits:  Position  Original+Context  Edited+Context  Bitted+Context  Edited+Context  Edited+Context  12018  Edited+Context  Edited+Conte

```
Young, G., Zainoun
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                      49578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human.
                                                                                                                                                                                                                                                                                                                             RESULT 14
AC015706/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTG 12-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Huf; Hucs. Frans. Proposica cultivar-group).
Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Subararyophyta; Virighjalnata; Streptcophyta; Embryophyta; Poaceae;
Enrhartoideae; Oryzae; Oryza.
1 (pasea I to 174623)
1 (pasea I to 174623)
1 Abdran, T.R., McCombie, W., Mohapatra, T. and Singh, N.K.
Genomic sequence for Oryza sativa chromosome 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (26-JAN-2002) Indian Initiative for Rice Genome
Submitted (26-JAN-2002) Indian Initiative for Rice Genome
Submitted, Nava Road, New Delhi 110012, India
Institute, Pusa Road, New Delhi 110012, India
3 (bases 1 to 174623)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-JUN-2002) IIRGS, NRC on Plant BioTechnology, Indian Agricultural Research Institute, LBS Centre, New Delhi, Delhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa (japonica cultivar-group) chromosome 11 clone OSJUBA0038F07, *** SEQUENCING IN PROGRESS ***, 4 ordered pieces
                                                                                                                        /rpt_family="Aludb"
complement(4544. .4681)
/rpt_family="MIR"
/rpt_family="MIR"
/rpt_family="MIR"
/rote="Region similar to Hs#S953417 oa06g05.sl Homo sapiens cDNA: AA765439"
5553. .5859
/note="Region similar to Hs#S1195593 qt69f10.xl Homo sapiens cDNA: AI285403"
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110012, India
On Jun 12, 2002 this sequence version replaced gi:20564464.

* NOTE: This is a 'working daft' sequence. It currently
* consists of 4 contigs. Gaps between the contigs
* are represented as runs of N. The order of the piaces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
3585. .3735
//note="Region similar to Hs#S936143 aj27d02.s1 Homo
sapiens CDNA: AA789222"
3885. .3910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence will be replaced as soon as it is available and by the finished sequence as soon as it is available and the accession number will be preserved.

1 3956: contig of 3956 bp in length 4057 8421: contig of unknown length 8422 73067; contig of 4365 bp in length 8521: gap of unknown length 8527 73067; contig of 64546 bp in length 73068 73167; captig of unknown length 73168 174623; contig of 101456 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                          Length 142971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sharma, T.R., McCombie, W., Mohapatra, T. and Singh, N.K. Direct Submission
                                                                                                                                                                                                                                                                                                                                      Score 18.8; DB 9; Length 1
Pred. No. 2.4e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174623 bp
                                                                                 /rpt family="(TA)n"
complement (3917. .4030)
/rpt family="AluJb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .174623
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 133396 GACGITGACAACAGGGTCTCI 133375
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GACGTTGACAACGGCGGTTTCT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC108224.3 GI:21392687
HTG; HTGS_PHASE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 174623)
                                                                                                                                                                                                                                                                                                                                             85.5%;
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 90.9
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Singh, N.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC108224
                                                                        repeat_region
                                                                                                                 repeat_region
                                                                                                                                                          repeat_region
                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                    misc_feature
      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
AC108224
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

source

```
Mipublished

Biren, B. Linton, L. Nusbaum, C., Lander, E., Allen, N., Anderson, M., Biren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Bara, M., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Blown, M., Casllano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Caslera, C., Candagelo, M., Collins, S., Collymore, A., Horton, L., Galagan, J., Gardyna, S., Garant, G., Rann, L., Karatas, A., Hotton, L., Galagan, J., Gardyna, S., Grant, G., Kann, L., Karatas, A., Klein, J., Hehoraky, J., Lieu, C., Looke, K., Mcdonald, P., Marquis, N., Lehoczky, J., Lieu, C., Looke, K., Mcdonald, P., Marquis, N., Lehoczky, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Fastage, S., Tirkell, A., Vassiliev, H., Vo'Connor, T., O'Donnell, P., Naylor, J. Stojanovic, N., Subramanian, A., Talams, J., Tesfaye, S., Tirkell, A., Vassiliev, H., Vo'A., Wheeler, J., Wu, X., Tesfaye, S., Tirkell, A., Vassiliev, H., Vo'A., Wheeler, J., Wu, X., Nayman, D., Ye, W.J., Zimmer, A. and Zody, M.

Albases 1 to 182695

Biren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Biren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Barren, B., Linton, L., Nusbaum, C., Lander, R., Patzhigh, M., Gastle, A., Gooke, P., Dekrellano, K., Dewar, K., Diaz, J. S., Cooke, P., Castle, A., Horton, L., Karatas, A., Hollow, J., Gardyna, S., Goyette, M., Graham, L., Kalein, J., Lavine, R., Lieu, C., Ling, S., Goyette, M., Graham, L., Kalein, J., Lavine, R., Lieu, C., Ling, S., Hagos, B., Heaford, A., Horton, L., Kalein, J., Lavine, R., Lieu, C., Ling, S., Goyette, M., Grand, Pierre, N., Grand, G., Hagos, B., Heaford, A., Horton, L., Kalein, J., Lavine, R., Schauer, S., Goyette, M., Grand, V., Morrow, P., McCarth, M., Meneus, L., Michon, S., Seprecer, B., Seprecer, B., Seprecer, B., Seprecer, B., Seprecer, B., Seprecer, B., Seprecer, B., Seprecer, B., Seprecer, B., Seprece
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182695 bp. DNA linear HTG 24-AUG-2002
Homo sapiens chromosome 1 clone RP11-325P15 map 1, WORKING DRAFT
SEQUENCE, 17 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 182695)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 1, clone RP11-325P15
                                                                                                                                                                                                                                                                                                                                             Gaps
/organism="Oryza sativa (japonica cultivar-group)"
/db_xref="taxon:39947"
/chromosome="11"
                                                                                                                                                                                                                                                               Length 174623;
                                                                                                                                                                                                                                                                                                                                             ..
                                                                                                                                                              441 others
                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                       Score 18.8; DB 2;
Pred. No. 2.3e+02;
0; Mismatches 2;
                                                                                                                                                                  37968 g 48745 t
                                                                                                                        /clone="OSJNBa0038F07"
a 37891 c 37968 g 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC015706
AC015706.3 GI:8096833
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 150055 GACGGTGACAACGGTGGTTTCT 150076
                                                                                                                                                                                                                                                                                                                                                                                                                              1 GACGTTGACAACGGCGGTTTCT 22
                                                                                                                                                                                                                                                                               Query Match 85.5%;
Best Local Similarity 90.9%;
Matches 20; Conservative
```

```
56372
                                                                                                                  misc_feature
                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
NGU43735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
A Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On MAY 26, 2000 this sequence version replaced gi:6454072.

All repeats were identified using RepeatMasker:
Smit, A.P.A. & Green, P. (1996-1997)
http://frp.genome.washington.edu/RM/RepeatMasker.html
Center: Whitehead Institute/ MIT Center for Genome Research
Center: Whitehead Institute/ MIT Center for Genome Research
Center: Code: MIE
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center project name: 11.182
Center clone name: 11.182
Center clone name: 325 p 15
Center clone name: 325 p 25
Center clone name: 325 p 25
Center clone name: 325 p 25
Center clone name: 11.182
Center project name: 11.182
Center project name: 11.182
Center project name: 11.182
Center project name: 11.182
Center clone name: 325 p 25
Center clone name: 325 p 25
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Center clone name: 325 p 35
Ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert size: 181000; agarose-fp
Insert size: 181095; sum-of-contigs
Quality coverage: 4.2 in Q20 bases; agarose-fp
Quality coverage: 4.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93231 93330: gap of 100 bp 93331 116951: contig of 23621 bp in length 116952 177051: gap of 100 bp 117052 143611: contig of 26560 bp in length 143712 182695: contig of 38984 bp in length Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75145 75244: gap of 100 bp
75245 93230: contig of 17986 bp in length
93231 93330: gap of 100 bp
93331 116951: contig of 23621 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 2035: contig of 2035 bp in length
2036 2135: gap of 100 bp
2136 6069: contig of 3934 bp in length
6070 6169: gap of 100 bp
6170 10460: contig of 4291 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37001 37100: gap of 100 bp 1.0 mg 137101 45183: contig of 8083 bp in length 45184 45289; gap of 100 bp 53421: contig of 8138 bp in length 53422 53521: gap of 100 bp 53522 64476: contig of 10955 bp in length 64472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64576: gap of 100 bp
75144: contig of 10568 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10461 10560: gap of 100 bp 10561 14300: contig of 3740 bp in length 14301 14400: gap of 100 bp 14401 18480: contig of 4080 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18481 18580: gap of 100 bp 18581 23093: contig of 4513 bp in length 23094 23193: gap of 100 bp 23194 28213: contig of 5020 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ip of 100 bp contig of 4495 bp in length ap of 100 bp contig of 4092 bp in length contig of 4092 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32809 32908; gap of
32909 37000; cont
37001 37100; gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28214 28313: gap of 28314 32808: con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53522 53521:
53522 6447
64477 64576:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bource
              JOURNAL
                                                                              COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
```

/map="1

```
BCT 30-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGU43735
Neisseria gonorrhoeae restriction/modification system, M.NgoV cytosine methylase (dcmE) gene, complete cds, and R.NgoV Testriction endonuclease (dcrE) gene, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stein, D.C., Gunn, J.S., Radlinska, M. and Piekarowicz, A. Restriction and modification systems of Neisseria gonorrhoeae 95331562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria gonorrhoeae strain=WR302.
Neisseria gonorrhoeae
Bacteria, Proteobacteria, beta subdivision, Neisseriaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 182695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
clone lib="RPCI-11 Human Male BAC" 1. .2035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.5%; Score 18.8; DB 2;
90.9%; Pred. No. 2.3e+02;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lote="assembly_fragment"
36165 c 37419 g 51126 t
                                                                                                                                  14401. .18480
/note="assembly_fragment"
                                           2136. .6069
/note="assembly_fragment"
                                                                       6170. 10460
/note="assembly_fragment"
                                                                                                  10561. 14300 // note="assembly_fragment"
                                                                                                                                                                 note="assembly_fragment"
                                                                                                                                                                                                                                                                                                 note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                             53522. ...64476
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                         64577, 75144
/note="assembly_fragment"
75245, 93230
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28314. .32808
/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                 15284. .53421
'note="assembly_fragment
                                                                                                                                                                                                                                                                    vector_side:right"
32909. .37000
                                                                                                                                                                                                                                                                                                                                                                                  clone_end:SP6 __
vector_mide:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 19692 GACGTTGACAACAGTGGTTTCT 19671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .43712, .182695
note="assembly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GACGTTGACAACGGCGGTTTCT 22
                                                                                                                                                                                                                                                         clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U43735.1 GI:1165240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 2219)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7607490
2 (bases 1 to 2219)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 90.9°
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stein, D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
```

```
/translation="MikLTAQQIFDKLLDEEKILSANGQIRFFLGDVDIIVKQKDVVG
NIOGMIAKMETEFDVGTNTQMPPDFFLNKKDRSRELLEVKAFNRNACPGFDIA
DFKMYSDESFISPISGCRLFNIGYDMDDNGNVTIKDLWLKKVWQITRSMDGWAINFKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVLKQNYPDEVPYGDITKIETGDIPPDILLAGFPCQAFSFACKRLGFEDTRGTLFFD
VARILKAKKPKGFILENVEGLVTHDRKDSTQKIGRTLTVILETLEALGYYVSWKVLNA
KEFGIPQNRKRIYLTGSLKSKPDLSFETSPSPKLKNILESGLPTESSPFIKKLLKKFP
                                                                                                                                                                                                                                                                                                                 /trans]_table=11
/product="isopropylmalate isomerase"
/protein id="AAA86267.1"
/borein id="GI:1165247.1"
/translation="VDRPFKEVFANEGYRLSIDLAEQTLTTPGGETFTFDITEHRKHC
/translation="VDRPFKEVFANEGYRLSIDLAEQTLTTPGGETFTFDITEHRKHC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MQQIKFIDLFSGMSGIRKGFEQACRKQSVACECVFTSEIKPAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SELYGKSYKDKRGGKUNIHSWDIELKGAYTEEEKQLLNILLKERRKKNGLQKIGIDW
DGMPLTKAQISTFYKHPDLQNILDSLTDKGYLVLEHPKQKIGGGRIKDESLPKGYNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKKSFEINKILDPNDVAPTLFAMDMEHLFVVDNGGLRTLTGKEGLRLFGYPDDYPF
Direct Submission.
Submitted (20-DEC-1995) Daniel C. Stein, Microbiology, Univ.
Maryland, College Park, MD 20742, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon_start=1
|transT_table=11
|producE=*R.NgoV_restriction_endonuclease"
|protein_id=*RAAA86269.1"
|db_xref="GI:1165243"
                                                                                     1. .2219
/organism="Neisseria gonorrhoeae"
/dstrain="WR302"
/db_xref="taxon:485"
/clone="pJM5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PKKDRCDLLGNTVAVPVIKAVSERLLHTL"
                                                                                                                                                                                                                                                                               function="leucine biosynthesis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'transI_table=11
'product="M.NgoV DNA methylase"
'protein_id="AAA86268.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unction="restriction enzyme"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unction="cytosine methylase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            575 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    db xref="GI:1165242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 476 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKAWCIKSARVFGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      695. .>2219
gene="dcrE"
                                                                                                                                                                                                                                                                                                        codon start=
transl_table
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .695. .2219
gene="dcrE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           08. .1679
gene="dcmE"
                                                                                                                                                                                                                    gene="leuD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08. .1679
gene="dcmE"
                                                                                                                                                                                                                                                                 gene≂"leuD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 427 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   741 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
         TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                             CDS
                                                                        FEATURES
```

Query Match
83.6%; Score 18.4; DB 1; Length 2219;
Best Local Similarity 95.0%; Pred. No. 5.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0;
Qy 1 GACGTIGACAACGGCGGTTT 20

ö

Gaps

 Search completed: April 18, 2003, 06:31:06 Job time : 501 secs

· -

Н

```
April 18, 2003, 04:12:35 ; Search time 98 Seconds (without alignments) 505.551 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N_Geneseq_101002:*
|:_/SIDSZ/gcgdata/geneseq/genesegn-embl/NA1980.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS2/gcgdata/geneseq/geneseqn-emb/NA1984.
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   geneseqn-embl/NA1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genesegn-emp1/NA1989
                                                                                                                                                                                                                                                                                                                                                                                                                                        4370478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991
GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /SIDS2/gcgdata/geneseq/geneseqn-emb
                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                              2185239 seqs, 1125999159 residues
                                                                            OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                  1 gacgttgacaacggcggtttct 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gcgdata/geneseg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /SIDS2/gcgdata/geneseg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDS2/gcgdata/geneseg/
                                                                                                                                                                                                                                                                                                             IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                       US-09-270-437D-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIDS2
                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                          Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                            Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description		FCK primer for DNA	Human colon cancer	DNA encoding novel	An alternative for	DNA encoding cance	DNA encoding novel	Himan CONT nemil	Manual Court encount	DNA polymerase III	DNA nolvmerses III
SUMMARIES		10	AA236160	AAHATOTT	AAS 70081	1000000	C 10 10 10 10 10 10 10 10 10 10 10 10 10	AA436152	AAS / 0982	AAS26150	ABI.87975	201010	9/6/0704
		DB	5	21	16	5	16	1 0	2	22	24		9
		re Match Length DB I	22	424	2010	3283	3412	7770	000	4000	666	000	
df	Query	Match	100.0	100.0	100.0	100.0	100.0	0.0		7007	83.6	83.6	•
		Score	22	22	22	22	22	20	3 6	77	18.4	18.4	
	ult	و	н	N	m	4	ហ	v		٠,	20	σ	
	Result			υ	U	υ	υ	U	•	) :	υ	U	

DNA polymerase III	7 '	N moningitial ba	Notes of a mental particular part	Notes a meningic	Neighberia meningit	n. meningicials B	nervous	human secreted pro	Diosophila melanog	Diceopula melanog		Prosopiila melanog		_	m	Arabidopsis thalls	Human ORFX polynuc			Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Human ORFX polynuc	Bacillus lichenifo	. licheniformis		DNA encoding the m	Bacillus lichenifo	Xanthomonas campes	7.47	מקר דוום/ כוודם	gene	o action of	DIA Sequence of Bu	ropionipacteriu	N. meningitidis pa
ABL87977 ABL87978	AAA8173	AAA8146		AAF21609		ABA11525	AAC27430	ABT.0649	ABI.0649	AAH4122	ABLZOOD	AAF12699	AAC47512	AAC34520	AACA3435	ARNOGRA			0.000			AMC#OUV		AAABY4B3	AA231556	MA25230	AACBESS	ABK /535	<b>AAT7543</b>	AAL42599	AAV5873	AAA7530	AAA7530	AAS59549	4448147	
999 24	1289	02634	_	49980	43766	_			543	9980		512												9 0	1026 20	9 0		010	157	390				6050	56485 21	
83.6 83.6	ø	9	9	ø	9					N			76.4	76.4	73.6	73.6	73.6	73.6	73.6	73.6	73.6	73.6	73.6	7.50	73.0		73.0	9 0	73.6	73.6	73.6	73.6	73.6			
α. ω.	18.4	ω.	18.4	18.4	18.4	17.2	17.2	17.2	7	6	17	ġ	Ġ	ø	6	œ.	6	ú						٠.,	16.2			;,	ė,	ċ	ė.	16.2	ů.	ė	9	
c 10						17		c 19	20	c 21		23	24	25	•	c 27	. 28	•	•	c 31			34	35	36	17	3.6	9 6		<b>7</b> 7	41	42	43	44	45	

## ALIGNMENTS

AAZ36160 standard; DNA; 22 BP

RESULT 1

Cancer associated antigen; KOC-1; cancer; vaccine; CT7; PCR primer; ss. PCR primer for DNA encoding cancer associated antigen KOC-3. (LUDW-) LUDWIG INST CANCER RES. 99WO-US05766. 98US-0061709 11-FEB-2000 (first entry) WO9954738-A1. Homo sapiens 17-APR-1998; 16-MAR-1999; 28-OCT-1999. Synthetic. AAZ36160; 

Nucleotides representing cancer-associated genes, used to develop products for the diagnosis, monitoring and treatment of cancers WPI; 2000-013284/01.

Knuth A, Old LJ;

Jager E,

Gure A, Tsang S, Stockert E,

Chen Y,

```
PCR primers AAZ36159-60 were used to amplify a cancer associated antigen gene designated XCC-3. The specification also describes a cancer gene designated ACC-3. The specification also describes a cancer associated antigen designated CT7. The CT7 polymucleotide was isolated from SK-MEL-37 melanoma cells. The polymucleotide has some homology with from SK-MEL-37 melanoma cells. The polymetide has some homology with the protein has a repetitive pattern, with repeats rich in terminal of the protein has a repetitive pattern, with repeats rich in terminal of the protein, and ending a repetitive pattern, with repeats rich in the peptide given in AAY43877. The CT7 polypetide can be processed to the peptides which provoke lysis by cytolytic T cells. The polymucleotides peptides which provoke lysis by cytolytic T cells. The polymucleotides and polypeptides can be used for treating a cancerous condition and a cancer associated attigens can be used as an immunogenic or vaccine composition with an attigens can be used as an immunogenic or vaccine composition with an adjuvant, e.g. a cytokine, a saponin, or granulocyte macrophage-colony cadjuvant, e.g. a cytokine, a saponin, or granulocyte macrophage-colony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention describes a library of polymucleotides comprising mucleotide sequences (given in AAH10067 to AAH11145). Also described (1) an isolated polymucleotide (1) having at least 90% identity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human colon cancer cell line Km12L4-A cDNA library derived sequence #945.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Labat I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; diagnosis; colon cancer; cancer; màlignant; chromosome mapping;
detection; colon cancer cell line Kml2L4-A; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sudduth-Klinger J;
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger (Glese K, Randazzo F, Kennedy GC, Pot D, Kassam A); manac R, Crkvenjakov R, Dickson M, Drmanac S, Labx Kita D, Garcia V, Jones LW, Stache-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotide library comprising 1079 defined sequences, useful the form of an array to detect cancer or susceptibility to cancer
                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                    100.0%; Score 22; DB 21; Length 22; 100.0%; Pred. No. 0.36;
                                                                                                                                                                                                                                                                                                                                                                         0, Indels
                                                                                                                                                                                                                                                                                                   Sequence 22 BP; 4 A; 5 C; 7 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 454; 502pp; English.
Claim 108; Page 13; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH31011 standard; cDNA; 424 BP
                                                                                                                                                                                                                                                                                                                                                                                                               1 GACGITGACAACGGCGGITTCT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GACGTTGACAACGGCGGTTTCT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0102161.
98US-0102180.
98US-0102380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0103815.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US22226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d C, Giese K, F
C. Drwanac R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leshkowitz D, Kita D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-293155/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHIRON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200018916-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Williams LT,
Reinhard C,
Lamson G, D:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-0CT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH31011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CHIR )
                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH31011/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

```
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of terrape seq sequence tags polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques for reacte normal activity of (II) or to treat disease states involving (II). II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as
                                                                                                                                                                                                                                                                                                                                                                                         ö
            one of the 1079 sequences; (2) a recombinant host cell containing (17); (4) an inclated polypeptide (II) encoded by (I); (4) an antibody that specifically binds to (II); (5) a vector comprising (I); and (6) a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell comprising detecting a gene product encoded by state of a mammalian cell comprising detecting a gene product encoded by of the 1079 sequences given in the specification. The polymucleotides are used to monitor patients having (or susceptible) to cancer to detect potentially malignant events at a molecular level before they are potentially malignant events at a molecular level before they are petectable at a gross morphological level. The polymucleotides are also useful for monitoring the efficacy of various therapies and preventive useful for chromosome mapping and detection of transcription levels. The 1079 polymucleotide sequences were derived from a human colon cancer cell line Km12L4-A cDNA library.
(2) a recombinant host cell containing (I);
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 22; DB 21; Length 424; 100.0%; Pred. No. 0.43; ... ... ... ... ... ... ... ... ... Indels (
                                                                                                                                                                                                                                                                                                             Sequence 424 BP; 117 A; 106 C; 111 G; 90 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding novel human diagnostic protein #6785.
                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID No 6785; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1981/c
AAS70981 standard; cDNA; 2010 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                      GACGTTGACAACGGCGGTTTCT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 GACGTTGACAACGCCGGTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity ...
                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-639362/73.
P-PSDB; ABG06794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS70981;
                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS70981/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
```

```
a food supplement. (II) and its binding partners are useful in medical limaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and disposetic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fib. wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                                                                                       Sequence 2010 BP; 565 A; 552 C; 532 G; 361 T; 0 other;
  888888888888888888
```

```
Score 22; DB 23; Length 2010;
Pred. No. 0.48;
; Mismatches 0; Indels 0;
/ Match
Local Similarity 100.0%; Pi
188 22; Conservative 0;
                                                      1 GACGTTGACAACGGCGGTTTCT 22
   Query Match
                Best Loca
Matches
                                                                                  g
                                                        ઠે
```

Gaps

ö

421 GACGTTGACAACGCGGTTTCT 400

```
AAZ36154/c
ID AAZ36154 standard; DNA; 3283 BP
   AAZ36154;
```

11-FEB-2000 (first entry)

An alternative form of DNA encoding cancer associated antigen KOC-3.

Cancer associated antigen; KOC-3; cancer; vaccine; CT7; ss.

Homo sapiens

WO9954738-A1

28-OCT-1999,

99WO-US05766 16-MAR-1999;

98US-0061709 17-APR-1998; (LUDW-) LUDWIG INST CANCER RES

Knuth A, Jager E, Stockert E, Gure A, Tsang S, WPI; 2000-013284/01 Chen Y,

old LJ;

Nucleotides representing cancer-associated genes, used to develop products for the diagnosis, monitoring and treatment of cancers

Claim 55; Page 42-43; 44pp; English.

The present sequence represents an alternative form of a cancer associated antigen gene designated KOC-3. The specification also describes a cancer associated antigen designated CT7. The CT7 describes a cancer associated artigen designated CT7. The CT7 polynciactide was isolated from SK-MSL-37 melanoma calls. The Colyneptide has some homology with MAGB-10, limited to about 210 carboxy cerminal amino acids. The amino terminal of the protein has a repetitive pattern, with repeats rich in serine, proline, glutamine and leucine, and an almost invariable core of the peptide given in AAY43877. The CT7 polypeptide can be processed to peptides and polypeptides can be used for treating a cancerous condition and screening for or diagnosing cancerous conditions. The cancer associated antigens can be used as an immunogenic or vaccine composition with an adjuvant, e.g. a cytokine, a saponin, or

Sequence 3283 BP; 945 A; 833 C; 779 G; 725 T; 1 other;

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a cancer associated antigen gene designated KOC-3. The specification also describes a cancer associated antigen designated Trom SK-MEL-37 melanoma cells. The CT7 polymucleotide was isolated from SK-MEL-37 melanoma cells. The polypeptide has some homology with terminal of the protein has a repetitive pattern, with repeats rich in serine, proline, glutamine and leucine, and an almost invariable core of peptide given in AAY43877. The CT7 polypeptide can be processed to peptides which provoke lysis by cytolytic T cells. The polymucleotides and polypeptides can be used for treating a cancerous condition and antigens can be used an annexe associated antigens can be used an annexe on an almost invariable core and polypeptides an an immunogenic or vaccine composition with an antigens can be used as an immunogenic or vaccine composition with an
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         old LJ;
                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleotides representing cancer-associated genes, used to develo
products for the diagnosis, monitoring and treatment of cancers
       100.0%; Score 22; DB 21; Length 3283; 100.0%; Pred. No. 0.49;
                                                                                                                                                                                                                                                                                     Cancer associated antigen; KOC-3; cancer; vaccine; CT7; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Knuth A,
                                          Indela
                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jager E,
                                                                                                                                                                                                                                                       DNA encoding cancer associated antigen KOC-3.
                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stockert E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 55; Page 41; 44pp; English.
                                                                              AAZ36152 standard; DNA; 3412 BP
                                       ö
                                                                 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LUDW-) LUDWIG INST CANCER RES.
                                                                1 GACGTTGACAACGGCGGTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US05766.
                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0061709.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tsang S,
                                                                                                                                                                                                                           11-FEB-2000 (first entry)
                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-013284/01.
                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gure A,
Query Match
Best Local Simi]
Matches 22; (
                                                                                                                                                                                                                                                                                                                                                                                                                                       17-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                           16-MAR-1999;
                                                                                                                                                                                                                                                                                                                                               WO9954738-A1
                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                AAZ36152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen Y,
                                                                                                                                                      AAZ36152/c
                                                                                                                                      RESULT 5
                                                              ઠે
```

100.0%; Score 22; DB 21; Length 3412; 100.0%; Pred. No. 0.49; 1. Indels 0; Mismatches 0; Indels 0; 444 GACGITGACAACGGCGGTTTCT 423 1 GACGIIGACAACGCCGGIITCI 22 l Similarity 100.0%; 22; Conservative ( Query Match Best Local Similarity Best Loca Matches

ö

Gaps

ö

adjuvant, e.g. a cytokine, a saponin, or granulocyte macrophage-colony stimulating factor (GM-CSF).

Sequence 3412 BP; 970 A; 887 C; 804 G; 750 T; 1 other;

AAS70982 standard; cDNA; 3667 BP. RESULT 6 AAS70982/c ID AAS709 XX

AAS70982;

```
07-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                     WO200155322-A2.
                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUG-2000
                                                                                                                                                                                                                                                                                                                     02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2-AUG-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0-JUN-2
     The invention relates to isolated polymucleotide (I) and colored (II) sequences. (I) is useful as hybridisation probes, collypeptide (II) sequences. (I) is useful as hybridisation probes, collymerase chain reaction (PCR) primers, oligomers, and for chromosome polymerase chain reaction (PCR) primers, oligomers, and for chromosome companies are also used in diagnostics as expressed sequence tags continuation of (II) is useful in gene therapy techniques for identifying expressed genes. (I) is useful in gene therapy techniques continuity in useful for generating antibodies against it, detecting or continuitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating ciscorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in the polypeptide and polymucleotide sequences have applications in the polypeptide of genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human and manner in the medical manner.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 22; DB 23; Length 3667; ilarity 100.0%; Pred. No. 0.5; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3667 BP; 1081 A; 882 C; 846 G; 858 T; 0 other;
                                                                              DNA encoding novel human diagnostic protein #6786.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID No 6786; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
AAS26150/c
ID AAS26150 standard; cDNA; 3694 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                810 GACGTTGACAACGGCGGTTTCT 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22
                                                                                                                                                                                                                                                                                                                                                                                                        Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GACGITGACAACGGCGGTTTCT
                                                                                                                                                                                                                                                                                 30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                   31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                     13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
---- 22; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                          Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; ABG06795
                                                                                                                                                                                                                WO200175067-A2
                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                   11-OCT-2001.
```

AAS26150

g

8

```
Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; carbiral ischaemia; anglogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; skin ageing; food additive; preservative; antiproliferation; skin ageing; food additive; preservative; antiproliferative.
Human cDNA encoding a novel secreted protein, Seq ID 329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               000US-0225213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JAN-2001; 2001WO-US01341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
```

```
08-NOV-2000; 2000US-0246475.
08-NOV-2000; 2000US-0246476.
08-NOV-2000; 2000US-0246477.
08-NOV-2000; 2000US-0246523.
08-NOV-2000; 2000US-0246524.
08-NOV-2000; 2000US-0246525.
08-NOV-2000; 2000US-0246526.
08-NOV-2000; 2000US-0246526.
08-NOV-2000; 2000US-0246529.
08-NOV-2000; 2000US-0246611.
08-NOV-2000; 2000US-0246611.
08-NOV-2000; 2000US-0246611.
17-NOV-2000; 2000US-0246611.
17-NOV-2000; 2000US-0246611.
17-NOV-2000; 2000US-0246611.
17-NOV-2000; 2000US-0246611.
17-NOV-2000; 2000US-0246611.
                                                                                                                                                                                                                                               000US-0241826
                                                                                                                                                                                                                                                                                                                                                                                                                              17-NOV-2000; 2000US-0249215.
17-NOV-2000; 2000US-0249216.
17-NOV-2000; 2000US-0249217.
17-NOV-2000; 2000US-0249217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0250160
                                                                                                                                                                                                                                                                                                                                                                                                   17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                            08-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                        17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                             17-NOV-2000;
```

```
The invention relates to isolated nucleic acid molecules and their coded secreted proteins. The nucleic acids and proteins are used to prevent, treat or annellorate a medical condition in e.g. humans, mice, cabbits, goats, horses, cats, dogs, chickens or sheep. They to a pathological condition. Antibodies to the proteins can also to a pathological condition. Antibodies to the proteins can also condition. Antibodies to the proteins can also compared in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassay or enzyme linked immunosophant assays (ELISA). Disorders which are diagnosed or treated include autoimmune disease e.g. rheumatoid arthitis, cardiovascular disorders e.g. rheumatoid arthitis, hyperproliferative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. corneal infections caused by bacteria, viruses and fungical social cardisorders e.g. corneal infection, and many other and ocular disorders e.g. corneal infection, and many other cardisorders e.g. corneal infection, and many other and ocular disorders e.g. corneal infection, and many other corneal infection, and many other corneal infection, and many other and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to resent skin aging due to sunburn, to maintain organs before corneal and other nutritional components. The polypeptides can also be used capabilities, fat content, lipid, protein, carbohydrate, vitamins, capabilities, fat content, lipid, protein, carbohydrate, vitamins, centent encodes a novel secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA polymerase III holoenzyme delta subunit related DNA SEQ ID NO:61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA polymerase III holoenzyme deltá subunit; DNA polymerase III;
DnaX; holA; holB; antibacterial; tuberculostatic; antileprotic;
bacterial infection; DNA replication modulation; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 22; DB 22; Length 3694; Best Local Similarity 100.0%; Pred. No. 0.5; Matches 22; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID No 329; 980pp; English.
                                                                                                                                                                                                                                                                                                                           Rosen CA, Barash SC, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0251988.
2000US-0256719.
2000US-0251479.
2000US-0251856.
2000US-0251868.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1975/c
ABL87975 standard; DNA; 999 BP.
                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                11-DEC-2000; 2000US-0254097
05-JAN-2001; 2001US-0259678
                                                                                                                                                                         2000US-0251989
2000US-0251990
                                                                                                                                                    2000US-0251869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-488783/53.
P-PSDB; AAU16163.
                                                                                                                                                  08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL87975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABL87975/
XX AC ABL8
XX AC ABL8
XX 16-M
DT 16-M
XX DNA
XX DNA
XW DNA
KW DNA
KW DNA
ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

ô

McHenry CS;

Bullard JJ, Janjic N, (REPL-) REPLIDYNE INC.

14-JUL-2000; 2000US-218246P. 28-MAR-2001; 2001US-0818780.

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes nucleic acid sequences encoding a DNA polymerase III holoenzyme delta subunit (I) from bacteria. (I) has antibacterial; tuberculostatic; antileprotic. Methods from the present invention can be used for screening for bacterial DNA polymerase holoenzyme delta subunit proteins and agents that modulate their activity. The agents are useful in the treatment of bacterial activity. The agents are useful in the treatment of bacterial wyersinia, Corynebacterium, Salmonella, Mycobacterium tuberculosis or M. leprae. The invention provides a convenient means of identifying compounds which modulate DNA replication in bacteria and therefore provide antibacterial targets, and which are also useful for amplification of DNA. ABL89335 to ABL88071 and ABB84724 to ABB84816 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid encoding a DNA polymerase III holoenzyme delta subunit from bacteria, useful for screening agents that modulate the subunit activity which is useful in the treatment of bacterial infections e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA polymerase III holoenzyme delta subunit related DNA SEQ ID NO:62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA polymerase III holoenzyme delta subunit; DNA polymerase III; DnaX; holA; holB; antibacterial; tuberculostatic; antileprotic; bacterial infection; DNA replication modulation; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
83.6%; Score 18.4; DB 24; Length 999;
Best Local Similarity 95.0%; Pred. No. 25;
Matches 19; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 999 BP; 219 A; 262 C; 328 G; 190 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 282; 500pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                  McHenry CS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABL87976 standard; DNA; 999 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 621 GACGTTGGCAACGGCGGTTT 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GACGTTGACAACGGCGGTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-JUL-2001; 2001WO-US22395.
                                                                                                                                                                                             .6-JUL-2001; 2001WO-US22395.
                                                                                                                                                                                                                                                       14-JUL-2000; 2000US-218246P.
28-MAR-2001; 2001US-0818780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S. pyogenes and S. aureus -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                      Bullard JJ, Janjic N,
Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                     (REPL-) REPLIDYNE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-164785/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; ABB84744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200206532-A1.
                                                                WO200206532-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JAN-2002
                                                                                                                                24-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL87976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL87976/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
```

ઠે g

```
The present invention describes nucleic acid sequences encoding a DNA polymerase III holoenzyme delta subunit (I) from bacteria. (I) has antibacterial; tuberculostatic; antileprotic. Methods from the present invention can be used for screening for bacterial DNA polymerase holoenzyme delta subunit proteins and agents that modulate their activity. The agents are useful in the treatment of bacterial affections e.g. S. progenes, S. aureus S. pneumoniae, Mycoplasma, infections e.g. S. progenes, S. aureus S. pneumoniae, Mycoplasma, versinia, Corynebacterium, Salmonella, Mycobacterium tuberculosis or M. leprae. The invention provides a convenient means of identifying compounds which modulate DNA replication in bacteria and therefore provide antibacterial targets, and which are also useful for amplification of DNA. ABL887935 to ABL88071 and ABB84724 to ABB84816 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA polymerase III holoenzyme delta subunit related DNA SEQ ID NO:64.
                                                                                                                                                             Nucleic acid encoding a DNA polymerase III holoenzyme delta subunit from bacteria, useful for screening agents that modulate the subunit activity which is useful in the treatment of bacterial infections e.g. S. pyogenes and S. aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA polymerase III holoenzyme delta subunit; DNA polymerase III; bnaX; holA; holB; antibacterial; tuberculostatic; antileprotic; bacterial infection; DNA replication modulation; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18.4; DB 24; Length 999;
Pred. No. 25;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 999 BP; 219 A; 263 C; 327 G; 190 T; 0 other;
                                                                                                                                                                                                                                                    Disclosure; Page 283-284; 500pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bullard JJ, Janjic N, McHenry CS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1977/c
ABL87977 standard; DNA; 999 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  621 GACGTTGGCAACGGCGGTTT 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-JUL-2000; 2000US-218246P.
28-MAR-2001; 2001US-0818780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-JUL-2001; 2001WO-US22395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GACGTTGACAACGGCGGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (REPL-) REPLIDYNE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 19; Conserv
                                                                                                                         WPI; 2002-164785/21.
                                                                                                                                            P-PSDB; ABB84744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200206532-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL87977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL87977,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

WPI; 2002-164785/21

Disclosure; Page 287-289; 500pp; English

```
The present invention describes nucleic acid sequences encoding a DNA polymerase III holoenzyme delta subunit (I) from bacteria. (I) has antibacterial; tuberculostatic; antileprotic. Methods from the present invention can be used for screening for bacterial DNA polymerase holoenzyme delta subunit proteins and agents that modulate their activity. The agents are useful in the treatment of bacterial infections e.g. S. pyogenes, S. aureus, S. pneumoniae, Mycoplasma, Yersinia, Corynebacterium, Salmonella, Mycobacterium tuberculosis or Compounds which modulate DNA replication in bacteria and therefore provide antibacterial targets, and which are also useful for amplification of DNA. ABL87935 to ABL88071 and ABB84724 to ABB84816
                                                            Nucleic acid encoding a DNA polymerase III holoenzyme delta subunit from bacteria, useful for screening agents that modulate the subunit activity which is useful in the treatment of bacterial infections e.g. S. pyogenes and S. aureus -
                                                                                                                                                                       Disclosure, Fig 4U; 500pp; English.
                       P-PSDB; ABB84745
```

ö 83.6%; Score 18.4; DB 24; Length 999; 95.0%; Pred. No. 25; Live 0; Mismatches 1; Indels 0 621 GACGTTGGCAACGGCGGTTT 602 20 1 GACGTTGACAACGGCGGTTT Local Similarity 95.0 Query Match Best Local Si Matches 19; ઠે 유

Sequence 999 BP; 222 A; 260 C; 327 G; 190 T; 0 other;

ö

'978/c ABL87978 standard; DNA; 999 16-MAY-2002 (first entry) ABL87978; 

DNA polymerase III holoenzyme delta subunit related DNA SEQ ID NO:65.

DNA polymerase III holoenzyme delta subunit; DNA polymerase III; DnaX; holA; holB; antibacterial; tuberculostatic; antileprotic; bacterial infection; DNA replication modulation; gene; ds.

Neisseria meningitidis.

WO200206532-A1.

24-JAN-2002.

16-JUL-2001; 2001WO-US22395.

Tettelin H, Venter JC; Ratti G, Scarselli M, Scarlato V;

Peterson J, C, Mora M,

Frazer CM, Hickey E, Masignani V, Galeotti Rappuoli R, Pizza M;

WPI; 2000-318079/27.

14-JUL-2000; 2000US-218246P. 28-MAR-2001; 2001US-0818780.

(REPL-) REPLIDYNE INC

S, McHenry Bullard JJ, Janjic N,

WPI; 2002-164785/21. P-PSDB; ABB84745 Nucleic acid encoding a DNA polymerase III holoenzyme delta subunit from bacteria, useful for screening agents that modulate the subunit activity which is useful in the treatment of bacterial infections e.g. S. pyogenes and S. aureus

The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82214 represent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA81260 to AAA81303 and AAB25620 to AAB25653 represent Neisseria DNA sequences and their corresponding proteins; AAA81254 to AAA81259 and AAA81321 represent PCR primers used in the

Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea -

Claim 7; Page 1561-1565; 1760pp; English.

```
ö
                    The present invention describes nucleic acid sequences encoding a DNA polymerase III holoenzyme delta subunit (1) from bacteria. (I) has antibacterial; tuberculostatic; antileprotic. Methods from the present invention can be used for screening for bacterial DNA polymerase holoenzyme delta subunit proteins and agents that modulate their activity. The agents are useful in the treatment of bacterial infections e.g. S. pyogenes, S. aureus, S. pneumonlae, Mycoplasma, Yersinia, Corynebacterium, Salmonella, Mycobacterium tuberculosis or W. leprae. The invention provides a convenient means of identifying compounds which modulate DNA replication in bacteria and therefore provide antibacterial targets, and which are also useful for amplification of DNA ABL87935 to ABL8901 and ABB4724 to ABB84816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis, Neisseria gonorrheae, genome; immunogenic;
antigen; vaccine; diagnosis; infection; antibacterial; identification;
Meningococcus B; MenB; ds.
                                                                                                                                                                                                                                                                                                 Gape
                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                         represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                  DB 24; Length 999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N. meningitidis partial DNA sequence gnm_280 SEQ ID NO:280.
                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                 Sequence 999 BP; 222 A; 260 C; 327 G; 190 T; 0 other;
                                                                                                                                                                                                                                                               83.6%; Score 18.4; C
95.0%; Pred. No. 25;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    AAA81733 standard; DNA; 12893
                                                                                                                                                                                                                                                                                                                                                621 GACGTTGGCAACGCCGTTT 602
                                                                                                                                                                                                                                                                                                                        20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US23573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0103794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0132068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                    1 GACGITGACAACGGCGGTTT
                                                                                                                                                                                                                                                                                           19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200022430-A2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-APR-2000.
                                                                                                                                                                                                           nvention.
                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
AAA81733/C
ID AAA81
ઠ
```

```
isolation of Neisseria meningitidis DNA sequences; and AAA81322 to
AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF
CC AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF
CC sequences, which are all used in the exemplification of the present
CC invention. The nucleic acid sequences, protein sequences, and antibodies
composition can be used in the manufacture of a composition. The
composition can be used as a medicament (or in the manufacture of a
composition. The composition can be used as medicament (or in the manufacture of a
composition. The composition of sequences we seemed to against all serotypes;
cc medicaments of vaccines against Meningococcus B; against all serotypes;
cc and/or against all pathogenic Neissariae. Identification of sequences
cc and/or against all pathogenic Neissariae. Identification of sequences
cc and/or against all pathogenic Neissariae. Identification of sequences
cc medicamenty organism-specific probes. Attempts to make efficacious
particularly organism-specific probes. Attempts to make efficacious
cc multivalent vaccines have also been tried but none have successfully
covercome antigenic variability. The provision of further, complete
cc sequences may provide an opportunity to identify secreted or surface
cc exposed proteins that may be presumed targets for the immune system and
which are not antigenically variable or at least more conserved than
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tettelin H, Venter JC;
Ratti G, Scarselli M, Scarlato V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis, Neisseria gonorrheae; genome; immunogenic;
antigen; vaccine; diagnosis; infection; antibacterial; identification;
Meningococcus B; MenB; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                DB 21; Length 12893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                                            Sequence 12893 BP; 2829 A; 3164 C; 3741 G; 3159 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N. meningitidis partial DNA sequence gnm_12 SEQ ID NO:12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  83.6%; Score 18.4; E
95.0%; Pred. No. 29;
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peterson J,
C, Mora M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA81464 standard; DNA; 102634 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2453 GACGTTGGCAACGGCGGTTT 2434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0103794.
99US-0132068.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US23573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GACGITGACAACGGCGGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Frazer CM, Hickey E,
Masignani V, Galeotti
Rappuoli R, Pizza M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-318079/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200022430-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA81464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
AAA81464/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 원
                       5555555555555555555555555555555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
```

Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea

The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Neisseria meningitidis genomic DNA

Claim 7; Page 353-383; 1760pp; English.

```
Sequences, AAA81260 to AAA81303 and AAB25620 to AAB25663 represent CC Neisseria DNA sequences and their corresponding proteins, AAA81254 to AAA81259 and AAA81321 represent PCP primers used in the isolation of Neisseria meningitidis DNA sequences, and AAA8132 to AAA81322 represent Neisseria meningitidis MenB polynucleotide ORF AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF composition. The nucleic acid sequences, protein sequences, and antibodies invention. The nucleic acid sequences, protein sequences, and antibodies composition can be used in the manufacture of a composition of the present composition can be used in the manufacture of a composition can be used as a medicament (or in the manufacture of a composition can be used as a medicament (or in the manufacture of a composition can be used as a medicament (or in the manufacture of a components of vaccines against Meningococcus B, against all serotypes; be components of vaccines against Meningococcus B, against all serotypes; components of vaccines against All pathogenic Neissariae. Identification of sequences conforted particularly organism-specific probes. Attempts to make efficacious particularly organism-specific probes. Attempts to make efficacious conserved proteins have also been tried but none have successfully overcome antigenic variability The provision of further, complete exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Masignani V.
Rappuoli R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis B full length genome sequence and open reading frames are used to detect, treat and prevent Neisserial infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine;
diagnosis; antigen; detection; infection; gene therapy; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21; Length 102634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence 102634 BP; 23871 A; 24828 C; 27888 G; 26042 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis B nucleotide sequence SEQ ID NO:109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter JC,
Scarlato V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peterson J, Tettelin H,
Ratti G, Scarselli M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18.4; 1
Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; Appendix A; 692pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF21608 standard; DNA; 349980 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 44045 Gredrichehadedededrir 44026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-APR-1999; 99US-0132068.
08-OCT-1999; 99WO-US23573.
28-FEB-2000; 2000GB-0004695.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GACGTTGACAACGGCGGTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAR-2000; 2000WO-US05928
                                                                                                                                                                                                                                                                                                                                                                                                                             other more variable regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHIRON CORP.
INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 95.03
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pizza M, Hickey E,
Galeotti C, Mora M,
Frazer CM, Grandi G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-647603/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200066791-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF21608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CHIR )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
AAF21608/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          $$$$$$$$$$$$$$$$$$$$$$$$$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
```

Claim 7; Appendix A; 692pp; English.

The present invention describes the full length genome of
Neisseria meningitidis B (NMB). The sequences in AAP21544 and AAF21607
To AAP21613 represent fragments of the NMB genomic sequence, as the
sequence was too long to go in a record on its own it was split into 8
sequences which overlap each other at the beginning and end of each
sequence by 49980 bp (1.e. the last 49980 bp of AAF21544 is repeated at
the beginning of AAF21609, and so on). AAF21545 to AAF21589 encode the
consistent a proteins given in AAF35850 to AAF31589 encode the
consistent a proteins given in AAF35850 to AAF31589 to
the present invention. The NMB genome and fragments from it have
contibacterial activity, and can be used in the exemplification of
antibacterial activity, and can be used in vaccines and gene therapy.
Contibacterial compositions for treating or preventing infection
contibacterial bacteria or as a diagnostic reagent for detecting the
presence of Neisserial bacteria or of antibodies raised to Neisserial
contibacteria. Computers, computer memory, computer storage medium or computer
contibacteria. Computers of an as a diagnostic reagent for detecting the
contibacteria. Computers computer memory, computer storage medium or computer
contibacteria. Computers within the NMB genome. The DNA sequences provide
cor coding sequences within the NMB genome. The DNA sequences provide
contibacterial reads.
Contibacterial pacterial or of antibacterial and contibacterial activity of the contibacterial activity.
Contibacterial computers within the NMB genome contibacterial activity of the contibacterial activity of the contibacterial activity of the contibacterial activity of the contibacterial activity of the contibacterial activity of the contibacterial activity of the contibacterial activity of the contibacterial activity of the contibacterial activity of the contibacterial activity of the contibacterial activity of the contibacterial activity of the contibacterial activity of the contibacterial activity of the contibacterial activity of the \$

Sequence 349980 BP; 82523 A; 82940 C; 96712 G; 87805 T; 0 other;

0; Gaps 83.6%; Score 18.4; DB 21; Length 349980; 95.0%; Pred. No. 36; tive 0; Mismatches 1; Indels 0; ( Conservative Query Match Best Local Similarity

ö

Db 140350 GACGTTGGCAACGGCGTTT 140331 8 1 GACGTTGACAACGGCGGTTT

ઠે

AAF21609 standard; DNA; 349980 BP.

AAF21609;

(first entry) 13-MAR-2001

Neisseria meningitidis B nucleotide sequence SEQ ID NO:110.

Nelsseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine; diagnosis; antigen; detection; infection; gene therapy; antibacterial;

Neisseria meningitidis.

WO200066791-A1

09-NOV-2000.

08-MAR-2000; 2000WO-US05928.

30-APR-1999; 99US-0132068 08-OCT-1999; 99WO-US23573. 28-FEB-2000; 2000GB-0004695.

(CHIR ) CHIRON CORP. (GENO-) INST GENOMIC RES.

Masignani V; Rappuoli R; Venter JC, Scarlato V, Pizza M, Hickey B, Peterson J, Tettelin H, Galeotti C, Mora M, Ratti G, Scarselli M, Frazer CM, Grandi G; 

WPI; 2000-647603/62.

Neisseria meningitidis B full length genome sequence and open reading frames are used to detect, treat and prevent Neisserial infections -

The Purchason describes the full tengen genome or Neisseria meningitidis B (NMB). The sequences in AAF21644 and AAF21607 to AAF21613 represent fragments of the NMB genomic sequence, as the sequence was too long to go in a record on its own it was split into 8 sequences which overlap each other at the beginning and end of each sequence by 49980 bp (i.e. the last 49980 bp of AAF2164 is repeated at sequence by 49980 bp (i.e. the last 49980 bp of AAF2164 is repeated at the beginning of AAF21607, the last 49980 bp of AAF21607 are repeated to the beginning of AAF21608, and 80 on). AAF2165 to AAF21689 and code the Neisseria proteins given in AAB5850 to AAB58593, and AAF21589 to AAF21606 represent PCR primers which are used in the exemplification of the present invention. The NMB genome and fragments from it have antibacterial activity, and can be used in vaccines and gene therapy.

Neisseria nucleic acids, proteins and/or antibodies which binds to the presence of Neisserial bacteria or as a diagnostic reagent for deceting the computer. Computers, computer memory, computer storage medium or computer databases can be used in a search to identify open reading frames (ORFs) or coding sequences within the NMB genome. The DNA sequences provide comportunities to find antigenic or immunogenic proteins which are near an effective in vaccines than the outer membrane proteins currently present invention describes the full length genome of 

Sequence 349980 BP; 81351 A; 86755 C; 95584 G; 86290 T; 0 other;

Gaps Score 18.4; DB 21; Length 349980; Pred. No. 36; 0; Mismatches 1; Indels 0; ( ô 1; Indels 95.08; 83.68; Query Match Best Local Similarity 95.0 Matches 19, Conservative

ö

Db 147755 Gregrigacaacgecegrir 147736 1 GACGTTGACAACGGCGGTTT 20 ò

Search completed: April 18, 2003, 05:48:05 Job time : 251 secs

				•			!
	•						
				•			
					•		
e village e vill							
ings -					•		
					-4		
j. evi							. :
	•	•					
						#	
E.			en en en en en en en en en en en en en e				
ili Agent Agent Magaza							<i>#</i>
			•				
			•				
						. :	
			Service of the Servic				
	*					a a	
				કે <del>વ</del>		* 3	
							•
			en ger Grander (1984) Grander (1984)				
6.	is Second		en de la companya de la companya de la companya de la companya de la companya de la companya de la companya de La companya de la companya de la companya de la companya de la companya de la companya de la companya de la co			•	
					A Company of the Company		
					•		
		en en en en en en en en en en en en en e			•		
*				•			
Si di	A.M.					·	S. Sec.
				· · · · · · · · · · · · · · · · · · ·			
							i di Santa Santa Santa Santa Santa Santa Santa Santa Santa Santa Santa Santa Santa Santa Santa Santa Santa San Santa Santa Santa Santa Santa Santa Santa Santa Santa Santa Santa Santa Santa Santa Santa Santa Santa Santa Sa
				•	•	·	\$ P.

```
APPLICANT: Teang, Solam
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Jager, Elke
APPLICANT: Muth, Alexander
APPLICANT: Muth, Alexander
APPLICANT: Old, Lloyd J.

IITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated
TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
FILE REFERENCE: LUD 5538
CURRENT APPLICATION NUMBER: US/09/061,709B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gure, Ali
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13, Appl
Sequence 290, Appl
Sequence 12, Appl
Sequence 15, Anni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Appl
Sequence 1, Appli
                                                                                                            April 18, 2003, 04:53:41 ; Search time 21.5 Seconds (without alignments) 313.809 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Appl
Sequence 6, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18,
Sequence 3, A
Sequence 10,
Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 23,
Sequence 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, /
Sequence 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3
Sequence 1
Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cgn2_6/ptodata/1/ina/5A_COMB.seg:*
/cgn2_6/ptodata/1/ina/5B_COMB.seg:*
/cgn2_6/ptodata/1/ina/6A_COMB.seg:*
/cgn2_6/ptodata/1/ina/B_COMB.seg:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seg:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seg:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-061-709-6
US-08-328-322-16
US-08-328-322-16
US-09-30-328-132-13
US-09-198-956-7
US-09-188-956-7
US-09-188-956-3
US-09-546-500-1
US-09-546-501-3
US-09-64-531-3
US-09-64-531-3
US-09-670-141-7
US-09-670-141-7
US-09-670-141-7
US-09-670-141-7
US-09-670-141-7
US-09-670-141-7
US-09-670-141-7
US-09-670-141-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-835-500A-3
US-08-816-500A-1
US-08-916-1979A-13
US-09-654-289-13
US-08-998-416-290
US-08-91-9570-12
US-08-91-9570-12
US-08-91-918-15
                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                441362 seqs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-635-121-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                      - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0*
Maximum Match 100*
Listing first 45 summaries
                                                                                                                                                                                                                                     1 gacgttgacaacggcggtttct 22
                                                                                                                                                                                                                                                                      IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Issued_Patents_NA:*
                                                                                                                                                                                           US-09-270-437D-14
                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
                                                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                                                                                      Scoring table:
                                                                      OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database:
                                                                                                                                                                                                                                   Seguence:
                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0 0
```

Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 92, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 1, Appli Sequence 19, Appli Sequence 19, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli	ncoding Cancer Associated Uses Thereof	ngth 3283; Indels 0; Gaps 0;
6718 2 US-08-962-284-1 10718 3 US-08-325-426B-1 20235 1 US-07-642-734C-3 20235 3 US-08-439-009A-3 50 4 US-08-237-712-92 397 4 US-09-237-712-92 111282 4 US-09-754-250-3 4403765 4 US-09-103-840A-1 341 2 US-09-103-840A-1 341 4 US-09-103-840A-1 409 2 US-08-975-316-39 409 4 US-09-615-192A-11 1155 2 US-08-169-192A-118 1155 2 US-08-169-915 1155 2 US-08-169-915 1165 4 US-08-382-452D-15	ALIGNMENTS  1-8/C Application US/09061709B 6293364 Chen, Yao-Tseng Gure, Ali Tsang, Solam Stocker, Elisabeth Jager, Elke Kutth, Alexander Old, Lloyd J. NVENTION: Isolated Nucleic Acid Molecules Encoding NVENTION: Isolated Nucleic Acid Molecules Encoding NVENTION: Antigen, The Antigens Per Se, And Uses TI ELICATION NUMBER: US/09/061,709B LING DATE: 1998-04-17 SEQ ID NOS: 8 Homo sapiens	; Score 22; DB 4; Le ; Pred. No. 0.062; 0; Mismatches 0; 22 423 61709B
28 15.2 69.1 6 31 15.2 69.1 10 31 15.2 69.1 20 32 15.2 69.1 20 33 15.2 69.1 20 34 14.8 67.3 440 38 14.6 66.4 41 14.6 66.4 42 14.6 66.4 44 14.6 66.4 45 14.6 66.4 45 14.6 66.4 46 14.6 66.4 47 14.6 66.4 48 14.6 66.4 49 14.6 66.4 49 14.6 66.4 49 14.6 66.4 49 14.6 66.4 49 14.6 66.4	1 661-709-8/c ence 8, Application int No. 6297364 RAL INFORMATION: LICANT: Chen, Yao-7 LICANT: Grae, Ali LICANT: Grae, Ali LICANT: Stocker, Ble LICANT: Stocker, Ble LICANT: Jager, Elke LICANT: Jager, Elke LICANT: Old, Lloyd LE OF INVENTION: Is REFERRACE: LUD 55 RENT FILING DATE: 1 BER OF SEQ ID NOS: LD NO 8 ENT APPLICATION NO RENT FILING DATE: 1 DNO 8 ENT APPLICATION NO RENT FILING DATE: 1 DNO 8 ENT APPLICATION NO RENT FILING DATE: 1 DNO 8 ENT APPLICATION NO RENT FILING DATE: 1 DNO 8 ENT APPLICATION NO RENT FILING DATE: 1 DNO 8 ENT APPLICATION NO RENT FILING DATE: 1 DRA 9 FRINT FILING DATE: 1 DRA 9 FRINT FILING DATE: 1 DRA 1283 FRINT FILING BATE: 1 DRA 1283 FRINT FILING BATE: 1 DRA 1283 FRINT FILING BATE: 1 DRA 1283 FRINT FILING BATE: 1 DRA 1283 FRINT FILING BATE: 1 DRA 1283 FRINT FILING BATE: 1 DRA 1283 FRINT FILING BATE: 1 DRA 1283 FRINT FILING BATE: 1 DRA 1283 FRINT FILING BATE: 1 DRA 1283 FRINT FILING BATE: 1 DRA 1283 FRINT FILING BATE: 1 DRA 1283 FRINT FILING BATE: 1 DRA 1283 FRINT FILING BATE: 1 DRA 1283 FRINT FILING BATE: 1 DRA 1283 FRINT FILING BATE: 1 DRA 1283 FRINT FILING BATE: 1	Query Match  Best Local Similarity 100.0%; Sco  Bast Local Similarity 100.0%; Pre  Matches 22; Conservative 0; M  1 GAGGTTGACAACGCGGTTTCT 22
· · · · · · · · · · · · · · · · · · ·	RESULT Seque Pace Pace Pace Pace Pace Pace Pace Pac	Quer Best Matc Qy Db Db NS-09- ; Sequ- ; Pate:

```
436 GACATTGACAAGGACGGTTTC 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GACGITGACAACGGCGGTITC 21
307 GACATIGACAAGGACGGITIC 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
181..652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INDIVIDUAL ISOLATE: INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54..104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 350 Cambz
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , NAME/KEY:
, LOCATION:
US-08-328-322-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
US-09-073-684-1
                                                                                                                                                         RESULT 4
US-08-328-322-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, Application US/08328322
| Sequence 16, Application US/08328322
| Patent No. 5723436
| CENERAL INFORMATION:
| APPLICANT: Huang, Laidiang | Applicant: Cyert, Martha S. | TITLE OF INVENTION: Calcineurin Interacting Protein Compositions | TITLE OF INVENTION: and Methods | NUMBER OF SEQUENCES: 23 | CORRESPONDENCE ADDRESS: ADDRESSE: Dehlinger & Associates | STREET: 350 Cambridge Avenue, Suite 250 | CITY: Palo Alto | CITY: Palo Alto | CITY: Correspondence | Correspondence | Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: Correspondence | CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: CITY: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.6%; Score 16.2; DB 1; Length 524; 85.7%; Pred. No. 33; tive 0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Score 22; DB 4; Length 3412;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: USA

ZIP: 94306

COMPUTER READABLE FORM:
MEDILUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
SOFTWARE: PATENTIN RALEASE #1.0, Version #1.25
CLASSIPICATION DATE: 24-OCT-1994
CLASSIPICATION NUMBER: US/08/328,322
FILING DATE: 24-OCT-1994
CLASSIPICATION: 530
CLASSIPICATION: 530
TTCARSIPICATION: MADER: B600-0151.10
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
ORIGINAL SOURCE: coding sequence of CNB1
INDIVIDUAL ISOLATE: coding sequence of CNB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          444 GACGTTGACAACGGCGGTTTCT 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GACGTTGACAACGGCGGTTTCT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                        CURRENT FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 6
LENGTH: 3412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY:
; LOCATION:
US-08-328-322-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
US-08-328-322-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                          US-09-061-709-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
                                                                                                                                                                                                                                                                                                                                                      FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

```
Sequence 13, 4p3

Bequence 13, 743436

GENERAL INFORMATION
GENT Huang, Laidiang
APPLICANT: Cyert, Martha S.
TITLE OF INVENTION: Calcineurin Interacting Protein Compositions
TITLE OF INVENTION: Calcineurin Interacting Protein Compositions
TITLE OF INVENTION: Calcineurin Interacting Protein Compositions
TITLE OF INVENTION: Calcineurin Interacting Protein Compositions
OUNDER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Deblinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 73.6%; Score 16.2; DB 1; Length 812; Best Local Similarity 85.7%; Pred. No. 35; Matches 18; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genomic DNA fragment containing full CNB1 coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SUGNERRY APPLICATION DATA:
APPLICATION NUMBER: US/08/328,322
FILING DATE: 24-OCT-1994
CLASSIFICATION NUMBER: B38,615
REPRENCE/DOCKET NUMBER: 8600-0151.10
TELECOMMUNICATION NUMBER: 8600
TELEFRONE: (415) 324-0860
TELEFRONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTER STICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gequence 1, Application US/09073684
| Sequence 1, Application US/09073684
| Patent No. 6124127
| GENERAL INFORMATION:
| APPLICANT: Andersen, Lene No. 6124127boe | APPLICANT: Sch lein, Martin APPLICANT: Lange, Niels Erik Krebs
```

; 0

1 GACGITGACAACGGCGGTITC 21

8

```
51 GTCATTGACAGCGGCGGTTTC 71
                       1 GACGTTGACAACGGCGGTTTC 21
                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
              AUMBER OF SEQUENCES: NO. 014414/61 FECCACE LYBEES

CORRESPONDENCE ADDRESS:
ADDRESSEE No. 61241270 No. 6124127th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STRET: NY
COUNTRY: USA
ZIP: 10174
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: SEADABLE FORM:
MEDIUM TYPE: OF Windows Version 2.0
COMPUTER: FASESOG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,684
FILING DATE: 6 MAX-1998
CLASSIFICATION: 0506
ATTORNEY/AGENT INFORMATION:
NAME: Carol E. ROZZEK
REGISTRATION NUMBER: 35,993
TELEBHONE: 212-867-0123
TELEBHONE: 212-867-0123
TELEBHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73.6%; Score 16.2; DB 3; Length 1026; llarity 85.7%; Pred. No. 36; Conservative 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.6%; Score 16.2; DB 4; Length 1026; 85.7%; Pred. No. 36; tive 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Addersen, Lene N.
APPLICANT: Schuled.n, Martin
APPLICANT: Schuled.n, Martin
APPLICANT: Lange, Niels Erik K.
APPLICANT: Lange, Niels Erik K.
APPLICANT: School.n, Mads E.
APPLICANT: School.n, Kirk
ITLE OF INVENTION: Pectin Degrading Enzymes From Bacillus
ITLE OF INVENTION: Licheniformis
FILE REFERRNCE: 537, 200-120
CURRENT FILING DATE: 1998-11-24
EARLIER APPLICATION NUMBER: 1344/97
EARLIER FILING DATE: 1997-11-24
EARLIER FILING DATE: 1997-11-24
SERLIER FILING DATE: 1997-12-02
NUMBER OF SO ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
LENGTH: 1026
TYPE: DNA

CNGANISM: Bacillus licheniformis
US-09-198-956-7
TITLE OF INVENTION: No. 6124127el Pectate Lyases
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
US-09-198-956-7
; Sequence 7, Application US/09198956
; Patent No. 6165769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1026 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

i TOPOLOGY: linear

US-09-073-684-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GACGTTGACAACGGCGGTTTC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 Grcarrdacaccccccrrrc 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              유
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.6%; Score 16.2; DB 4; Length 1026; 85.7%; Pred. No. 36; 1ive 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-395-858A-11

Sequence 11, Application US/09395858A

Sequence 11, Application US/09395858A

Factor No. 642014

GENERAL INFORMATION:
APPLICANT: Feng Xu
TITLE OF INVEXTION: Machods For Using Pectate Lyases In
TITLE OF INVEXTION: Baking
FILE REFERENCE: 5670.200-US

CURRENT APPLICATION NUMBER: US/09/395,858A

CURRENT APPLICATION NUMBER: 09/156,298

PRIOR APPLICATION NUMBER: 09/156,298

PRIOR FILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FRSESEQ for Windows Version 3.0

SEQ ID NO 11

LENGTH: 1026
                                                                                                                                                                                                                                                                                        APPLICANT: Moller, Soren
APPLICANT: Glad, Sanne O. S.
APPLICANT: Kauppinen, Markus S.
APPLICANT: Kauppinen, Markus S.
APPLICANT: Kongsbak, Lars
ITILE OF INVENTION: No. 6187580el Pectate Lyases
ITILE OF INVENTION: No. 6187580el Pectate Lyases
FILE REFERENCE: 5378, 200-US
CURRENT FILING DATE: 1997-11-24
FRIOR FILING DATE: 1997-11-24
FRIOR PELICATION NUMBER: 1344/97
FRIOR FILING DATE: 1997-11-24
FRIOR PELICATION NUMBER: 60/067, 249
FRIOR APPLICATION NUMBER: 60/067, 249
FRIOR APPLICATION NUMBER: 09/073, 684
FRIOR APPLICATION NUMBER: 09/073, 684
FRIOR APPLICATION NUMBER: 09/073, 684
FRIOR APPLICATION NUMBER: 09/184, 217
FRIOR APPLICATION NUMBER: 09/184, 217
FRIOR APPLICATION NUMBER: 09/184, 217
FRIOR APPLICATION NUMBER: 09/184, 217
FRIOR APPLICATION NUMBER: 09/184, 217
FRIOR APPLICATION NUMBER: 09/184, 217
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRI
Sequence 3, Application US/09198955A
Patent No. 6187580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Bacillus liceniformis
US-09-395-858A-11
                                                                                                                         Andersen, Lene N.
Schulein, Martin
Lange, Niels E.
Bjornvad, Mads E.
Moller, Soren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 GTCATTGACAGCGGCGGTTTC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 85.7
Matches 18; Conservative
```

```
10174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-694-531-3
                                                                                                                                     COUNTRY:
                                                                         ö
                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09546500
; Patent No. 6280995;
APPLICANT: Andersen, Lene No. 6280995boe
APPLICANT: Lange, Niels Erik Krebs
APPLICANT: Lange, Niels Erik Krebs
APPLICANT: Lange, Niels Erik Krebs
APPLICANT: Lange, Niels Erik Krebs
APPLICANT: Lange, Niels Erik Krebs
APPLICANT: Lange, Niels Erik Krebs
APPLICANT: Lange, Niels Erik Krebs
APPLICANT: Lange, Niels Erik Krebs
APPLICANT: Lange, Niels Erik Krebs
APPLICANT: Lange, Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
APPLICANT: Niels Erik Krebs
A
                                                                             Gaps
                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16.2; DB 4; Length 1026;
Pred. No. 36;
0; Mismatches 3; Indels 0:
   Length 1026;
                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Andersen, Lene No. 6284524boe
APPLICANT: Sch lein, Martin
APPLICANT: Lange, Niels Brik Krebs
TITLE OF INVENTION: No. 6284524el Pectate Lyases
CORRESPONDENCES: 10
              DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
CHOFFWARE: FRE4CSEQ for Windows Version 2.0
SUFFRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/546,500
ch 73.6%; Score 16.2; 1 Similarity 85.7%; Pred. No. 36; 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/073,684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-546-762-1; Sequence 1, Application US/09546762; Patent No. 6284524; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: CARCI E. ROZEK
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 5543
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.6%;
milarity 85.7%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 Grcarrdácágcegegerrre 71
                                                                                                                                                              21
                                                                                                                                                                                                                          sı drcarrdacaccececerrrc 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1026 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GACGITGACAACGGCGGTITC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1026 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 212-867-0123
                                                                                                                                                              1 GACGITGACAACGGCGGITIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 18; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
           Query Match
Best Local Similarity
Matches 18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-546-500-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                            RESULT 9
US-09-546-500-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                        셤
```

```
62845240 No. 6284524disk of No. 6284524th America, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 1026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kongsbak, Lars
TITLE OF INVENTION: No. 6368843el Pectate Lyases
FILE REPERENCE: 5378.200.US
CURRENT APPLICATION NUMBER: US/09/694,531
CURRENT FILING DATE: 2000-10-23
                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/546,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 73.6%; Score 16.2; Best Local Similarity 85.7%; Pred. No. 36 Matches 18; Conservative 0; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 5543.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 1334/97
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/067,249
PRIOR PELING DATE: 1997-12-02
PRIOR APPLICATION NUMBER: 60/067,240
PRIOR PELING DATE: 1997-12-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1997-12-02
PRIOR APPLICATION UNMBER: 09/073,684
PRIOR FILING:DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 09/184,217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/198,955
                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/073,684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09694531 Patent No. 6368843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1998-11-24
PRIOR APPLICATION NUMBER: 1343/97
PRIOR FILING DATE: 1997-11-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glad, Sanne O. S.
Kauppinen, Markus S.
Schnorr, Kirk
                                    405 Lexington Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GACGITGACAACGGCGGITIC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sı Grcarrdacaccececerric 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schulein, Martin
Lange, Niels E.
Bjornvad, Mads E.
                                                                                                                                                                                        COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Carol E. Rozek
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Andersen, Lene N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
                                                            New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
```

```
Tarrytown
                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-028-934-23
                                                                                                                                                                                                                Ouery Match 73.6%; Score 16.2; DB 4; Length 1026; Best Local Similarity 85.7%; Pred. No. 36; . . . Matches 18; Conservative 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Schulein, Martin
APPLICANT: Andersen, Lene N.
APPLICANT: Andersen, Lene N.
APPLICANT: Genlein, Martin
APPLICANT: Bornord, Mada E.
APPLICANT: Bjornvad, Mada E.
APPLICANT: Bjornvad, Mada E.
TITLE OF INVENTION: Lichenifermis
FILE REPERENCE: 5377.200-US
CURRENT APPLICATION NUMBER: US/09/670,141
FILE APPLICATION NUMBER: US/09/670,141
FRIOR PRING DATE: 1998-11-24
PRIOR APPLICATION NUMBER: 13344/97
PRIOR APPLICATION NUMBER: 60/198,956
PRIOR APPLICATION NUMBER: 1344/97
PRIOR APPLICATION NUMBER: 1997-11-24
PRIOR APPLICATION NUMBER: 60/067,240
PRIOR PRING DATE: 1997-12-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
LENGTH: 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 1026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23, Application US/08729214

Sequence 23, Application US/08729214

PERNEAL INFORMATION:
APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight Steven
APPLICANT: Hill, Dwight Steven
APPLICANT: Hyals, John Andrew
APPLICANT: Hyals, John Andrew
APPLICANT: Wan Pee, Kal-Heinz
APPLICANT: Wan Pee, Ral-Heinz
ITLE OF INVENTION: Genes for the synthesis of
ITLE OF INVENTION: Genes for the synthesis of
ITLE OF INVENTION: Antipathogenic substances
CORRESPONDENCE ADDRESS:
STREFT:
STREFT:
                                                                  ; SEQ ID NO 3
i LENGTH: 1026
i TYPE: DNA
i OKGANISM: Bacillus licheniformis - AICC 14580
US-09-694-531-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 73.6%; Score 16.2; I Best Local Similarity 85.7%; Pred. No. 36; Matches 18; Conservative 0; Mismatches
                      NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/09670141
Patent No. 6429000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-670-141-7
                                                                                                                                                                                                                                                                                                            1 GACGITGACAACGGCGGITTC 21
                                                                                                                                                                                                                                                                                                                                                       51 GreatfacageGeegette 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 Grcarrdacaccccccrrrc 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GACGTTGACAACGCCGGTTTC 21
PRIOR FILING DATE: 1998-11-02
                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   윱
```

```
COMPUTER READABLE TONE:
MEDIUM TETER: Florey disk.
COMPUTER: IN PETER: Florey disk.
COMPUTER: IN PC Compatible
COMPUTER: IN PC Compatible
COMPUTER: IN PC Compatible
COMPUTER: IN PC Compatible
COMPUTER: IN PC Compatible
COMPUTER: IN PC Compatible
COMPUTER: IN PC COMPATIBLE
MANEY. MEDILATION NDATA:
ATTORNER'/GERT THYORANTION:
MANEY. MEDILATION NOMER: US /G/07729, 214
ATTORNER'/GERT THYORANTION:
MANEY. MEDILATION NOMER: US /G/07729, 214
TELERONOWING THE SEG UT THOSE /GOVERNOR SEG UT ON COMPATIBLE SEG UT THE MEDILATION NOMER: US /G/07729, 214
TELERONOR SEG UT ON COMPATIBLE ON COMPATIBLE NOW SEG UT ON COMPATIBLE SEG UT AND GENERAL SEG UT AND GENERAL SEG UT ON COMPATIBLE SEG UT AND GENERAL SEG UT ON COMPATIBLE SEG UT AND GENERAL SEG UT ON COMPATIBLE SEG UT OF SEG UT ON COMPATIBLE SEG UT OF SEG UT ON COMPATIBLE SEG UT OF SEG UT OF SEG UT ON COMPATIBLE SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF SEG UT OF
```

```
APPLICANT: Hammer, Philip E.
APPLICANT: van Pee, Karl-Heinz
APPLICANT: Kirner, Sabine
TITLE OF INVENTION: Pyrrolnitrin Biosynthesis Genes and Uses
TITLE OF INVENTION: Pyrrolnitrin Biosynthesis Genes and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 37
CORRESONDENCE ADDRESS:
STORTES OND FAILTIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3; Length 8931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                   ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: APPLICATION DATA:
SOFTWARE: PATCHILL Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/028,934
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.6%; Score 16.2; L
85.7%; Pred. No. 48;
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:

PRIOR APPLICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/729,214

FILING DATE: 09-0CT-1996

PRIOR APPLICATION NUMBER: US 08/258,261

ATTORNEY AGENT INFORMATION:

NAME: Meigs, J. Timothy:

REGISTRATION NUMBER: 38,24

REGISTRATION NUMBER: 38,24

REGISTRATION NUMBER: 38,24

REGISTRATION NUMBER: 38,24

RETERBHORE: 919-541-8689

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE GHARACTERISTICS:

LENGTH: 8931 base pairs

TYPE: nucleic acid

STRANDEDMESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:
                                                                                                                                                                                                                                                          ADDRESSEE: No. 6117670artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS

! LOCATION: 5145..6266

! OTHER INFORMATION: /product= "PrnD"

US-09-028-934-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 2270..3355
OTHER INFORMATION: /product= "PrnB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 3421..5121
OTHER INFORMATION: /product= "PrnC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 657..2267
OTHER INFORMATION: /product= "PrnA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GACGTTGACAACGGCGGTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: 2270..3355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                NC
USA
                                                                                                                                                                                                                                                                                                                                          STATE: NO COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 85.7%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                 COUNTRY: USA ZIP: 27709

ZIP: 27709

COMPUTER: READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: LIBM PC COMPATIBLE
COMPUTER: EN PACE COMPATIBLE
COMPUTER: DATE PC-DS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
SOFTWARE: PATENTIN BATE:
APPLICATION NUMBER: US/09/028,934
FLING DATE: 09-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/729,214
FILING DATE: 09-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/258,261
FILING DATE: 09-OCT-1996
PRIOR APPLICATION NUMBER: US 08/258,261
FILING DATE: 09-OCT-1996
THING DATE: 09-OCT-1996
THING DATE: 09-OCT-1996
THING DATE: 09-OCT-1996
THING DATE: 09-OCT-1996
THING DATE: 09-OCT-1996
THING DATE: 09-OCT-1996
THELEPATION NUMBER: 38,241
REPERRICE/DOCKET NUMBER: CGC1506/CIP7
TELEPAX: 919-541-8689
TREERANTION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 6250 base pairs
TYPE: MUCHEL
                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6117670artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS

LOCATION: 5093..6202

OTHER INFORMATION: /product= "PrnD"

US-09-028-934-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: CDS
NAME/COS 3368..5065
OTHER INFORMATION: /product= "PrnC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 615..2228
OTHER INFORMATION: /product= "PrnA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 2231..3313
OTHER INFORMATION: /product= "PrnB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 28, Application US/09028934
Patent No. 6117670
GENERAL INFORMATION:
APPLICANT: Ligon, James M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5555 GACGTCGACAACGGCGACTTC 5575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GACGITGACAACGGCGGTITC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHEȚICAL: NO
                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-028-934-28
```

Gaps

.. 0

se13 dacdredachacddedacrrc se33

Ligon, James M. Hill, Dwight S. Lam, Steven T.

APPLICANT: APPLICANT:

RESULT 15

ઠ

```
Sequence 6, Appli
Sequence 329, Appli
Sequence 3, Appli
Sequence 689, Appli
Sequence 2650, Ap
Sequence 2650, Appli
Sequence 2650, Appli
Sequence 1028, Appli
Sequence 116, Appli
Sequence 1160, Appli
Sequence 1202, Appli
Sequence 1202, Appli
Sequence 1202, Appli
Sequence 1202, Appli
Sequence 1202, Appli
Sequence 1202, Appli
Sequence 1202, Appli
Sequence 243, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Appli
Sequence 6, Appli
                                                                                           April 18, 2003, 06:35:31; Search time 91.3333 Seconds (Without alignments) 241.975 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT Will Pub.seq:*
3: /cgn2_6/ptodata/1/pubpna/PCT Will Pub.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USO8_NEW PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USO8_NEW PUB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO8_NEW PUB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
11: /cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 US-09-899-651-8

10 US-09-899-651-6

10 US-09-764-864-329

10 US-09-938-842A-689

12 US-09-938-842A-689

13 US-09-97-152-3

14 US-09-90-419-28

15 US-09-90-419-28

16 US-09-913-153-59

17 US-09-913-153-59

18 US-09-914-1028

18 US-09-914-300-2660

18 US-09-976-419-28

18 US-09-918-842A-1028

18 US-09-974-300-260

18 US-09-974-300-260

18 US-09-960-352-11807

18 US-09-660-352-11807

18 US-09-660-352-11807

18 US-09-660-352-11807
                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-982-704-12
US-10-062-254-243
US-09-738-626-3451
                                                                                                                                                                                                                                                                                           639749 seqs, 502280978 residues
                                                            OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                       1 gacgttgacaacggcggtttct 22
                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0*
Maximum Match 100*
Listing first 45 summaries
                                                                                                                                                                                                                                       IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                      US-09-270-437D-14
22
                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           011100100000
0000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1026
1035
1653
11035
11462
11462
11462
3057
411
4319
531
1126
1128
11335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
                                                                                                                                                                                    Perfect score:
                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                                                                        Seguence:
                                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Result
```

```
C 20 15.6 70.9 1338 9 US-10-067-974-11 Sequence 11, Appl 22 15.6 70.9 1400 9 US-09-746-666A-43 Sequence 43, Appl 22 15.6 70.9 1596 9 US-09-746-666A-43 Sequence 785, Appl 24 15.6 70.9 330470 9 US-09-738-626-1 Sequence 18, Appl 25 15.4 70.0 3222 10 US-09-738-626-1 Sequence 11, Appl 26 15.2 69.1 266 10 US-09-974-7377 Sequence 7377, Appl 27 15.2 69.1 176 10 US-09-974-730-108 Sequence 7377, Appl 28 15.2 69.1 1376 10 US-09-974-300-108 Sequence 581, Appl 30 15.2 69.1 1376 10 US-09-974-300-2336 Sequence 2135, Appl 27 15.2 69.1 1378 10 US-09-974-300-2336 Sequence 2135, Appl 27 15.2 69.1 1378 10 US-09-974-300-2336 Sequence 2135, Appl 27 15.2 69.1 12860 10 US-09-974-300-2336 Sequence 315, Appl 28 15.2 69.1 12860 10 US-09-974-300-2336 Sequence 3150, Appl 28 15.2 69.1 12860 10 US-09-974-300-2346 Sequence 3150, Appl 28 15.2 69.1 3798 10 US-09-974-300-2346 Sequence 3150, Appl 28 15.2 69.1 3798 10 US-09-974-300-2346 Sequence 3150, Appl 28 15.2 69.1 3798 10 US-09-974-300-315 Sequence 3150, Appl 38 14.8 67.3 3123 10 US-09-974-300-1122 Sequence 3150, Appl 40 14.8 67.3 31257 9 US-09-974-300-322 Sequence 3122, Appl 29 14.8 67.3 3130440 9 US-09-974-300-322 Sequence 3137, Appl 24 14.8 67.3 3130440 9 US-09-974-300-322 Sequence 31, Appl 26 14.8 67.3 3130440 9 US-09-974-300-322 Sequence 31, Appl 26 14.8 67.3 3130440 9 US-09-974-300-322 Sequence 31, Appl 26 14.8 67.3 3130440 9 US-09-974-300-322 Sequence 31, Appl 26 14.8 67.3 3130440 9 US-09-974-300-322 Sequence 31, Appl 26 14.8 67.3 3130440 9 US-09-974-300-322 Sequence 31, Appl 26 14.8 67.3 3130440 9 US-09-974-300-322 Sequence 31, Appl 26 14.8 67.3 3130400 9 US-09-974-300-322 Sequence 31, Appl 36 Sequence 31, Appl 36 Sequence 31, Appl 36 Sequence 32, Appl 36 Sequence 32, Appl 36 Sequence 32, Appl 36 Sequence 32, Appl 36 Sequence 32, Appl 36 Sequence 32, Appl 36 Sequence 32, Appl 36 Sequence 32, Appl 36 Sequence 32, Appl 36 Sequence 32, Appl 36 Sequence 32, Appl 36 Sequence 32, Appl 36 Sequence 32, Appl 36 Sequence 32, Appl 36 Sequence 32, Appl 36 Sequence 32, Appl 36 Sequence 32, Appl 36
```

## ALIGNMENTS

```
US-09-899-651-8/C

Sequence 8, Application US/09899651

Sequence 8, Application US/09899651

Sequence 8, Application US/09899651

Sequence 8, Application US/09899651

Sequence 8, Application US/02011147041

APPLICANT: Gure, Ali

APPLICANT: Tang, Solam

APPLICANT: Stockert, Ellsabeth

APPLICANT: Stockert, Ellsabeth

APPLICANT: Old, Lloyd J.

TITLE OF INVENTION: Associated

TITLE OF INVENTION: Associated

TITLE OF INVENTION: Associated

TITLE OF INVENTION: Associated

TITLE OF INVENTION: Associated

TITLE OF INVENTION: Associated

TITLE OF INVENTION: Associated

TITLE OF INVENTION: Associated

TITLE OF INVENTION: Associated

TITLE OF INVENTION: Associated

TITLE OF INVENTION: Associated

TITLE OF INVENTION: Associated

TITLE OF INVENTION: Associated

TITLE OF INVENTION: Associated

TITLE OF INVENTION: Associated

TITLE OF INVENTION: Associated

TITLE OF INVENTION: Associated

TITLE OF INVENTION: Associated

TITLE OF INVENTION: Associated

TITLE OF INVENTION: Associated

TITLE OF INVENTION: Associated

TITLE OF INVENTION: Associated

TITLE OF INVENTION: Associated

TITLE OF INVENTION: Associated

TITLE OF INVENTION: Associated

TITLE OF INVENTION: Associated

TITLE OF INVENTION: Associated

CURRENT APPLICATION NUMBER: US/09/061,709

NUMBER OF SEQ ID NOS: 8

CURRENT ASSOCIATED

SEQ ID NO 8

TERMINE: DAM

CORGANISM: Homo sapiens

PRACTICACA ASSOCIATED

OUS-09-699-651-8

OUS-09-699-651-8

DA 444 GACCTTGACARCAGCGGGTTTCT 22

OUS-09-699-671-8

DA 444 GACCTTGACARCAGCGGGTTTCT 23
```

ö

US-09-899-651-6/c
; Sequence 6, Application US/09899651
; Patent No. US20020111470A1
; GENERAL INFORMATION:

```
RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                              APPLICANT: Jack. Alexander Applicant: Jack. Applicant: Jack. Alexander Applicant: Jack. Alexander Applicant: Muth, Alexander Applicant: Old, Lloyd J.
TITLE OF INVENTION: Associated TITLE OF INVENTION: Associated TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof TITLE OF INVENTION: ANTIGEN, The Antigens Per Se, And Uses Thereof CURRENT FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: US/09/061,709
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 6
LENGTH: 3412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 329, Application US/09764864

Sequence 329, Application US/09764864

Sequence 329, Application US/09764864

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

TITLE OF INVENTION: NUMBER: US/09/764,864

CURRENT APPLICATION NUMBER: US/09/764,864

CURRENT PILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NOTWHER OF SEQ ID NOS: 1792

SOTUMBER OF SEQ ID NOS: 1792

SEQ ID NO 329

LINGTH: 3694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 22; DB 10; Length 3694; Best Local Similarity 100.0%; Pred. No. 0.06; O; Indels O; Mismatches 22; Conservative O; Mismatches 0; Indels O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 22; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   467 GACGTTGACAACGGCGGTTTCT 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 444 GACGTTGACAACGGCGGTTTCT 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GACGTTGACAACGGCGGTTTCT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CT 22
                                         Tsang, Solam
Stockert, Elisabeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GACGITGACAACGGCGGITI
Chen, Yao-Tseng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
CORGANISM: Homo sapiens
US-09-764-864-329
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-09-764-864-329/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-899-651-6
                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
```

```
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL APPLICANT: Kreps, Joe1
APPLICANT: Kreps, Joe1
APPLICANT: Wang, Xun
APPLICANT: ALN, TONE
TITLE OF INVENTION: SAME, AND METHODS OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REPRENCE: SCRIP1300-3
CURRENT PRILING DATE: 2001-08-24
CURRENT PILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR PELING DATE: 2001-01-16
PRIOR PELING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 689
                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 76.4%; Score 16.8; DB 9; Length 486; Best Local Similarity 90.0%; Pred. No. 23; Matches 18; Conservative 0; Mismatches 2; Indels C
                                                                                                                                                                                                                                                                                                             Query Match 76.4%; Score 16.8; DB 10; Length 369; Best Local Similarity 90.0%; Pred. No. 22; Astches 18; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kongsbak, Lars
TITLE OF INVENTION: No. US20020142438Alel Pectate Lyases
FILE REFERENCE: 5378.200-US
NUMBER OF SEQ ID NOS: 900
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/10072152
Sequence 3, Application US/10072152
Patent No. US20020142438A1
GENERAL INFORMATION:
APPLICANT: Andersen, Lene N.
APPLICANT: Schulein, Martin
APPLICANT: Lange, Niels E.
APPLICANT: Bjornvad, Mads E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 689, Application US/09938842A Patent No. US20020160378A1 GENERAL INFORMATION:
                                                                                                                                                                                                             ; LOCATION: (1)...(369)
; OTHER INFORMATION: n = A,T,C or G
US-09-924-035A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glad, Sanne O. S.
Kauppinen, Markus S.
Schnorr, Kirk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONGANISM: Arabidopsis thaliana US-09-938-842A-689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197 cerrakcakerecerrier 216
                                                                                                                TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAWE/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 CGTTGACAACGGCGGTTTCT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48 cerraacaacreceerricr 67
                                                                                                                                                                                                                                                                                                                                                                                                                             3 CGTTGACAACGGCGGTTTCT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-938-842A-689
```

```
RESULT 9
US-10-169-953-1
                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 12; Length 1026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10; Length 1035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2650, Application US/09974300
| Patent No. US20020146721A1
| GENERAL INFORMATION:
| APPLICANT: Berka, Randy M. APPLICANT: Clausen, ID Groth
| TITLE OF INVENTION: Methods For Monitoring Multiple Gene; TITLE OF INVENTION: Methods For Monitoring Multiple Gene; TITLE OF INVENTION: Expression
| FILE REFERENCE: 10085.500-US
| CURRENT FILING DATE: 2001-10-05
| PRIOR APPLICATION NUMBER: 09/680,598
| PRIOR FILING DATE: 2000-10-06
| PRIOR FILING DATE: 2001-03-27
| NUMBER OF SEQ ID NOS: 8481
| SOFTWARE: PSECSEQ for Windows Version 4.0
| SEQ ID NO 2650
| LENGTH: 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3,
                                                                                                                                                                                                                                                                                                                                                                                                                                             p TYPE: DNA
p ORGANISM: Bacillus licheniformis - ATCC 14580
US-10-072-152-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
73.6%; Score 16.2; I Best Local Similarity 85.7%; Pred. No. 52; Matches 18; Conservative 0; Mismatches
                CURRENT FILING DATE: 2002-02-07
PRIOR APPLICATION NUMBER: US/09/198,955
PRIOR FILING DATE: 1998-11-24
PRIOR FILING DATE: 1998-11-24
PRIOR FILING DATE: 1997-11-24
PRIOR PELING DATE: 1997-11-24
PRIOR PELING DATE: 1997-11-24
PRIOR PELING DATE: 1997-11-24
PRIOR PELING DATE: 1997-11-24
PRIOR PELING DATE: 1997-12-02
PRIOR APPLICATION NUMBER: 60/067,240
PRIOR PELING DATE: 1997-12-02
PRIOR PELING DATE: 1997-12-02
PRIOR PELING DATE: 1997-12-02
PRIOR PELING DATE: 1998-10-02
PRIOR PELING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FRAESEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
73.6%; Score 16.2; E
Best Local Similarity 85.7%; Pred. No. 52;
Matches 18; Conservative 0; Mismatches
CURRENT APPLICATION NUMBER: US/10/072,152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 28, Application US/09906419
Publication No. US20030037357A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-2650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GACGITGACAACGCCGCTTTC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 GTCATTGACAGCGGGGTTTC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GACGTTGACAACGGCGGTTTC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 Grcarrcacaccececirric 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Shockey, Jay
APPLICANT: Schnurr, Judy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
US-09-974-300-2650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
US-09-906-419-28/c
                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1026
                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

```
Sequence 1. Application US/10169953

Sequence 1. Application US/10169953

Sequence 1. Application NO. US20030044915A1

GENERAL INFORMATION:

APPLICANT: PRACE DELNESTE

APPLICANT: PRACE DELNESTE

APPLICANT: PRACE DELNESTE

APPLICANT: PRACE DELNESTE

APPLICANT: PRACE DELNESTE

APPLICANT: PRACE DELNESTE

APPLICANT: PRACE DELNESTE

APPLICANT: PRACE DELNESTE

APPLICANT: PRACE DELNESTE

APPLICANT: PRACE DELNESTE

APPLICANT: PRACE DELNESTE

APPLICANT: MATHOD FOR PREPARING A POLYPEPTIDE SOLUBLE IN AN AQUEOUS SOLVENT

TITLE OF INVENTION: MIT ABSENCE OF DETERGENT

TITLE OF INVENTION: MIT ABSENCE OF DETERGENT

TITLE OF LING DATE: 2002-07-03

CURRENT FILING DATE: 2002-07-03

PRIOR FILING DATE: 2000-01-04

NUMBER OF SEQ ID NOS: 2

SOPTWARE: PATENTING DATE: 2.1

TENCH OF ALL OF THE DATE: 2.1

TENCH OF ALL OF THE DATE: 2.1

TENCH OF ALL OF THE DATE: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                        Score 16.2; DB 9; Length 1653; Pred. No. 56; 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1035;
                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indele
TITLE OF INVENTION: Plant Acyl-CoA Synthetases FILE REFERENCE: DOW-04679 CURRENT APPLICATION NUMBER: US/09/906,419 CURRENT FILING DATE: 2001-07-16 PRIOR PAPLICATION NUMBER: 60/220,474 PRIOR FILING DATE: 2000-07-21 NUMBER OF SEQ ID NOS: 120 SOFTWARE: Patentin version 3.0 LENGTH: 1653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09:813-153-59.
Sequence 59, Application US/09813153
Publication No. US20030045459A1
GENERAL INFORMATION:
TITLE OF INVENTION: 67 Human secreted proteins
TILE REFERENCE: PZ023
CURRENT APPLICATION NUMBER: US/09/813,153
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
71.8%; Score 15.8; Dest Local Similarity 89.5%; Pred. No. 84; Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1014 GACGATTACACCGGCGGTTTC 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1035
TYPE: DNA
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Arabidopeis thaliana
US-09-906-419-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GACGITGACAACGCCGGITIC 21
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 85.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 cerreacaacecrerre 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGTTGACAACGCCGGTTTC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(1032)

FEATURE:

CTHER INFORMATION: P40

US-10-169-953-1
```

```
ID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15.8; DB 10; Length 3057; Pred. No. 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9; Length 1842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2660, Application US/09974300
; Sequence 2660, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
    APPLICANT: Clausen, Ib Groth
    TITLE OF INVENTION: Methods For Monitoring Multiple Gene
    TITLE OF INVENTION: Methods For Monitoring Multiple Gene
    TITLE OF INVENTION: Expression
    TITLE OF INVENTION: Expression
    TITLE OF INVENTION: Expression
    TITLE OF INVENTION: Expression
    TITLE OF INVENTION: Expression
    TITLE OF INVENTION: DO09974,300
    CURRENT FILING DATE: 2001-10-05
    PRIOR FILING DATE: 2001-10-06
    PRIOR FILING DATE: 2001-0-06
    PRIOR FILING DATE: 2001-03-27
    NUMBER: OF EAC ID NOS: 8481
    SOFTWARE: FastSEQ for Windows Version 4.0
    SEQ ID NO 2660
    LENGTH: 3057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLITITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15.8; DF; Pred. No. 91; 0; Mismatches
SAME, AND METHODS OF USE
                        FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11807, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-2660
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA; CRGANISM: Arabidopsis thaliana; US-09-938-842A-1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 1780 GACGATGACCACGGCGGTT 1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 CATTGACAACGCCGATTTC 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 CGTTGACAACGGCGGTTTC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GACGITGACAACGGCGGIT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-09-974-300-2660/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-960-352-11807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Yun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 15.8; DB 9; Length 1279;
Pred. No. 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 9; Length 1462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 957
SOFTMARE: PatentIn Ver. 2.0
SEQ ID NO 515
LENGTH: 1462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PALS
CURRENT APPLICATION NUMBER: US/09/764,872
CURRENT FILING DATE: 2001-01.17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 15.8;
Pred. No. 8
                  PRIOR APPLICATION NUMBER: US/09/363,044
PRIOR FILING DATE: 1999-07-29
PRIOR PELING DATE: 1999-07-30
PRIOR PELING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1028, Application US/09938842A Patent No. US20020160378A1 GENERAL INFORMATION:
                        APPLICATION NUMBER: US/09/363,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-764-872-516
Sequence 516, Application US/09764872; Publication No. US20030050231A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            umery Match 71.8%;
Best Local Similarity 89.5%;
Matches 17; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          740 Argardacaackackirr 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 71.8%;
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               815 Accarcacarceccectrr 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ACGITGACAACGCCGGITT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 ACGITGACAACGCCGGIII 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-872-516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CORGANISM: Homo sapiens
US-09-813-153-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
US-09-938-842A-1028
```

셤

g

ઠ

Search completed: April 18, 2003, 10:16:07 Job time : 96.5 secs

1 GACGITGACAACGGCGGITTCT 22

ઠે

a win	\$; .					
ľ			•			
			•			i
100 m						
E.						
No.						
			•			, 22
F - 7		• •		•		
	•					
No.						·
1000 1000 1000	·					
				•		
1						
**						4
1		•				
			and the second			
P.			•			
14. 14.			*			
, 18°						2.04
						nige.
₩.						
Ì						
1			A STATE OF THE STA		v · · · ·	
4						
					•	
í h						
1						
	$\frac{1}{2} \left( \frac{1}{2} \right) \right) \right) \right) \right)}{1} \right) \right) \right)} \right) \right) \right)} \right) \right) \right) \right)} \right) \right)} \right) \right)} \right) \right)}}}}}}}}$				*.	
					÷	
•						
		ar in the second		The second of th		
						A COLUMN TO THE STATE OF THE ST
Est.					i se s	
						Line and the second sec
			e e e e e e e e e e e e e e e e e e e			
						₩ •
			is the second se		•	*
<b>₹</b>			• • • • • • • • • • • • • • • • • • •		tana di Pinangan di Pinangan di Pinangan di Pinangan di Pinangan di Pinangan di Pinangan di Pinangan di Pinang Pinangan di Pinangan di Pinangan di Pinangan di Pinangan di Pinangan di Pinangan di Pinangan di Pinangan di Pi	- <del></del>
51			en en en en en en en en en en en en en e	et e e e e e e e e e e e e e e e e e e		
				y <del>-</del>		* *
						***
			a .			1
*		er (				

Search completed: April 18, 2003, 07:34:42 Job time : 30.5 sec8

us-09-270-437d-14.rni

						·
		• · · · · · · · · · · · · · · · · · · ·		·		
in the second se						
						d
				wiz j		
k						
		•		•		
		:		•		Constitution of the consti
					1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
- Ter						
				: 5	•	<u>.</u>
		• • • • • • • • • • • • • • • • • • •				
in the second se						
				ą.		
					÷ .	
3					*	
-						
			•			ÿ
	•					. 0

Run on:

```
22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77
                                                                                                                                                                                             April 18, 2003, 05:48:17; Search time 1211 Seconds (without alignments) 456.759 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pending Patents NA Main:*

1: cgn2 6/ptodata/1/pna/USO6 COMB.seq:*
2: cgn2 6/ptodata/1/pna/USO6 COMB.seq:*
3: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
5: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
6: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
7: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
8: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
9: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
11: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
12: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
13: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
14: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
15: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
16: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
17: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
18: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
19: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata/1/pna/USO8 COMB.seq:*
10: cgn2 6/ptodata
GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cgn2_6/ptodata/1/pna/US102A_COMB.seq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24791104 segs, 12571243825 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                        OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                    gacgttgacaacggcggtttct 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                    US-09-270-437D-14
22
                                                                                                                                                                                                                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
```

```
| cgn2_6/ptodata/1/pna/US6000_COMB.seq:*
| cgn2_6/ptodata/1/pna/US6001_COMB.seq:*
| cgn2_6/ptodata/1/pna/US6001_COMB.seq:*
| cgn2_6/ptodata/1/pna/US6002_COMB.seq:*
| cgn2_6/ptodata/1/pna/US6003_COMB.seq:*
| cgn2_6/ptodata/1/pna/US6005_COMB.seq:*
| cgn2_6/ptodata/1/pna/US6005_COMB.seq:*
| cgn2_6/ptodata/1/pna/US6005_COMB.seq:*
| cgn2_6/ptodata/1/pna/US6001_COMB.seq:*
| cgn2_6/ptodata/1/pna/US6010_COMB.seq:*
| cgn2_6/ptodata/1/pna/US6010_COMB.seq:*
| cgn2_6/ptodata/1/pna/US6011_COMB.seq:*
| cgn2_6/ptodata/1/pna/US6012_COMB.seq:*
| cgn2_6/ptodata/1/pna/US6013_COMB.seq:*


Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Description              | Semience 2440 by   |                     |                    |                     | , -                 | Segmence 32161 A    | • • •               | • • •              |                   |                   |                     |                     |                      |                   | Semience 6785 An    | ٠.              | ò              | ٠.               | Seguence 113, App  | _                 |                 | ġ Ġ             |  |
|--------------------------|--------------------|---------------------|--------------------|---------------------|---------------------|---------------------|---------------------|--------------------|-------------------|-------------------|---------------------|---------------------|----------------------|-------------------|---------------------|-----------------|----------------|------------------|--------------------|-------------------|-----------------|-----------------|--|
| ID                       | US-08-959-395-2440 | US-09-539-334-17512 | US-09-652-121-1684 | US-09-289-768-12874 | US-09-939-397-12874 | US-09-289-768-32161 | US-09-939-397-32161 | US-09-652-918-3592 | US-09-304-649-680 | US-09-840-424-680 | US-09-528-409-49810 | US-09-933-524-49810 | US-09-933-524A-49810 | US-60-125-787-430 | PCT-US01-08631-6785 | US-09-270-437-8 | US-09-89-651-8 | 0 100 to 100 EDG | FCI-0201-0130/-113 | US-10-092-302-113 | US-09-270-437-6 | US-09-899-651-6 |  |
| DB                       | 13                 | 20                  | 25                 | 16                  | 35                  | 16                  | 35                  | 25                 | 11                | 32                | 19                  | 35                  | 35                   | 26                | -1                  | 16              | 33             |                  | 4                  | 39                | 16              | 33              |  |
| Query<br>Match Length DB | 272                | 272                 | 347                | 349                 | 349                 | 363                 | 363                 | 409                | 465               | 465               | 467                 | 467                 | 467                  | 546               | 2010                | 3283            | 3283           | 2274             | 7                  | 3374              | 3412            | 3412            |  |
| Query<br>Match           | 100.0              | 100.0               | 100.0              | 100.0               | 100.0               | 100.0               | 100.0               | 100.0              | 100.0             | 100.0             | 100.0               | 100.0               | 100.0                | 100.0             | 100.0               | 100.0           | 100.0          | 000              |                    | 100.0             | 100.0           | 100.0           |  |
| Score                    | 22                 | 22                  | 22                 | 22                  | 22                  | 22                  | 22                  | 22                 | 22                | 22                | 22                  | 22                  | 22                   | 22                | 22                  | 22              | 22             | 22               | 4 (                | 22                | 22              | 22              |  |
| ult<br>No.               | 1                  | <b>6</b>            | m                  | 4                   | D.                  | ø                   | 7                   | æ                  | σ                 | 10                | 11                  | 12                  | 13                   | 14                | 12                  | 16              | 17             | α                | 2 6                | 7                 | 20              | 21              |  |
| Result<br>No.            | υ                  | υ                   | υ                  | υ                   | ט                   | υ                   | υ                   | υ                  | υ                 | υ                 | U                   | U                   | υ                    | υ                 | υ                   | υ               | U              | C                | ) (                | υ                 | υ               | U               |  |

```
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
   TYPE: DNA ORGANISM: Homo sapiens
   RESULT 2
US-09-539-334-17512/c
  à
                      Sequence 27552, A Sequence 6786, Ap Sequence 146, App Sequence 146, App Sequence 129, App Sequence 329, App Sequence 329, App Sequence 9906, Ap Sequence 9743, App Sequence 9743, App Sequence 6556, App Sequence 656, App Sequence 
   Sequence 76081, A
Sequence 60934, A
  APPLICANT: Stuve, Laura L.
APPLICANT: Stuve, Laura L.
APPLICANT: Ito, Laura Y.
APPLICANT: Ito, Laura Y.
APPLICANT: ARCEDION, Ingrid E.
APPLICANT: Maughton, Rebecca E.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Naughton, Research E.
TITLE OF INVENTION: HUMAN PANCREATIC ISLET CELLS
CORRESPONDENCE ADDRESS:
ADDRESSEE: INVYTE PHARMACEUTICALS, INC.
   Sequence Sequence 6
  Sequence
  Sequence
   Sequence
   Sequence
   Sequence
  Sequence
  Sequence
  Sequence
  CORRESPONDENCE ADJUGESS:
ADDRESSE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: WORD PATR:
APPLICATION NUMBER: 60/030,755
FILING DATE: OCTOBER 28, 1996
PRIOR APPLICATION NUMBER: 60/033,551
FILING DATE: DECEMBER 20, 1996
ATTORNEY/AGENT INFORMATION:
NAMM: CYRENDAE INFORMATION:
NAMM: CYRENDAE INFORMATION:
NAMM: CYRENDAE INFORMATION:
                  1 US-60-172-360-27652

PCT-US01-08631-6786

PCT-US02-07826-146

9 US-10-097-340-146

4 US-60-406-385-48

PCT-US01-01341-329

US-09-76-864-329

US-09-64-869-8906

105-09-644-869-8906

105-09-644-869-8906

105-09-644-869-8906

105-09-644-869-8906

105-09-644-869-8906

105-09-644-869-8906

105-09-652-355-3571

US-09-614-353A-20241

US-09-652-355-3571

US-09-677-417-514

US-09-535-356-356
  US-09-815-264-45836
US-09-702-134-11032
US-09-815-264-76081
US-09-620-392-60934
   ALIGNMENTS
   NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PD-0259 US
TELECOMMUNICATION INFORMATION:
   Sequence 2440, Application US/08959395
  Gooding, Douglas H.
   (650) 855-0555
   (650) 845-4166
   3650
3667
3667
3667
3694
3694
3694
3896
3896
3905
   100.0
100.0
100.0
100.0
100.0
100.0
100.0
   RESULT 1
US-08-959-395-2440/c
```

```
ö
   ö
   Gaps
   Gaps
   APPLICANT: Sellhamer, Jeffrey J.
APPLICANT: Sellhamer, Jeffrey J.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Laura L.
APPLICANT: Stuve, Laura L.
APPLICANT: Mulahy, Sara J.
APPLICANT: Maughton, Rebecca E.
TITLE OF INVENTION: POLIVICLEOTIDES OF ENDOCRINE SYSTEM TISSUE
FILE REPERENCE: DP-10.26 CLP
CURRENT PILING DATE: 2000-03-30
CURRENT PILING DATE: 2000-03-30
PPLIOR APPLICATION NUMBER: US/09/539,334
CURRENT PILING DATE: 2000-03-30
WHERE OF SEQ ID NOS: 38381
SSOTIMARE: FERL PROGRAM
SSO ID NO 17512
LENGTH: 272
   ö
  US-09-652-121-1684/C
US-09-652-121-1684/C
Sequence 1684, Application US/09652121
Sequence 1684, Application US/09652121
Sequence 110FORMATION:
TITLE OF INVENTION: DISTERENCE:
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
STILE REPERENCE: 1600-1188-001
CURRENT PILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,129
PRIOR FILING DATE: 1999-08-30
PRIOR FILING DATE: 1999-08-30
SROPHWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1684
LENGTH: 347
   ö
  100.0%; Score 22; DB 20; Length 272; 100.0%; Pred. No. 1.6;
   Query Match
100.0%; Score 22; DB 13; Length 272;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 22; Conservative 0; Mismatches 0; Indels
  Indels
  FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: hu00470097
US-09-539-334-17512
  0; Mismatches
   ; Sequence 17512, Application US/09539334 ; GENERAL INFORMATION:
  179 GACGTTGACAACGGCGGTTTCT 158
   179 dacetreachacececetrici 158
   1 GACGITGACAACGGCGGITTCT 22
  Query Match
Best Local Similarity 100.0
Matches 22; Conservative
LENGTH: 272 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
  TYPE: DNA ORGANISM: Homo sapiens
   STRANDEDNESS: sing

TOPOLOGY: linear

MOLECULE TYPE: CDNA

| IMMEDIATE SOURCE:

| CLONE: 2077095H2

US-08-959-395-2440
```

```
US-09-652-918-3592/c
  US-09-939-397-32161
  g
                    ð
   ઠે
  ö
   ö
   ö
   Gaps
   ö
  ö
   DB 25; Length 347;
1.7;
  US-09-939-397-12874/c

Sequence 12874, Application US/09939397

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES

FILE REFERENCE: 20411-765

CURRENT FAPLICATION NUMBER: US/09/939,397

CURRENT FILING DATE: 1090-04-08

PRIOR PILING DATE: 1999-04-08

NUMBER OF SEQ ID NOS: 39996

SOCTUMENT: RastSEQ for Windows Version 3.0

LENGTH: 349
   7;
0, Indels
  Indels
  APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: ROW VARIOUS CDNA LIBRARIES
FILE REPERENCE: 20411-765
CURRENT APPLICATION NUMBER: US/09/289, 768
CURRENT FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 39996
SEQ ID NOS: 39996
SEQ ID NOS: 39996
LENGTH: 349
  Query Match
100.0%; Score 22; DB 35;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 22; Conservative 0; Mismatches 0;
  Query Match
100.0%; Score 22; DB 16;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 22; Conservative 0; Mismatches 0;
  Query Match 100.0%; Score 22; DE Best Local Similarity 100.0%; Pred. No. 1.7 Matches 22; Conservative 0; Mismatches
  US-09-289-768-12874/c
; Sequence 12874, Application US/09289768
; GENERAL INFORWATION:
NAME/KEY: misc_feature

! LOCATION: (1)._.(347)

! OTHER INFORMATION: n = A,T,C or G

US-09-652-121-1684
   NAME/KEY: misc_feature

| LOCATION: (1)...(349)

| OTHER INFORMATION: n = A,T,C or G

US-09-289-768-12874
   // NAME/KEY: misc_feature
// LOCATION: (1)...(349)
// CTHER INFORMATION: n = A,T,C or G
US-09-939-397-12874
   323 GACGTTGACAACGCCGGTTTCT 302
   1 GACGITGACAACGGCGGITTCT 22
   122 GACGITGACAACGCCGCITICI 101
  1 GACGTTGACAACGGCGGTTTCT 22
   TYPE: DNA
ORGANISM: Homo sapiens
  ORGANISM: Homo sapiens
  TYPE: DNA
   g
   ሯ
  ઠ
```

```
ô
   Gaps
  ö
   100.0%; Score 22; DB 16; Length 363; 100.0%; Pred. No. 1.7;
  Length 363;
   A CURRENT HYSEG, INC.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-765
CURRENT APPLICATION NUMBER: US/09/939,397
CURRENT FILING DATE: 2001-08-24
PRIOR RILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 39996
SOFTWARE: FESTENCE for Windows Version 3.0
IENGTH: 363
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: 
   0; Indels
   APPLICANT: Hyseq, inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: ROW VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-765
CURRENT APPLICATION NUMBER: US/09/289,768
CURRENT FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 39996
SOFTWARE: PastSEQ for Windows Version 3.0
LENGTH: 363
  Sequence 3592, Application US/09652918
GENERAL INFORMATION:
APPLICANT: Galvin, Katherine
APPLICANT: Galvin, Natherine
APPLICANT: Holfman, Douglas A.
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1187-001
CURRENT APPLICATION NUMBER: US/09/652,918
CURRENT FILING DATE: 2000-08-30
   100.0%; Score 22; DB 35; 100.0%; Pred. No. 1.7;
   0; Mismatches
   Mismatches
   US-09-289-768-32161/c
; Sequence 32161, Application US/09289768
; GENERAL INFORMATION:
  US-09-939-397-32161/c
; Sequence 32161, Application US/09939397
; GENERAL INFORMATION:
122 GACGTTGACAACGCCGGTTTCT 101
  276 GACGTTGACAACGGCGGTTTCT 255
   .
  276 GACGTTGACAACGGCGGTTTCT 255
   1 GACGITGACAACGGCGGITICI 22
   1 GACGITGACAACGGCGGIIICI 22
   Query Match
Best Local Similarity 100.0
Matches 22; Conservative
  Query Match
Best Local Similarity 100.0
....hes 22; Conservative
   TYPE: DNA
CORGANISM: Homo sapiens
US-09-289-768-32161
```

```
ORGANISM: Homo sapiens
   TYPE: DNA ORGANISM: Homo sapiens
  US-09-528-409-49810
  ò
   Gaps
  ö
   Sequence 680, Application US/09304649

Sequence 680, Application US/09304649

GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Gearing, David P.
APPLICANT: McCarthy, Sean A.
ITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A.
ITLE OF INVENTION: HUMAN MICROVASCULAR ENDOTHELIAL LIBRARY FILE OF INVENTION: HUMAN MICROVASCULAR ENDOTHELIAL LIBRARY FILE OF INVENTION: 1999-05-04
EARLIER APPLICATION NUMBER: 60/084,098
EARLIER PILING DATE: 1999-05-05-04
EARLIER PILING DATE: 1999-03-08
EARLIER FILING DATE: 1999-03-08
EARLIER FILING DATE: 1999-03-08
SARLIER FILING DATE: 1999-03-08
SARLIER FILING DATE: 1999-03-08
SARLIER FILING DATE: 1999-03-08
SARLIER FILING DATE: 1999-03-08
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 680
LENGTH. ACE
  Query Match
Best Local Similarity 100.0%; Score 22; DB 17; Length 465;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 22; Conservative 0; Mismatches 0; Indels (
  Length 409;
  S-U3-U3-LINFORMATION:
Sequence 680, Application US/09840424
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: MCCARTHY, Sean A.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
TITLE OF INVENTION: HUMAN MICROVASCULAR ENDOTHELIAL LIBRARY
FILE REPERENCE: 1600.1010-002
CURRENT APPLICATION NUMBER: US/09/840,424
CURRENT APPLICATION NUMBER: US 60/084,098
   0; Indels
PRIOR APPLICATION NUMBER: 60/151,130
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 8985
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3592
   100.0%; Score 22; Best Local Similarity 100.0%; Pred. No. Matches 22; Conservative 0; Mismatch
   ; LOCATION: (1)...(465)
; OTHER INFORMATION: n = A,T,C or G
US-09-304-649-680
  ; LOCATION: (1) ... (409)
; OTHER INFORMATION: n = A,T,C or G
US-09-652-918-3592
   464 GACGTTGACAACGGCGGTTTCT 443
   262 GACGTTGACAACGGCGGTTTCT 241
  1 GACGITGACAACGGCGGITICI 22
   1 GACGTTGACAACGGCGGTTTCT . 22
  NAME/KEY: misc feature
  TYPE: DNA
ORGANISM: Homo sapiens
  NAME/KEY: misc_feature
   TYPE: DNA
ORGANISM: Homo sapien
   RESULT 10
US-09-840-424-680/c
   셤
  ઠ
```

```
Gaps
  ö
   Length 467;
   Length 465;
  APPLICANT: Labet, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Birgit
APPLICANT: Dickson, Mark
APPLICANT: Dickson, Mark
APPLICANT: Unces, Lee W
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
FITLE OF INVENTION: Prom Various Libraries
FILE REPERENCE: 774
CURRENT APPLICATION NUMBER: US/09/528,409
PRIOR APPLICATION NUMBER: 60/125,453
PRIOR FILING DATE: 1999-00-19
  Indels
  Query Match
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 22; Conservative 0; Mismatches 0;
   Query Match
100.0%; Score 22; DB 32;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 22; Conservative 0; Mismatches 0;
PRIOR FILING DATE: 1998-05-04
PRIOR APPLICATION NUMBER: US 60/123,523
PRIOR APPLICATION NUMBER: US 60/126,974
PRIOR APPLICATION NUMBER: US 60/126,974
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 1311
SOFTWARE: PEBESEQ for Windows Version 4.0
SOFTWARE: 465
   Sequence 49810, Application US/09933524 GENERAL INFORMATION:
   RESULT 11
US-09-528409-49810/c
; Sequence 49810, Application US/09528409
; GENERAL INFORMATION:
  NUMBER OF SEQ ID NOS: 116231
SOTTWARE: Hy patent.pl Version 3.1
SEQ ID NO 49810
LENGTH: 467
  FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(467)
OTHER INFORMATION: n = A,T,C or G
  NAME/KEY: misc_feature;
COCATION: (1)...(465)
CHER INFORMATION: n = A,T,C or G
US-09-840-424-680
  457 dacerreacaaceecerrrer 436
  464 GACGTTGACAACGCCGGTTTCT 443
   1 GACGITGACAACGCCGGITTCT 22
   APPLICANT: Drmanac, Radoje T.
```

```
Query Match
  Query Match
   ò
  ö
  ö
   100.0%; Score 22; DB 35; Length 467; 100.0%; Pred. No. 1.7;
  100.0%; Score 22; DB 35; Length 467; 100.0%; Pred. No. 1.7;
APPLICANT: Jones, Lee W.
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 77 2000 CURRENT FILID BATE: 2001-08-20
CURRENT APPLICATION NUMBER: 09/528,409
PRIOR APPLICATION NUMBER: 09/528,409
PRIOR PILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 116231
SOFTWARE: Hy-patent.pl Version 3.1
SEQ ID NO 49810
   Sequence 49810, Application US/09933524A
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Mark
APPLICANT: Jones, Lee W
ITILE OF INVENTION: Novel Nucleic Acid Sequences Obtained
ITILE OF INVENTION: From Various Libraries
FILE REFERENCE: 774
CURRENT APPLICATION NUMBER: US/09/933,524A
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 2001-08-17
NUMBER OF SEQ ID NOS: 116231
SOFTWARE: HY-Patent: pl Version 3.1
LENGTH: 467
  0; Indels
   Indela
  0; Mismatches
   Mismatches
   US-60-125-787-430/c

Sequence 430 Application US/60125787

GENERAL INFORMATION:

APPLICANT: Hodgeon, David M.

APPLICANT: Lincoln, Stephen E.

APPLICANT: Russo, Frank D.
   FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(467)
OTHER INFORMATION: n = A,T,C or G
US-09-933-524-49810
   // NAME/KEY: misc_feature
// LOCATION: (1)...(467)
// OTHER INFORMATION: n = A,T,C or G
US-09-933-524A-49810
   457 GACGTTGACAACGCCGTTTCT 436
   457 GACGTTGACAACGGCGGTTTCT 436
   ö
  1 GACGTTGACAACGGCGGTTTCT 22
   22
   1 GACGITGACAACGGCGGTITCI
   Best Local Similarity 100.
Matches 22; Conservative
  Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
   TYPE: DNA
ORGANISM: Homo sapiens
  TYPE: DNA
ORGANISM: Homo sapiens
   US-09-933-524A-49810/c
   Query Match
  ઠે
  g
```

```
FEATURE:
NAME/KEY: SIMILAR
LOCATION: (50).. (1843)
OTHER INFORMATION: 100% homologous to Homo sapiens IGF-II mRNA-binding protein
OTHER INFORMATION: 2, accession number AF117107, Smith-Waterman Score=3059.
  ö
  ö
  Gape
  ö
  ö
  100.0%; Score 22; DB 1; Length 2010; 100.0%; Pred. No. 1.9;
  100.0%; Score 22; DB 56; Length 546; 100.0%; Pred. No. 1.7;
  Sequence 6785, Application PC/TUS0108631
GENERAL INFORMATION:
APPLICANT: Hyaeq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-049;
CURRENT PELING DATE: 2001-03-30;
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/549,167
PRIOR APPLICATION NUMBER: 2006-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SEQ ID NO 6785
LENGTH: 2010
   0; Indels
   0; Indels
  APPLICANT: Yu, Jimmy Y.
APPLICANT: Yu, Jimmy Y.
APPLICANT: Greenawalt, Lila B.
APPLICANT: Roseberry, Ana M.
APPLICANT: Wright, Rachel J.
ITILE OF INVENTION: TRANSCRIPTION FACTOR MOLECULES
FILE REFERENCE: PT-0017 P
CURRENT APPLICATION NUMBER: US/60/125,787
CURRENT FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 591
SOFTWARE: PERL Program
SOFTWARE: PERL Program
SENGTH: 546
  Mismatches
   0; Mismatches
  ó
   453 GACGTTGACAACGCCGTTTCT 432
   421 GACGTTGACAACGCCGGTTTCT 400
  1 GACGITGACAACGCCGGITICI 22
  1 GACGTTGACAACGCCGGTTTCT 22
APPLICANT: Dufour, Gerard E. APPLICANT: Cohen, Howard J. APPLICANT: Rosen, Bruce APPLICANT: Shah, Purvi APPLICANT: Chalup, Michael S. APPLICANT: Hillman, Jennifer L. APPLICANT: Jones, Anissa L.
   FEATURE: -
; OTHER INFORMATION: 22091.1
US-60-125-787-430
   Best Local Similarity 100.
Matches 22; Conservative
   Best Local Similarity 100.
Matches 22; Conservative
  TYPE: DNA
ORGANISM: Homo sapiens
   TYPE: DNA
ORGANISM: Homo sapiens
   PCT-US01-08631-6785/c
   PCT-US01-08631-6785
  à
```

Search completed: April 18, 2003, 09:35:49 Job time : 1213 secs

us-09-270-437d-14.rnpm

```
GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
```

OM nucleic - nucleic search, using sw model

April 18, 2003, 06:35:28; Search time 245.167 Seconds (without alignments) 400.770 Million cell updates/sec Run on:

US-09-270-437D-14 22

Title: Perfect score:

1 gacgttgacaacggcggtttct 22 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

5897297 seqs, 2233080881 residues Searched:

11794594 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pending\_Patents\_NA\_New:\*

1: /cgn2\_6/ptodata/1/pna/PCT\_NEW\_COMB.seq:\*

2: /cgn2\_6/ptodata/1/pna/USO6\_NEW\_COMB.seq:\*

3: /cgn2\_6/ptodata/1/pna/USO8\_NEW\_COMB.seq:\*

4: /cgn2\_6/ptodata/1/pna/USO8\_NEW\_COMB.seq:\*

5: /cgn2\_6/ptodata/1/pna/USO8\_NEW\_COMB.seq:\*

6: /cgn2\_6/ptodata/1/pna/USO9\_NEW\_COMB.seq:\*

7: /cgn2\_6/ptodata/1/pna/USO9\_NEW\_COMB.seq:\*

8: /cgn2\_6/ptodata/1/pna/USO9\_NEW\_COMB.seq:\*

9: /cgn2\_6/ptodata/1/pna/USO9\_NEW\_COMB.seq:\*

10: /cgn2\_6/ptodata/1/pna/USO0\_NEW\_COMB.seq:\*

11: /cgn2\_6/ptodata/1/pna/USO0\_NEW\_COMB.seq:\* **Database**:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description    |   | Segmence 14. April | Seminary a concerner | TIDAY 'O DOWNSON  | Semica of Appril    | Semience 218/0, A                       | , , , ,            | Semience 3834, Ap   |                    |                 |                    |                                           | Seguence 30361, A   | Sequence 20375, A   |                     |                     | 203                 | 9                 | ,                | adductice 33, Appl | Seguence 5179. Ap  | Sequence 612 App  | 492               | Semience 102, and | 705              | sequence 3237, Ap  |
|-----------|----------------|---|--------------------|----------------------|-------------------|---------------------|-----------------------------------------|--------------------|---------------------|--------------------|-----------------|--------------------|-------------------------------------------|---------------------|---------------------|---------------------|---------------------|---------------------|-------------------|------------------|--------------------|--------------------|-------------------|-------------------|-------------------|------------------|--------------------|
| SUMMARIES | , qı           |   | US-09-270-437D-14  | US-09-270-437D-8     | US-09-270-437D-6  | US-10-170-235-21870 | US-60-453-135-3834                      | US-60-453-050-3834 | US-10-170-235-22086 | US-60-453-135-3835 | 118-60-63-05-01 | 118-60-469-600-600 | TG 700 - 20 - 20 - 20 - 20 - 20 - 20 - 20 | US-60-452-680-30361 | US-60-453-135-20375 | US-60-453-135-20385 | US-60-453-050-20375 | US-60-453-050-20385 | PCT-US02-31357-39 | US-10-262-445-39 | 110 110 110 110    | 02-10-1/0-232-2179 | US-60-452-680-612 | US-60-453-135-482 | US-60-453-050-482 | TIG-60-03-03-011 | 1575-000-761-00-00 |
|           | DB             | - | 'n                 | 'n                   | Ŋ                 | 8                   | ======================================= | 11                 | 8                   | 11                 | 1               | -                  | 1:                                        | 1:                  | 7                   | 11                  | 11                  | 1                   | -                 | σ                | •                  | 0                  | 11                | 11                | 11                | ;                | ;                  |
|           | Length         |   | 22                 | 3283                 | 3412              | 3427                | 3427                                    | 3427               | 3475                | 3475               | 3475            | 200                | 6                                         | 7 0 0               | 107                 | 201                 | 201                 | 201                 | 1707              | 1707             | 2227               | 753                | 3237              | 3237              | 3237              | 3445             |                    |
| . de      | Query<br>Match |   | 100.0              | 100.0                | 100.0             | 100.0               | 100.0                                   | 100.0              | 100.0               | 100.0              | 100.0           | 6                  |                                           | ,                   | 0 1                 | 85.5                | 85.5                | 85.5                | 85.5              | 85.5             | A.                 |                    | 85.5              | 85.5              | 85.5              | 85.5             |                    |
|           | Score          |   | 22                 | 22                   | 22                | 22                  | 22                                      | 22                 | . 22                | 22                 | 22              | 18.8               | 9                                         | 9 0                 | 0.0                 | 18.8                | 18.8                | 18.8                | 18.8              | 18.8             | α                  |                    | 18.8              | 18.8              | 18.8              | 18.8             |                    |
|           | Regult<br>No.  |   | ٠,                 | o<br>U               | ო<br><sub>U</sub> | Ω<br>4              | Ω<br>Ω                                  | υ                  | 0                   | ω<br>U             | O               | 0 10               | 2                                         | 1:                  | 9 6                 | 7 .<br>O            |                     | G 15                |                   | c 17             |                    |                    |                   | C 50              | c 51              | 25<br>C          |                    |

| Sequence 1, Appli<br>Sequence 1, Appli<br>Sequence 31514, A<br>Sequence 26, Appl<br>Sequence 31037, A<br>Sequence 31037, A<br>Sequence 397, App<br>Sequence 519026, A<br>Sequence 38972, A<br>Sequence 38972, A<br>Sequence 38972, A<br>Sequence 38972, A<br>Sequence 38973, A<br>Sequence 38973, A<br>Sequence 38973, A<br>Sequence 64771, A<br>Sequence 64771, A<br>Sequence 64893, Ap<br>Sequence 63821, A                                                                                                                                                           | Sequence 14654, A<br>Sequence 46168, A<br>Sequence 8986, Ap<br>Sequence 44760, A<br>Sequence 46167, A |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------|
| 9 US-10-018-470-1<br>9 US-10-018-470A-1<br>5 US-09-513-990C-31514<br>11 US-60-427-166-43<br>11 US-60-427-166-26<br>9 US-10-282-122A-31037<br>9 US-10-144-77-134698<br>11 US-60-449-155-997<br>12 US-10-35-577-519026<br>13 US-10-35-977-519026<br>14 US-09-613-1013-38953<br>15 US-09-531-113-38953<br>15 US-09-837-604A-4761<br>15 US-09-837-604A-4761<br>16 US-09-837-604A-7761<br>16 US-09-837-604A-7761<br>16 US-09-837-604A-7761<br>16 US-09-837-604A-7761<br>16 US-09-837-604A-7761<br>17 US-09-837-604A-7761<br>18 US-09-837-604A-7761<br>18 US-09-837-604A-7761 | 3 US-10-391-339-14654<br>US-09-837-604A-46168<br>US-10-401-229-8986<br>US-09-837-604A-44760           |
| 222<br>1122<br>122<br>122                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 612 8<br>619 7<br>645 8<br>671 7                                                                      |
| 8887 6887 6887 6888 6887 6888 6887 6887                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 73.6<br>73.6<br>73.6<br>73.6                                                                          |
| 4.4.6.2.6.6.8.8.9.9.9.9.9.9.9.9.9.9.9.9.9.9.9.9                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 16.22.2                                                                                               |
| 0000 0000<br>0000<br>00000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 0 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4                                                               |

## ALIGNMENTS

```
APPLICANT: Teang, Solam
APPLICANT: Teang, Solam
APPLICANT: Teang, Solam
APPLICANT: Jackert, Elisabeth
APPLICANT: Jackert, Elisabeth
APPLICANT: Jackert, Alexander
APPLICANT: Gunth, Alexander
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: Incolated Nucleic Acid Molecules Encoding Cancer Associated Antiger
TITLE OF INVENTION: Antigens Per Se, And Uses Thereof
TITLE OF INVENTION: Antigens Per Se, And Uses Thereof
CURRENT APPLICANTION NUMBER: 18709/051,709
PRIOR APPLICATION NUMBER: 09/061,709
PRIOR APPLICATION NUMBER: 1998-04-17
SEQ ID NO 14
ELENGTH: 22
   Gapa
  .
0
   Query Match
100.0%; Score 22; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 22; Conservative 0; Mismatches 0; Indels
                            Sequence 14, Application US/09270437D GENERAL INFORMATION:
   APPLICANT: Chen, Yao-Tseng
APPLICANT: Gure, Ali
  TYPE: DNA
ORGANISM: Homo sapiens
US-09-270-437D-14
  US-09-270-437D-14
   FEATURE:
   ઠે
```

; Sequence 8, Application US/09270437D; GENERAL INFORMATION: APPLICANT: Chen, Yao-Teeng
APPLICANT: Gure, Ali
APPLICANT: Teang, Solam
APPLICANT: Stockert, Elisabeth
APPLICANT: Jager, Elke
APPLICANT: Knuth, Alexander 22 1 GACGITGACAACGCCGGITICI 22 1 GACGTTGACAACGCCGGTTTCT US-09-270-437D-8/c RESULT 2 Q

ö

```
Sequence 3384, Application US/60453135
Sequence 3814, Application US/60453135
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: TAKORILL, Michele
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPERENCE: CLO01456
FULLE REPUBLICATION AND USES
FULLE REPUBLICATION AND USES
FULLE REPUBLICATION AND USES
FULLE REPUBLICATION AND USES
FULLE REPUBLICATION AND USES
FULLE REPUBLICATION AND USES
FULLE REPUBLICATION AND USES
FULLE REPUBLICATION AND USES
FULLE REPUBLICATION AND USES
FULLE REPUBLICATION AND USES
FULLE REPUBLICATION AND USES
FULLE REPUBLICATION AND USES
FULLE REPUBLICATION AND USES
FULLE REPUBLICATION AND USES
FULLE REPUBLICATION AND USES
FULLE REPUBLICATION AND USES
FULL REPUBLICATION AND USES
FULL REPUBLICATION AND USES
FULL REPUBLICATION AND USES
FULL REPUBLICATION AND USES
FULL REPUBLICATION AND USES
FULL REPUBLICATION AND USES
FULL REPUBLICATION AND USES

  ö
  ö
  US-60-453-050-3834/C
US-60-453-050-3834/C
IS-60-453-050-3834, Application US/60453050
| Sequence 3834, Application US/60453050
| GENERAL INFORMATION:
| APPLICANT: CARGILL; Michele
| APPLICANT: LUKE, MAY
| TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
| TITLE OF INVENTION: GENETIC POLYMORPHISMS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: GENETIC POLYMORPHISMS OF DETECTION AND USES THEREOF
| CURRENT APPLICATION NUMBER: US/60/453,050
| CURRENT FILING DATE: 2003-03-10
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 3834
   ö
   100.0%; Score 22; DB 11; Length 3427; llarity 100.0%; Pred. No. 0.52; Conservative 0; Mismatches 0; Indels 0
  Query Match 100.0%; Score 22; DB 11; Length 3427; Best Local Similarity 100.0%; Pred. No. 0.52; Matches 22; Conservative 0; Mismatches 0; Indels 0;
  Query Match
100.0%; Score 22; DB 8; Length 3427;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 22; Conservative 0; Mismatches 0; Indels
  FILE REFERENCE: CL001380
CURRENT APPLICATION NUMBER: US/10/170,235
CURRENT FILING DATE: 2003-03-17
NUMBER OF SEQ ID NOS: 42514
SEQ ID NO 21870
LENGTH: 3427
  442 GACGTTGACAACGGCGGTTTCT 421
   442 GACGTTGACAACGGCGGTTTCT 421
  442 GACGTTGACAACGGCGGTTTCT 421
   1 GACGTTGACAACGGCGGTTTCT 22
   ; ORGANISM: Homo sapiens
US-60-453-050-3834
   TYPE: DNA
CORGANISM: Homo sapiens
US-60-453-135-3834
   Best Local Similarity
Matches 22; Conserv
  RESULT 5
US-60-453-135-3834/c
   ; TYPE: DNA
; ORGANISM: HUMAN
US-10-170-235-21870
  TYPE: DNA
  Query Match
  Matches
   ઠે
us-09-270-437

"TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Antige
; TITLE OF INVENTION: Antigens Per Se, And Uses Thereof
; TITLE OF INVENTION: Antigens Per Se, And Uses Thereof
; FILE REFERENCE: LUD 5538.1
; CURRENT APPLICATION NUMBER: US/09/270,437D
; PRIOR APPLICATION NUMBER: 09/061,709
; PRIOR PILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 8
; SEQ ID NO 8
; TITLE OF INVENTION TO BE TO 
   APPLICANT: Gure, Ali
APPLICANT: Gure, Ali
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Jager, Elke
APPLICANT: Jager, Elke
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Antige
TITLE OF INVENTION: Antigens Per Se, And Uses Thereof
FILE REFERENCE: LUD 5538.11
CURRENT FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 09/061,709
PRIOR FILING DATE: 1998-04-17
  Sequence 21870, Application US/10170235
; SEQUENCE INFORMATION:
; APPLICANT: VENTER, J. Craig
; ITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
; ITLE OF INVENTION: KITS, SUCH AS DETECTING EXPRESSION AND OTHER USES THEREOF
; ITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
   Gaps
   ö
   DB 5; Length 3412;
  100.0%; Score 22; DB 5; Length 3283; 100.0%; Pred. No. 0.51;
   0; Indels
   0; Indels
  0; Mismatches
   Query Match
Best Local Similarity 100.0%; Pred. No...
Matches 22; Conservative 0; Mismatch
   NAME/KEY: CDS
I LOCATION: 3372
COTHER INFORMATION: unsure of nucleotide us-270-4370-6
  LOCATION: 3243
OTHER INFORMATION: ungure of nucleotide
   US-09-270-437D-6/c
; Sequence 6, Application US/09270437D
; GENERAL INFORMATION:
   444 GACGTTGACAACGGCGGTTTCT 423
   444 GACGITGACAACGGCGGTTTCT 423
  1 GACGTTGACAACGGCGGTTTCT 22
   22
   Best Local Similarity 100.
Matches 22; Conservative
   APPLICANT: Chen, Yao-Tseng
   NUMBER OF SEQ ID NOS: 23
SEQ ID NO 6
LENGTH: 3412
   TYPE: DNA ORGANISM: Homo sapiens
   TYPE: DNA
ORGANISM: Homo sapiens
   RESULT 4
US-10-170-235-21870/c
   NAME/KEY: CDS
   US-09-270-437D-8
  Query Match
```

ద

ð

g

ð

```
Sequence 30351, Application US/60452680
GRNERAL INFORMATION:
GRNERAL INFORMATION:
GRNERAL INFORMATION:
GRNERAL GRUPE, Andrew
TITLE OF INVENTION: GRNETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001450
CURRENT APPLICATION WUMBER: US/60/452,680
CURRENT FILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 116213
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30351
LENGTH: 201
  18-60-452-680-30361/c

18-60-452-680-30361/c

18-60-452-680-30361, Application US/60452680

18-60-452-680-30361, Michele

18-8PELICANT: CREGILL, Michele

18-8PELICANT: CREGILL, Michele

18-8PELICANT: CREGILL, Andrew

18-8PELICANT: CREGILL, ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF

18-8PERENCE: CLO01450

18-8PELICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PELICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PELICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PELICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PELICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PELICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PELICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PELICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PELICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PELICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PELICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PELICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PELICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PELICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PELICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PELICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PELICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PELICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PELICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PERICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PERICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PERICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PERICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PERICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PERICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PERICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PERICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PERICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PERICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PERICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PERICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PERICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PERICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PERICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PERICANT: CREGILL ALZHEIMER: US/60/452,680

18-8PERICANT: CREGILL ALZHEIMER: US/60/452,
   ö
  ö
  ô
   Gaps
  Gape
  Gaps
   ö
  ö
  Score 22; DB 11; Length 3475;
Pred. No. 0.52;
   DB 11; Length 201;
   Length 201;
  Indels
  Indels
   DB 11;
   85.5%; Score 18.8; D
90.9%; Pred. No. 15;
iive 0; Mismatches
   85.5%; Score 18.8; ilarity 90.9%; Pred. No. 15 Conservative 0; Mismatche
  US-60-453-135-20375/c
; Sequence 20375, Application US/60453135
; GENERAL INFORMATION;
   ;
   439 GACGTTGACAACGGCGGTTTCT 418
  1 GACGITGACAACGGCGGTITCI 22
   Db 135 GACGTTGACAACAGTGGTTTCT 114
  CT 22
   171 GACGTTGACAACAGTGGTTTCT 150
  Query Match
100.0%;
Best Local Similarity 100.0%;
Matches 22; Conservative 0
  55
  APPLICANT: CARGILL, Michele APPLICANT: IAKOUBOVA, Olga
   20; Conservative
  TYPE: DNA
ORGANISM: Homo sapiens
  ; ORGANISM: Homo sapiens
US-60-452-680-30361
   Best Local Similarity
Matches 20; Conserv
  Query Match
Best Local Similarity
Matches 20; Conserv
   RESULT 10
US-60-452-680-30351/c
US-60-453-050-3835
   US-60-452-680-30351
   Query Match
  TYPE: DNA
  g
  ò
  ò
  a
a
   APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
FILE REPREBNCE: CL001380
CURRENT APPLICATION NUMBER: US/10/170,235
CURRENT FILING DATE: 2003-03-17
NUMBER OF SEQ ID NOS: 42514
SEQ ID NO 22086
LENGTH: 3475
  NSG-6-453-135-3835/c

| Sequence 3835, Application US/60453135 |
| Sequence 3835, Application US/60453135 |
| Sequence 3835, Application US/60453135 |
| GENERAL INFORMATION: |
| APPLICANT: CARGILL, Matchele |
| APPLICANT: IAKOUBOVA, Olga |
| TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH |
| TITLE OF INVENTION: MYMBER: US/60/453,135 |
| CURRENT APPLICATION NUMBER: US/60/453,135 |
| NUMBER OF SEQ ID NOS: 82762 |
| SOFTWARE: PastSEQ for Windows Version 4.0 |
| SEQ ID NO 3835 |
| LENGTH: 3475 |
  ö
  RESULT 9
US-60-453-050-3835/c
i General Information US/60453050
i General Information:
APPLICANT: CARGILL, Michele
APPLICANT: LUKE, May
ITILE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
ITILE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
ITILE OF INVENTION: WISHERS OF US/60/453,050
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
i NUMBER OF SEQ ID NOS: 82762
i NUMBER OF SEQ ID NOS: 82762
i NUMBER OF SEQ ID NOS: 82762
  Gaps
   ö
   DB 8; Length 3475;
   0; Indels
   0; Indels
  Mismatches
   0; Mismatches
  Query Match
100.0%; Score 22;
Best Local Similarity 100.0%; Pred. No. (Matches 22; Conservative 0; Mismatch)
   100.0%; Score 22;
100.0%; Pred. No.
  Sequence 22086, Application US/10170235 GENERAL INFORMATION:
  439 GACCTTGACAACGGCGGTTTCT 418
  1 GACGITGACAACGCCGGITICI 22
   439 GACGTTGACAACGCCGGTTTCT 418
   22
   Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-453-135-3835
  TYPE: DNA
ORGANISM: Homo sapiens
  US-10-170-235-22086/c
  ; TYPE: DNA
; ORGANISM: HUMAN
US-10-170-235-22086
  SEQ ID NO 3835
LENGTH: 3475
  ठे
   g
  g
```

```
135 GACGTTGACAACAGTGGTTTCT 114
1 GACGTTGACAACGGCGGTTTCT 22
   ð
  g
   Sequence 20385, Application US/60453135
Sequence 20385, Application US/60453135
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: TAKCOUGOVA, Olga
APPLICANT: TAKCOUGOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION WIMBER: US/60/453,135
CURRENT PILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20385

LENTH: 201
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INPARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001456
CURRENT PEPLICATION NUMBER: US/60/453,135
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: PatSEQ for Windows Version 4.0
SEQ ID NO 20175
LENGTH: 201
  ö
  ö
   US-60-453-050-20375/c
US-60-453-050-20375/c
US-60-453-050-20375, Application US/60453050
; GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
; APPLICANT: LUKE, May
TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REPERBRENCE: CL001457
; CURRENT APPLICATION NUMBER: US/60/453,050
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: PSESSO for Windows Version 4.0
; SEQ ID NO 20375
; LENGTH: 201
   Gaps
   Gaps
   ö
  ö
  Score 18.8; DB 11; Length 201;
Pred. No. 15;
0; Mismatches 2; Indels 0;
   ö
   DB 11; Length 201;
  Length 201;
  Indels
   Indels
  7
   5
  DB 11;
   85.5%; Score 18.8; D
90.9%; Pred. No. 15;
tive 0; Mismatches
   Pred. No. 15;
0; Mismatches
  Score 18.8;
Pred. No. 15
   135 GACGTTGACAACAGTGGTTTCT 114
   1 GACGITGACAACGGCGGITICT 22
  22
  Query Match
Best Local Similarity 90.9%;
Matches 20; Conservative
  Query Match
Best Local Similarity 90.9%;
Matches 20; Conservative
  1 GACGIIGACAACGGCGGIIICI
   Query Match
Best Local Similarity 90.9
Matches 20; Conservative
   TYPE: DNA
CORGANISM: Homo sapiens
US-60-453-050-20375
   TYPE: DNA
, ORGANISM: Homo sapiens
US-60-453-135-20385
  , ORGANISM: Homo sapiens US-60-453-135-20375
   TYPE: DNA
   요
   a
   ઠે
```

```
| Sequence 20185, Application US/60453050
| Sequence 20185, Application US/60453050
| GENERAL INFORMATION:
| APPLICANT: CARGILL, Michele
| APPLICANT: UNEX, May
| TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF;
| TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF;
| TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF;
| CURRENT APPLICATION UNMER: US/60/453,050
| CURRENT APPLICATION UNMER: 2003-03-10
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 20385
| LENGTH 201
  Gaps
  ö
  DB 11; Length 201;
  Indels
  Score 18.8; DE Pred. No. 15; 0; Mismatches
  Search completed: April 18, 2003, 10:50:34
Job time : 248.167 secs
  171 dacerreachachacherrer 150
   22
   Query Match 85.5%;
Best Local Similarity 90.9%;
Matches 20; Conservative
   1 GACGITGACAACGCCGGITICI
  TYPE: DNA
CORGANISM: Homo sapiens
US-60-453-050-20385
RESULT 15
US-60-453-050-20385/c
```

ö

BEG22021 601440673 BG221568 AGENCOURT BG480515 60250520 BG748346 602705902 BMR06132 AGENCOURT AG048517 PBH LYG91 BB852318 BB852318 BB852318 BB852318 BB852318 BB852318 BB673024 ULI-M-FIO-BIG55144 603280946 BB618115 BB618315 BB673209 BB643209 BB618115 BB618315 BB652701 BB853209 BB652701 BB853210 BB855310 BB855310 BG279958 b791209 BG279958 b791209 BB855310 BB855310 BG279958 b791209 BG279958 b791209 AL113568 T3 and of AQ091026 HS 3008 B BU026477 QHH14119 AUSCA BENGA CHI AUSCA BENGA CHI AUSCA BENGA CHI AUSCA BUNGA CHI BU026166 QHG13L05 BU026166 QHG13L05 BU026166 QHG13L05 BU02616 QHG13L05 BU02616 QHG13L05 BU02616 QHG13L05 BU02610 QHF18P04. BU025014 QHF9H06.y BU025014 QHF9H06.y

AG087457 BM977219 BM677219 BG221568 BG748346 BM66132 AG048517 BB852318 BB852318 BB852318 BB852318 BB852318 BB852318 BB852318 BB852318 BB852318 BB643209 BB618315 BB64462 BB852310 BB852310 BB852310 BB852310 BB852310

```
11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11000

11
  BG003431 RC1-GN019
AL121466 DKF2p762L
BG009869 QV1-GN032
BI858380 603383965
BF914566 IL3-UT011
AQ479871 RPCI-11-2
   April 18, 2003, 04:47:40 ; Search time 766 Seconds (without alignments).
465.145 Million cell updates/sec
   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  Description
  32308132
         GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
   16154066 segs, 8097743376 residues
   Total number of hits satisfying chosen parameters:
  SUMMARIES
   - nucleic search, using sw model
   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
  AL121466
BG009869
BI858380
BF914566
AQ479871
  BG003431
   1 gacgttgacaacggcggtttct
  IDENTITY NUC
Gapop 10.0 , Gapext 1.0
   a
   gss_other: *
  US-09-270-437D-14
   Minimum DB seq length: 0
Maximum DB seq length: 200000000
   em_esthum:
em_esthu:
em_esthu:
em_estro:
em_estro:
em_btc:
gb_est1:*
gb_est2:*
gb_est4:*
gb_est4:*
gb_est4:*
gb_est4:*
gb_est4:*
gb_est6:*
em_est6m:*
em_est6m:*
em_est6m:*
em_est6m:*
em_gss.*
  em gss pro: *
em gss rod: *
  em_gas_pln:*
  8
   estba:*
  em_988_v
em_988_f
   Length
  402
453
531
594
620
642
   EST: *
   Query
  1000.0
1000.0
1000.0
  Title:
Perfect score:
  Scoring table:
  Score
  222222
   OM nucleic
   Sequence:
   Searched:
  Database
  Run on:
   Result
  Š.
```

ALIGNMENTS

BG543604 AQ467039 BU026166 AZ178687 BQ488142 BM188239 BU0254011 BU025519

```
Query Match
Best Local Similarity
Matches 22; Conserv
  Simpson, A.J.
   Best Local Similarity
  BG009869.1
   20202663
   104
  human.
   Query Match
  source
  BASE COUNT
   DEFINITION
   ORGANISM
   Matches
   REFERENCE
  AUTHORS
   JOURNAL
  RESULT 4
   ACCESSION
  FEATURES
  BG009869
  KEYWORDS
   RESULT 3
  TITLE
   COMMENT
   ORIGIN
   VERSION
  ORIGIN
  g
   셤
  /organism="Homo sapiens"
/db xref="laxon:960"
/db xref="laxon:960"
/dlow_lib="GN0198"
/dev stage="Adult"
/note="Organ: placenta_normal; Vector: puc18; Site_1: Smal;
/note="Organ: placenta_normal; Vector: puc18; Site_1: Smal;
/site_2: Smal; A minl-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
17 a 98 c 109 g 78 t
   453 bp mRNA linear EST 25-FEB-2000
DKF29762L097 r1 762 (synonym: hmel2) Homo sapiens cDNA clone
DKF29762L097'5', mRNA sequence.
  ö
  Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by MediGenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project. No sl sequence
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCl&t2=RCl-GN0198-171100-021-f0?&t3=2000-11-17&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 15
High quality sequence stop: 400.
  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 453)
  This clone (DKFZp762L097) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
   Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
  Gaps
  /note="Vector: pSport1; Site_1: Not1; Site_2: Sal1" 121 c 137 g 78 t
  ö
  Query Match
Best Local Similarity 100.0%; Score 22; DB 12; Length 402;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 22; Conservative 0; Mismatches 0; Indels (
  /clone_lib="762 (synonym: hmel2)"
/tissue_type="melanoma (MeWo cell line)"
/dev_stage="adult"
/lab_host="DH10B"
  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp762L097"
   EST (Ottenwaelder, et al.)
Unpublished (1999)
   195 GACGTTGACAACGGCGGTTTCT 174
   Contact: Ottenwaelder B
   1 GACGTTGACAACGGCGGTTTCT 22
  AL121466
AL121466.1 GI:5927467
   1, .402
   Wiemann, S.
  117 a
  117
  BASE COUNT
   AL121466/c
  DEFINITION
  ORGANISM
  BASE COUNT
ORIGIN
  REFERENCE
AUTHORS
   JOURNAL
  ACCESSION
  VERSION
KEYWORDS
  FEATURES
  RESULT 2
  TITLE
   FEATURES
  COMMENT
  ð
  용
```

```
// Organisme."Homo sapiens"

/ Organisme."Homo sapiens"

/ db_xrefe_laxon:9606"

/ clone_lib="dx00320"

/ dev stage="Addult"

/ note="Crgan: placenta normal; Vector: puc18; Site_l: Smal

/ site_2: Smal; A mini_library was made by cloning

/ site_2: Smal; A mini_library was made by cloning

/ site_2: Smal; A mini_library was made by cloning

/ site_2: Smal; A mini_library was made by cloning

/ site_2: Smal; A mini_library was made by cloning

/ site_2: Smal; A mini_library was made by cloning

/ site_2: Smal; A mini_library was made by cloning

/ site_2: Smal; A mini_library was made by cloning

/ site_2: Smal; A mini_library was made by cloning

/ site_2: Smal

/ site_2: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

/ site_3: Smal

  ö
  This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV1&t2=QV1-GN0320-041200-532-c06&t2=2000-12-04&t4=1)
Seq primer: puc 18 forward fly forward High quality sequence stop: 531.
   l (bases 1 to 531)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., Gardin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
  BG009869 532-c06 GN0320 HRNA linear EST 24-JAN-2001 QVI-GN0320-041200-532-c06 GN0320 Homo sapiens CDNA, mRNA sequence.
   ö
   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
   Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
  Shotgun sequencing of the human transcriptome with ORF expressed
  Gaps
   Gaps
  .
   ö
   100.0%; Score 22; DB 12; Length 531; larity 100.0%; Pred. No. 4.9; Conservative 0; Mismatches 0; Indels
  sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
9; Length 453;
  Indels
          100.0%; Score 22; DB 9
100.0%; Pred. No. 4.5;
  Mismatches
   Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
   339 GACGTTGACAACGGCGGTTTCT 360
  1 GACGITGACAACGCCGGITTCT 22
   ;
  430 gacgrigacaacaccccirirci 409
   GI:12456498
   22
   Contact: Simpson A.J.G.
   1 GACGITGACAACGGCGGITICI
  Conservative
```

us-09-270-437d-14.rst

```
/organism="Homo sapiens"

/dx xref="taxon:966"

/clone_lib="uvol14"

/dev_stage="Adult"

/dev_stage="Adult"

/note="Corgan: uterus_tumor; Vector: pucl8; Site_l: Smal;

Site_2: Smal; A mini-library was made by cloning products

darived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

13 2 157 c 150 g 132 t
  Map Building
Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0200
Email: bbeeqipgr.org
Email: bbeeqipgr.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong
(pieterded-long med.buffallo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffallo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: T7.
   Tel: +55-11-2704922

Fax: +55-11-2707001

Email: selmpson@ludwig.org.br

Email: selmpson@ludwig.org.br

Project. This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-UT0114-011200-362-E06&t3=2000-12-01&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 619.
  AQ479871 642 bp DNA linear GSS 23-APR-1999
RPCI-11-274C8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-274C8,
                                      Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 642)
  1 (bases 1 to 642)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
  Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
  100.0%; Score 22; DB 12; Length 620; 100.0%; Pred. No. 5.3;
  Mismatches
  Location/Qualifiers
   385 GACGTTGACAACGGCGGTTTCT 364
   ö
  1 GACGITGACAACGCCGGITTCT 22
   AQ479871.1 GI:4661990
  22; Conservative
  DNA sequence.
   Homo sapiens
   Best Local Similarity
  181
  Brazil
   AQ4798
   human
  Query Match
   Bource
  AQ479871
LOCUS
DEFINITION
  BASE COUNT
   ORGANISM
   Matches
   ACCESSION
   VERSION
KEYWORDS
SOURCE
  REFERENCE
  AUTHORS
   PEATURES
   JOURNAL
               COMMENT
  FEATURES
  TITLE
   COMMENT
  ORIGIN
   RESULT
  g
  ò
   Humon sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Ramaalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 594)

NiH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CLone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Libra at:

found through the I.M.A.G.E. Consortium/Libra at:

High quality sequence stop: 594.
                       BI858380 594 bp mRNA linear EST 10-OCT-2001
  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 620)

Diss Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Ngal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
  620 bp mRNA linear EST 18-JAN-2001
IL3-UT0114-011200-362-E06 UT0114 Homo sapiens CDNA, mRNA sequence.
  /note="Organ: breast; Vector: pCMV-SPORT6; Site 1: Not1; Site 2: Sal1; Cloned unidirectionally; oligo-dT primed. Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH MGC Library."
   Gaps
   /tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
  ô
  sequence tags
Proc. Nall. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  Query Match
100.0%; Score 22; DB 13; Length 594;
Best Local Similarity 100.0%; Pred. No. 5.2;
   Indele
   ö
   Mismatches
   organism="Homo sapiens"
  /db_xref="taxon:9606"
/clone="IMAGE:5392792"
/clone_lib="NIH_MGC_87"
  150 g
  ö
   197 GACGTIGACAACGCCGGTTTCT 176
  BI858380.1 GI:15999127
  52
  BF914566.1 GI:12306024
  1 GACGITGACAACGGCGGITTCI
  Conservative
   mRNA seguence.
  BI858380
  human.
  human.
  22;
   KEYWORDS
SOURCE
ORGANISM
                         LOCUS
DEFINITION
   source
BI858380/c
   DEFINITION
ACCESSION
VERSION
KEYWORDS
  ACCESSION
VERSION
   TITLE
JOURNAL
COMMENT
   BASE COUNT
  RESULT 5
BF914566/c
  SOURCE
ORGANISM
  REFERENCE
   AUTHORS
  Matches
  REFERENCE
AUTHORS
  JOURNAL
MEDLINE
   FEATURES
   TITLE
  ORIGIN
  ઠે
  용
```

ö

Gaps

ö

0; Indels

```
321 GACGTTGACAACGGCGGTTTCT 342
   Query Match
Best Local Similarity
Matches 22; Conserv
  McCray Lab
  discovery
  97044477
  BM977219
   human.
  BASE COUNT
ORIGIN
   RESULT 8
BM977219/c
   LOCUS
DEFINITION
  ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
   REFERENCE
AUTHORS
TITLE
  MEDLINE
COMMENT
   JOURNAL
  FEATURES
   ò
   ö
   Pujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission
Submitted (O2-MG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@scriken.go.jp, Wir:http://hgp.gsc.riken.go.jp/, Trel:81-45-503-9111, Fax:81-45-503-9170)
Tlones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
  pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-086B21.F.
Pan troglodytes
  ö
   GSS 03-NOV-2001
  AG087457 688 bp DNA linear GSS 03-NOV-200
Pan troglodytes DNA, clone: PTB-086B21.F, genomic survey sequence.
AG087457
   Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
  /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
a 117 c 95 g 223 t.
   Gaps
  Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
   ö
  .;
0
  /gex="male"
/call_type="lymphoblast"
/clone lib="PTB Chimpanzee Male BAC Library"
153 c 120 g 198 t
   Query Match
Best Local Similarity 100.0%; Score 22; DB 17; Length 688;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 22; Conservative 0; Mismatches 0; Indels
  100.0%; Score 22; DB 17; Length 642; 100.0%; Pred. No. 5.4; tive 0; Mismatches 0; Indels
  1. .688
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-086B21.F"
                    1. 642

Organism="Homo sapiens"

/db_xref="GDB:7664887"

/db_xref="taxon:9606"

/clone="FRCI-11-274C8"

/clone lib="RPCI-11"

/sex="Male"
   Location/Qualifiers
   R.Site 1 : Saci
  Sequencing: -21M13
  AG087457.1 GI:16639259
  76 GACGTTGACAACGGCGGTTTCT 97
  1 GACGITGACAACGGCGGITICT 22
  clone tracking errors.
   (bases 1 to 688)
   Conservative
  Similarity
   LIBRAR
  207
   22;
   Query Match
  Local
   BASE COUNT
ORIGIN
  Best Loca
Matches
   DEFINITION
   ORGANISM
  BASE COUNT
  REFERENCE
AUTHORS
  TITLE
  ACCESSION
VERSION
KEYWORDS
SOURCE
   TITLE
JOURNAL
  RESULT 7
AG087457
LOCUS
  AUTHORS
   REFERENCE
   FEATURES
  COMMENT
   쉱
```

1 GACGITGACAACGGCGGTITCI 22

ò

```
PREFILT 6

DEFINITION

LOCATION - CONTROL - 12.0-UL 13 ULTC - DUI None appleans CDNA clone

LOCATION - CONTROL - 12.0-UL 13 ULTC - DUI None appleans CDNA clone

LOCATION - CONTROL - 12.0-UL 13 ULTC - DUI None appleans CDNA clone

LOCATION - MERCASA CONTROL - 13 ULTC - DUI None appleans CDNA clone

REPRESENCE

NUMBRAIL - CANADIAN - LANDA CONTROL - LANDA CONTROL - C
```

```
BG480515
   human.
   Bource
   RESULT 11
BG480515/c
   BASE COUNT
ORIGIN
  Bource
   DEFINITION
  ORGANISM
   REFERENCE
AUTHORS
TITLE
   JOURNAL
COMMENT
  ACCESSION
  VERSION
KEYWORDS
SOURCE
   FEATURES
   FEATURES
  셤
   ò
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
E 1 (bases 1 to 759)

S NH+MGC http://mgc.nci.nih.gov/.

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Arcc/DcTD/DTP
CONTact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Arcc/DcTD/DTP
CONTact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Arcc/DcTD/DTP
CONTact: Robert Strausberg, Ph.D.
CONTact: Robert Strausberg, Ph.D.
CONTact: Navayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be the http://image.llh.gov
Plate: LiAM9739 row: a column: 19
High quality sequence stop: 622.
Location/Qualifiers
I 759
//Ar verte | 1.759
//Ar verte | 1.759
   BEG22021

759 bp mRNA linear BST 20-OCT-2000

601440673F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915546 5',
   AGENCOURT 7559207 NIH_MGC_72 homo sapiens cDNA clone IMAGE:6046477 5', mRNA sequence. BQ221568 BQ221568.1 GI:20402968 BST.
   ö
   /db_xref="taxxx::9666"
/dclone="lundg::3915546"
/clone=lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/tissue_type="melanotic melanoma"
/lab_hogie="bylioB (phage-resistant)"
/note="Organ: skin; Vector: pCWV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life
  Eukaryoča, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 851)
   Gaps
   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
   ö
  Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
  134 t
  188 g
  164 GACGTTGACAACGGCGGTTTCT 143
  22
   BE622021.1 GI:9892961
  rechnologies.
  209 C
   22; Conservative
  mRNA sequence.
BE622021
  Homo sapiens
  Query Match
Best Local Similarity
Matches 22; Conserv
   Homo sapiens
  ø
  human.
  ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
  RESULT 10
BQ221568/c
RESULT 9
BE622021/c
                                       LOCUS
   TITLE
JOURNAL
COMMENT
   VERSION
KEYWORDS
SOURCE
ORGANISM
  BASE COUNT
ORIGIN
  REFERENCE
AUTHORS
  DEFINITION
  TITLE
JOURNAL
COMMENT
   ACCESSION
   REFERENCE
   AUTHORS
  FEATURES
```

ઠ

```
NIT-MGC http://mgc.nci.nih.gov/.

NIT-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammallan Gene Collection (MGC)

National Institutes of Health, Mammallan Gene Collection (MGC)

National Institutes of Health, Mammallan Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ArCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be http://image.llnl.gov

Plate: LLCMA43B row: h column: 06

High quality sequence stop: 661.

By Location/Qualifiers

I. .856

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_xref="taxon:9606"

AD_
   õ
  BG480515 887 21-MAR-2001 605529520F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4652981 5',
   đŢ.
   /db_xref="texxon:9606"
/clone="IMAGE:6046477"
/clone lib="NIH MGC 72"
/tlabue type="melanotic melanoma"
/lab host="Pall0B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT
Average insert size 2 kb. Library constructed by Life
   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 856)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13292 row: f column: 14
   Gapa
   ö
  DB 14; Length 851;
  0; Indels
  157 t
   100.0%; Score 22; DB
100.0%; Pred. No. 6.3
tive 0; Mismatches
  /organism="Homo sapiens"
  High quality sequence stop: 6
Location/Qualifiers
1. .851
   231 g
  398 GACGITGACAACGGCGGITTCI 377
   1 GACGITGACAACGCCGGITTCT 22
   BG480515.1 GI:13412705
  234 C
   Ouery Match
Best Local Similarity 100.
Matches 22, Conservative
  mRNA sequence.
   Homo sapiens
```

BASE COUNT ORIGIN

```
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Enkaryota; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 1089)

S NIH-Mach Lipp; //mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Ontact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAMI2276 row: c column: 13

High quality sequence stop: 688.
  Submitted (Q2-AUG-2001) Asao Fujiyama, The Institute of Physical Submitted (Q2-AUG-2001), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, WEL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9114, Fax:B1-45-503-9170)
Tel:81-45-503-9114, Fax:B1-45-503-9170)
  Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-028F21.F.
Pan troglodytes
   682 bp DNA linear GSS 02-NOV-2003
Pan troglodytes DNA, clone: PTB-028F21.F, genomic survey sequence.
AG048517.1 GI:16585409
GSS.
   /note="Organ: uterus, Vector: pCWV-SPORT6; Site 1: Not1; Site 2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. 1 to thers
  Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
   Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
  Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
   100.0%; Score 22; DB 14; Length 1089; 100.0%; Pred. No. 7.2;
   0; Indels
   Location/Qualifiers
1.089
1.089
Ab xref="texon:8606" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:555562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="IMAGE:55562" |
| clone="
   0; Mismatches
  244 GACGTTGACAACGGCGGTTTCT 223
  1 GACGITGACAACGGCGGTITCT 22
                          BM806132.1 GI:19122955
  (bases 1 to 682)
  22; Conservative
  Query Match
Best Local Similarity
   Homo sapiens
   human.
   LOCUS
DEFINITION
ACCESSION
   source
  ORGANISM
  TITLE
JOURNAL
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
   BASE COUNT
ORIGIN
  JOURNAL
REFERENCE
  Matches
  RESULT 14
AG048517
  REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
  AUTHORS
   AUTHORS
  REFERENCE
   VERSION
KEYWORDS
   TITLE
  COMMENT
   FEATURES
   SOURCE
  g
   /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone='InAgE:4842553"
/clone='InAgE:4842553"
/clone='InDagE:4842553"
/clone='InDagE:4842553"
/clone='InDagE:4842553"
/clone='InDage:resistant)"
/lab host='InDage:resistant)"
/note='Crogan: eye; Vector: pOTB7; Site 1: XhoI; Site_2:
/note='Crogan: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
/cloned into EcoRI/XhoI sites using the following 1/
cloned into EcoRI/XhoI sites using the following 1/
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
clifornia, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"
2 a 241 c 235 g 171 t
  I089 bp mRNA linear EST 05-MAR-2002
AGENCOURT_6553922 NIH_MGC:_71 Homo sapiens cDNA clone IMAGE:5555652
5', mRNA sequence.
   ö
  BG748346 889 bp mRNA linear EST 15-MAY-2001
   ô
   I toases I to susy,

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: cgapba-r@mail.nih.gov
Tissue Procurement: ATCC
Tobna Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Place: LLCML677 row: c column: 02
High quality sequence stop: 773.
High quality sequence stop: 773.
  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarhini, Hominidae, Homo.
1 (bases 1 to 889)
   Superscript II RT (Life Technologies)."
g 148 t
   Gaps
   Gaps
   .;
0
   ;
0
  DB 12; Length 889;
  Query Match
Best Local Similarity 100.0%; Score 22; DB 12; Length 856;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 22; Conservative 0; Mismatches 0; Indels (
   0; Indels
  Score 22; DB 1
Pred. No. 6.5;
   Mismatches
                      and
233
  ;
  374 GACGTTGACAACGGCGGTTTCT 353
   1 GACGITGACAACGGCGGTTTCT 22
  452 GACGTTGACAACGGCGGTTTCT 431
   100.0%;
100.0%;
   1 GACGITGACAACGGCGGTTTCT 22
  BG748346.1 GI:14058999
                      (Stratagene)
250 c
   Local Similarity 100.
   688. .1
   mRNA sequence.
BG748346
  Homo sapiens
   225 a
   242
  human.
```

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

BG748346/c DEFINITION

RESULT 12

GSS 02-NOV-2001

Query Match

Matches

BASE COUNT ORIGIN

BM806132/c LOCUS

RESULT 13

ô

Gaps

ö

```
Search completed: April 18, 2003, 07:32:04
Job time : 769.167 secs
   21;
   source
  BASE COUNT
ORIGIN
  Matches
   FEATURES
   셤
   SM Mus musculus

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,

Bukaryota, Metazoa, Chordata, Sciurognathi, Muridae, Murinae, Mus.

1 (Dases 1 to 448)

Kafumura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,

Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirazane, T., Imchani, K., Ishii,

Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,

Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,

Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,

Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa

A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T.,

Riken Encyclopedia of Mouse Full-length CDNAs (Akimura, T., et al.
   ö
  BB852457
BB852457 RIKEN full-length enriched, B16 F10Y cells Mus musculus cDNA clone G370007124 5', mRNA sequence.
BB852457.1 GI:17093911
   RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
  Unpublished (2001)
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Sciences Cenome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
T-722 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
Pax: 81-45-503-9216
  Email: genome-resignscriken.go.jp,

URL:http://genome.goc.riken.go.jp,

Carninci,P., Shibbata,Y., Hayatau,N., Sugahara,Y., Shibata,K., Itoh

Carninci,P., Shibbata,Y., Muramatau,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

Prepare full-length cDNA libraries for rappd discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

Wagdi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,

Wastaniki,M., Yoneda,Y., Ishikkwa,T., Ozawa,K., Tanaka,T., Matsuura

'S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
  Gaps
   ö
   /cell type="lymphoblast"
/clone lib="PTB Chimpanzee Male BAC Library"
147 c 112 g 199 t 7 others
  Query Match 95.5%; Score 21; DB 17; Length 682; Best Local Similarity 95.5%; Pred. No. 17; Matches 21; Conservative 0; Mismatches 1; Indels
  /organism="Pan troglodytes"
|db_xref="taxon:9598"
|clone="PTB-028F21.F"
   Location/Qualifiers
  255 GACGNTGACAACGCCGCTTTCT 276
  pKS145
   Sequencing: -21M13
   1 GACGTTGACAACGCCGGTTTCT 22
clone tracking errors.
  Saci
   /sex="male"
   R.Site 1
R.Site 2
  Vector
   nouse mouse.
                                PRIMERS
  LIBRARY
  217
   Bource
   RESULT 15
BB852457/c
  KEYWORDS
SOURCE
ORGANISM
   BASE COUNT
ORIGIN
  DEFINITION
  ACCESSION
VERSION
  JOURNAL
   REFERENCE
  AUTHORS
  FEATURES
```

ò

TITLE

```
/grain="CSTBL/GS"
/db xref="texon:1009"
/clone="G370007124"
/clone="G370007124"
/clone="Bararen:1009"
/cell_type="B16 F10Y cells"
/note="pooled tissues; (tissue_type=cerebellum,
dev_stage=16 days neonate, sex=mixed),
(tissue_type=cerebellum, dev stage=0 day neonate,
sex=male), (tissue_type=hippocampus, dev_stage=adult,
sex=male), (tissue_type=hippocampus, dev_stage=adult,
sex=male), (tissue_type=hippocampus, dev_stage=adult,
sex=male), (tissue_type=hippocampus, dev_stage=3 days
embryo, sex=mixed); (tissue_type=lung, dev_stage=13 days)
  ö
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details. e mouse tissues.
  Gaps
  ö
  92.7%; Score 20.4; DB 10; Length 448; 95.5%; Pred. No. 26; Live 0; Mismatches 1; Indels 0;
   75 t
  1. .448
/organism="Mus musculus"
   420 GACGTTGACAACGCCAGTTTCT 399
   22
   1 GACGTTGACAACGGCGGTTTCT
   Conservative
  Query Match
Best Local Similarity
```

